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(54) Title: METHODS OF DIAGNOSIS OF CANCER COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers. Related methods and compositions that can be used for diagnosis and treatment of those cancers are disclosed. Also described herein are methods that can be used to identify modulators of selected cancers.

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METHODS OF DIAGNOSIS OF CANCER, COMPOSITIONS AND METHODS OF
SCREENING FOR MODULATORS OF CANCER

5 CROSS-REFERENCES TO RELATED APPLICATIONS

This application claims priority to USSN 60/323,469, filed September 17, 2001; USSN 60/355,145, filed February 8, 2002; USSN 60/369,899, filed April 4, 2002; USSN 60/323,887, filed September 20, 2001; USSN 60/355,257, filed February 8, 2002; USSN 60/325,114, filed September 25, 2001; USSN 60/340,944, filed October 29, 2001; USSN 60/350,666, filed
10 November 13, 2001; and USSN 60/372,246, filed April 12, 2002; each of which is incorporated herein by reference for all purposes.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in cancer; and to the use of
15 such expression profiles and compositions in the diagnosis, prognosis, and therapy of cancer. The invention further relates to methods for identifying and using agents and/or targets that modulate cancer.

BACKGROUND OF THE INVENTION

Cancer is a major cause of morbidity in the United States. For example, in 1996, the
20 American Cancer Society estimated that 1,359,150 people were diagnosed with a malignant neoplasm and 554,740 died from one of these diseases. Cancer is responsible for 23.9 percent of all American deaths and is exceeded only by heart disease as a cause of mortality (33 percent). Unfortunately, cancer mortality is increasing and sometime early in this century, cancer is expected to become the leading cause of mortality in the United States as it already is
25 in Japan.

Cancers share the characteristic of disordered control over normal cell division, growth, and differentiation. Their initial clinical manifestations are extremely heterogeneous, with over 70 types of cancer arising in virtually every organ and tissue of the body. Moreover, some of those similarly classified cancer types may represent multiple different molecular diseases.
30 Unfortunately, some cancers may be virtually asymptomatic until late in the disease course, when treatment is more difficult, and prognosis grim.

Treatment for cancer typically includes surgery, chemotherapy, and/or radiation therapy. Although nearly 50 percent of cancer patients can be effectively treated using these methods, the current therapies all induce serious side effects which diminish quality of life. The identification of novel therapeutic targets and diagnostic markers will be important for
5 improving the diagnosis and treatment of cancer patients.

Recent advances in molecular medicine have increased the interest in tumor-specific antigens that could serve as targets for various immunotherapeutic or small molecule strategies. Antigens suitable for immunotherapeutic strategies should be highly expressed in cancer tissues, preferably accessible from the vasculature and at the cell surface, and ideally not expressed in
10 normal adult tissues. Expression in tissues that are dispensable for life, however, may be tolerated, e.g., reproductive organs. Examples of antigens that are currently available for the detection and treatment of certain cancers include Her2/neu and the B-cell antigen CD20. Humanized monoclonal antibodies directed to Her2/neu (Herceptin®/trastuzumab) are currently in use for the treatment of metastatic breast cancer. See Ross and Fletcher (1998) Stem Cells
15 16:413-428. Similarly, anti-CD20 monoclonal antibodies (Rituxin®/rituximab) are used to effectively treat non-Hodgkin's lymphoma. See Maloney, et al. (1997) Blood 90:2188-2195; Leget and Czuczman (1998) Curr. Opin. Oncol. 10:548-551.

The elucidation of a role for novel proteins and compounds in disease states for identification of therapeutic targets and diagnostic markers is valuable for improving the current
20 treatment of cancer patients. Accordingly, provided herein are molecular targets for therapeutic intervention in various defined cancers. Additionally, provided herein are methods that can be used in diagnosis and prognosis of cancer. Further provided are methods that can be used to screen candidate bioactive agents for the ability to modulate cancer.

SUMMARY OF THE INVENTION

25 The present invention provides methods for determining the presence or absence of a pathological cell in a patient, the method comprising detecting a nucleic acid comprising a sequence at least 80% identical to a sequence as described in Tables 2A-68 in a biological sample from the patient, thereby determining the presence or absence of the pathological cell. In certain embodiments of the method, the pathology is described in Table 1, including a
30 cancer; the biological sample comprises isolated nucleic acids; the nucleic acids are mRNA; the biological sample is tissue from an organ which is affected by the pathology of Table 1, including a cancer; a further step is used of amplifying nucleic acids before the step of detecting

the nucleic acid; the detecting is of a protein encoded by the nucleic acid; the nucleic acid comprises a sequence as described in Tables 2A-68; the detecting step is carried out by using a labeled nucleic acid probe, utilizing a biochip comprising a sequence at least 80% identical to a sequence as described in Tables 2A-68, or detecting a polypeptide encoded by the nucleic acid; or the patient is undergoing a therapeutic regimen to treat the pathology of Table 1, or is suspected of having the pathology or cancer.

Compositions are also provided, e.g., an isolated nucleic acid molecule comprising a sequence as described in Tables 2A-68, including, e.g., those which are labeled; an expression vector comprising such nucleic acid; a host cell comprising such expression vector; an isolated polypeptide which is encoded by such a nucleic acid molecule comprising a sequence as described in Tables 2A-68; or an antibody that specifically binds the polypeptide. In particular embodiments, the antibody is: conjugated to an effector component, is conjugated to a detectable label (including, e.g., a fluorescent label, a radioisotope, or a cytotoxic chemical), an antibody fragment, or is a humanized antibody.

Additional methods are provided, including methods for specifically targeting a compound to a pathological cell in a patient, the method comprising administering to the patient an antibody, as described, thereby providing the targeting. Others include, e.g., methods for determining the presence or absence of a pathological cell in a patient, the methods comprising contacting a biological sample with an antibody, as described. In more particular methods, the antibody is: conjugated to an effector component, or to a fluorescent label; or the biological sample is a blood, serum, urine, or stool sample.

Further methods include those for identifying a compound that modulates a pathology-associated polypeptide, the method comprising steps of: contacting the compound with a pathology-associated polypeptide, the polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-68; and determining the functional effect of the compound upon the polypeptide. Another drug screening assay method comprises steps of: administering a test compound to a mammal having a pathology of Table 1 or a cell isolated therefrom; and comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-68 in a treated cell or mammal with the level of gene expression of the polynucleotide in a control cell or mammal, wherein a test compound that modulates the level of expression of the polynucleotide is a candidate for the treatment of the pathology.

DETAILED DESCRIPTION OF THE INVENTION

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and prognosis evaluation for various disorders, e.g., angiogenesis, fibrosis, and various defined forms of cancer, including metastatic cancer, as well as methods for screening for compositions which modulate such conditions. Also provided are methods for treating such disorders or cancers. See, e.g., American Society of Clinical Oncology (ed. 2001) ASCO Curriculum: Symptom Management Kendall/Hunt, ISBN: 0787277851; Bonadonna, et al. (2001) Textbook of Breast Cancer (2d ed.) Dunitz Martin, ISBN: 1853178241; Devita and Hellman (eds. 2001) Cancer Principles and Practice of Oncology (2 vols.), Lippincott Williams, ISBN: 0781723876; Howell, et al. (2001) Breast Cancer Isis Medical Media, ISBN: 1901865584; Kaye and Laws (2001) Brain Tumours: An Encyclopedic Approach (2d ed.) Churchill Livingstone, ISBN: 0443064261; Mihm, et al. (2001) The Melanocytic Proliferation: A Comprehensive Textbook of Pigmented Lesions Wiley-Liss, ISBN: 0471252719; Montgomery and Aaron (2001) Clinical Pathology of Soft-Tissue Tumors Marcel Dekker, ISBN: 0824702905; Petrovich, et al. (eds. 2001) Combined Modality of Central Nervous System Tumors (Medical Radiology) Springer Verlag, ISBN: 3540660534; Rosen (2001) Rosen's Breast Pathology Lippincott Williams and Wilkins, ISBN: 0781723795; Shah, et al. (2001) Oral Cancer Isis Medical Media, ISBN: 189906687X; Weiss and Goldblum (2001) Enzinger and Weiss's Soft Tissue Tumors (4th ed.) Mosby, ISBN: 0323012000; Abelloff, et al. (eds. 2000) Clinical Oncology (2d ed.) Churchill Livingstone, ISBN: 044307545X; American Society of Clinical Oncology (ed. 2000) Cancer Genetics and Cancer Predisposition Testing Kendall/Hunt, ISBN: 0787276154; Fletcher (2000) Diagnostic Histopathology of Tumors (2 vols. 2d ed.) Churchill Livingstone, ISBN: 0443079927; Vogelzang (ed. 2000) Comprehensive Textbook of Genitourinary Oncology (2d ed.) Lippincott Williams and Wilkins, ISBN: 0683306456; Holland, et al. (eds. 2000) Holland-Frei Cancer Medicine (Book with CD-ROM 5th ed.) Decker, ISBN: 1550091131; Turrisi, et al. (2000) Lung Cancer Isis Medical Media, ISBN: 1901865428; Bartolozzi and Lencioni (eds. 1999) Liver Malignancies: Diagnostic and Interventional Radiology (Medical Radiology) Springer Verlag, ISBN: 3540647562; Gasparini (ed. 1999) Prognostic Variables in Node-Negative and Node-Positive Breast Cancer Kluwer, ISBN: 0792384474; Hansen (ed. 1999) The LASLC Textbook of Lung Cancer: International Association for the Study of Lung Cancer Dunitz Martin, ISBN: 1853177083; Raghavan, et al. (eds. 1999) Textbook of Uncommon Cancer (2nd ed.) Wiley, ISBN: 0471929212; Thawley, et

- al. (eds. 1999) Comprehensive Management of Head and Neck Tumors (2 vols.) Saunders, ISBN: 0721655823; Whittaker and Holmes (eds. 1999) Leukemia and Related Disorders (3d ed.) Blackwell Science, ISBN: 0865426074; Aapro (ed. 1998) OncoMedia: Medical Oncology (CD-ROM) Elsevier Science, ISBN: 0080427480; Abeloff (1998) Clinical Oncology (Library Version 2 CD-ROM Individual Version 2.0 Windows and Macintosh) Harcourt Brace, ISBN: 0443075557; Benson (ed. 1998) Gastrointestinal Oncology (Cancer Treatment and Research, CTAR 98) Kluwer, ISBN: 0792382056; Brambilla and Brambilla (eds. 1998) Lung Tumors: Fundamental Biology and Clinical Management (Vol 124) Marcel Dekker, ISBN: 0824701607; Canellos, et al. (eds. 1998) The Lymphomas Saunders, ISBN: 0721650309; Greenspan and Remagen (1998) Differential Diagnosis of Tumors and Tumor-Like Lesions of Bones and Joints Lippincott Williams and Wilkins Publishers, ISBN: 0397517106; Hiddemann (ed. 1998) Acute Leukemias VII: Experimental Approaches and Novel Therapies (Haematologie Und Bluttransfusion, Vol 39), Springer Verlag, ISBN: 3540635041; Husband and Reznick (1998) Imaging in Oncology (2 vols.) Mosby, ISBN: 1899066489; Leibel and Phillips (eds. 1998) Textbook of Radiation Oncology Saunders, ISBN: 0721653367; Maloney and Miller (eds. 1998) Cutaneous Oncology: Pathophysiology, Diagnosis, and Management Blackwell Science, ISBN: 0865425175; Mittal, et al. (eds. 1998) Advances in Radiation Therapy Kluwer, ISBN: 0792399811; Oldham (ed. 1998) Principles of Cancer Biotherapy (3d ed.) Kluwer, ISBN: 0792335074; Ozols (ed. 1998) Gynecologic Oncology Kluwer, ISBN: 0792380703; Parkin, et al. (eds. 1998) Cancer Incidence in Five Continents (Iarc Scientific Publications, No 143) Oxford University Press, ISBN: 9283221435; Perez and Brady (eds. 1998) Principles and Practice of Radiation Oncology Lippincott Williams and Wilkins, ISBN: 0397584164; Black, et al. (eds. 1997) Cancer of the Nervous System Blackwell Science, ISBN: 0865423849; Bonadonna, et al. (1997) Textbook of Breast Cancer: A Clinical Guide to Therapy Blackwell Science, ISBN: 1853173487; Pollock (ed. 1997) Surgical Oncology Kluwer, ISBN: 0792399005; Sheaves, et al. (eds. 1997) Clinical Endocrine Oncology Blackwell Science, ISBN: 086542862X; Vahrson (1997) Radiation Oncology of Gynecological Cancers Springer Verlag, ISBN: 0387567682; Walterhouse and Cohn (eds. 1997) Diagnostic and Therapeutic Advances in Pediatric Oncology Kluwer, ISBN: 0792399781; Aisner (ed. 1996) Comprehensive Textbook of Thoracic Oncology Lippincott, Williams and Wilkins, ISBN: 0683000624; Bertino, et al. (eds. 1996) Encyclopedia of Cancer (3 vols.) Academic, ISBN: 012093230X; Cavalli, et al. (1996) Textbook of Medical Oncology Dunitz Martin, ISBN: 1853172901;

Peckham, et al. (eds. 1995) Oxford Textbook of Oncology (2-Vols.) Oxford University Press, ISBN: 0192616854; and Freireich and Kantarjian (eds. 1996) Molecular Genetics and Therapy of Leukemia (Cancer Treatment and Research, V. 84) Kluwer, ISBN: 0792339126.

In particular, identification of markers selectively expressed on defined cancers allows for use of that expression in diagnostic, prognostic, or therapeutic methods. As such, the invention defines various compositions, e.g., nucleic acids, polypeptides, antibodies, and small molecule agonists/antagonists, which will be useful to selectively identify those markers. For example, therapeutic methods may take the form of protein therapeutics which use the marker expression for selective localization or modulation of function (for those markers which have a causative disease effect), for vaccines, identification of binding partners, or antagonism, e.g., using antisense or RNAi. The markers may be useful for molecular characterization of subsets of the diseases, e.g., as provided in Table 1, which subsets may actually require very different treatments. Moreover, the markers may also be important in related diseases to the specific disorders and cancers, e.g., which affect similar tissues in non-malignant diseases, or have similar mechanisms of induction/maintenance. Metastatic processes or characteristics may also be targeted. Diagnostic and prognostic uses are made available, e.g., to subset related but distinct diseases, or to determine treatment strategy. The detection methods may be based upon nucleic acid, e.g., PCR or hybridization techniques, or protein, e.g., ELISA, imaging, IHC, etc. The diagnosis may be qualitative or quantitative, and may detect increases or decreases in expression levels.

Tables 2B-66C provide unigene cluster identification numbers for the nucleotide sequence of genes that exhibit increased or decreased expression in cancer samples, particularly sequences involved in angiogenesis, prostate cancer (including androgen independent and taxol resistant prostate cancer), breast cancer, colorectal cancer, cervical cancer, bladder cancer, lung cancer, ovarian cancer, uterine cancer, glioblastoma, Ewing sarcoma, and lung fibrosis. Tables 2A-67 also provide an exemplar accession number that provides a nucleotide sequence that is part of the unigene cluster.

Definitions

The term "cancer protein" or "cancer polynucleotide" or "cancer-associated transcript" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologues that: (1) have a nucleotide sequence that has greater than about 60% nucleotide sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably about 92%, 94%, 96%, 97%,

98%, or 99% or greater nucleotide sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a nucleotide sequence of or associated with a gene of Tables 1-68; (2) bind to antibodies, e.g., polyclonal antibodies, raised against an immunogen comprising an amino acid sequence encoded by a nucleotide sequence of
5 or associated with a gene of Tables 1-68, and conservatively modified variants thereof; (3) specifically hybridize under stringent hybridization conditions to a nucleic acid sequence, or the complement thereof of Tables 1-68 and conservatively modified variants thereof; or (4) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, preferably 90%, 91%, 93%, 95%, 97%, 98%, or 99% or greater amino
10 sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acids, to an amino acid sequence encoded by a nucleotide sequence of or associated with a gene of Tables 1-68. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig, horse, sheep, or other mammal. A "cancer polypeptide" and a
15 "cancer polynucleotide," include both naturally occurring or recombinant forms.

A "full length" cancer protein or nucleic acid refers to a cancer polypeptide or polynucleotide sequence, or a variant thereof, that contains elements normally contained in one or more naturally occurring, wild type cancer polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translational processing or splicing,
20 including alternative splicing.

"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of a cancer protein, polynucleotide, or transcript. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and
25 autopsy samples, frozen sections taken for histologic purposes, archival samples, blood, plasma, serum, sputum, stool, tears, mucus, hair, skin, etc. Biological samples also include explants and primary and/or transformed cell cultures derived from patient tissues. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a
30 bird; reptile; or fish. Livestock and domestic animals are of interest.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an

animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues or materials, having treatment or outcome history, will be particularly useful.

5 The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (e.g., about 70% identity, preferably 75%, 80%, 85%, 90%, 91%, 93%, 95%, 97%, 98%, 99%, or higher identity over a specified region, when compared and aligned for maximum correspondence over
10 a comparison window or designated region) as measured using, e.g., a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site <http://www.ncbi.nlm.nih.gov/BLAST/> or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the complement of a test sequence. The definition also includes
15 sequences that have deletions and/or insertions, substitutions, and naturally occurring, e.g., polymorphic or allelic variants, and man-made variants. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

20 For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison
25 algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of contiguous positions selected from the group consisting typically of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150, in which a sequence may be compared to a
30 reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology

algorithm of Smith and Waterman (1981) Adv. Appl. Math. 2:482-489, by the homology alignment algorithm of Needleman and Wunsch (1970) J. Mol. Biol. 48:443-453, by the search for similarity method of Pearson and Lipman (1988) Proc. Nat'l. Acad. Sci. USA 85:2444-2448, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA
5 in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Ausubel, et al. (eds. 1995 and supplements) Current Protocols in Molecular Biology Wiley).

Preferred examples of algorithms that are suitable for determining percent sequence identity and sequence similarity include the BLAST and BLAST 2.0 algorithms, which are
10 described in Altschul, et al. (1977) Nuc. Acids Res. 25:3389-3402 and Altschul, et al. (1990) J. Mol. Biol. 215:403-410. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (<http://www.ncbi.nlm.nih.gov/>). This algorithm involves
15 first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul, et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are
20 extended in both directions along each sequence for as far as the cumulative alignment score can be increased.—Cumulative scores are calculated using, e.g., for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the
25 cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E)
30 of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62

scoring matrix (see Henikoff and Henikoff (1992) Proc. Natl. Acad. Sci. USA 89:10915-919) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences. See, e.g., Karlin and Altschul (1993) Proc. Nat'l. Acad. Sci. USA 90:5873-5787.

5 One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than
10 about 0.01, and most preferably less than about 0.001. Log values may be negative large numbers, e.g., 5, 10, 20, 30, 40, 40, 70, 90, 110, 150, 170, etc.

An indication that two nucleic acid sequences are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid. Thus, a
15 polypeptide is typically substantially identical to a second polypeptide, e.g., where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

20 A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be prokaryotic cells such as E. coli, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, e.g., the American Type Culture Collection catalog or web site,
25 www.atcc.org).

The terms "isolated," "purified," or "biologically pure" refer to material that is substantially or essentially free from components that normally accompany it as found in its native state. Purity and homogeneity are typically determined using analytical chemistry techniques such as polyacrylamide gel electrophoresis or high performance liquid
30 chromatography. A protein or nucleic acid that is the predominant species present in a preparation is substantially purified. In particular, an isolated nucleic acid is separated from some open reading frames that naturally flank the gene and encode proteins other than protein

encoded by the gene. The term "purified" in some embodiments denotes that a nucleic acid or protein gives rise to essentially one band in an electrophoretic gel. Preferably, it means that the nucleic acid or protein is at least about 85% pure, more preferably at least 95% pure, and most preferably at least 99% pure. "Purify" or "purification" in other embodiments means removing
5 at least one contaminant or component from the composition to be purified. In this sense, purification does not require that the purified compound be homogeneous, e.g., 100% pure.

The terms "polypeptide," "peptide," and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally
10 occurring amino acid, as well as to naturally occurring amino acid polymers, those containing modified residues, and non-naturally occurring amino acid polymers.

The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function similarly to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as
15 those amino acids that are later modified, e.g., hydroxyproline, γ -carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, e.g., an α carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs may have modified R groups (e.g.,
20 norleucine) or modified peptide backbones, but retain some basic chemical structure as a naturally occurring amino acid. Amino acid mimetic refers to a chemical compound that has a structure that is different from the general chemical structure of an amino acid, but that functions similarly to another amino acid.

Amino acids may be referred to herein by either their commonly known three letter
25 symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variant" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants
30 refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical or associated, e.g., naturally contiguous, sequences. Because of the degeneracy of the

genetic code, a large number of functionally identical nucleic acids encode most proteins. For instance, the codons GCA, GCC, GCG, and GCU each encode the amino acid alanine. Thus, at each position where an alanine is specified by a codon, the codon can be altered to another of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations," which are one species of conservatively modified variations. Every nucleic acid sequence herein which encodes a polypeptide also describes silent variations of the nucleic acid. In certain contexts each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally similar molecule. Accordingly, a silent variation of a nucleic acid which encodes a polypeptide is implicit in a described sequence with respect to the expression product, but not necessarily with respect to actual probe sequences.

As to amino acid sequences, one of skill will recognize that individual substitutions, deletions, or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds, or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid. Conservative substitution tables providing functionally similar amino acids are well known. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention. Typically conservative substitutions include for one another: 1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton (1984) Proteins: Structure and Molecular Properties Freeman).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts, et al. (eds. 2001) Molecular Biology of the Cell (4th ed.) Garland; and Cantor and Schimmel (1980) Biophysical Chemistry Part I: The Conformation of Biological Macromolecules Freeman. "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a

polypeptide that often form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional structure formed, usually by the noncovalent association of independent tertiary units. Anisotropic terms are also known as energy terms.

"Nucleic acid" or "oligonucleotide" or "polynucleotide" or grammatical equivalents used herein means at least two nucleotides covalently linked together. Oligonucleotides are typically from about 5, 6, 7, 8, 9, 10, 12, 15, 25, 30, 40, 50, or more nucleotides in length, up to about 100 nucleotides in length. Nucleic acids and polynucleotides are a polymers of any length, including longer lengths, e.g., 200, 300, 500, 1000, 2000, 3000, 5000, 7000, 10,000, etc. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have at least one different linkage, e.g., phosphoramidate, phosphorothioate, phosphorodithioate, or O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach Oxford Univ. Press); and peptide nucleic acid backbones and linkages. Other analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 of Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids. Modifications of the ribose-phosphate backbone may be done for a variety of reasons, e.g., to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip. Mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

A variety of references disclose such nucleic acid analogs, including, e.g., phosphoramidate (Beaucage, et al. (1993) Tetrahedron 49:1925-1963 and references therein; Letsinger (1970) J. Org. Chem. 35:3800-3803; Sprinzl, et al. (1977) Eur. J. Biochem. 81:579-589; Letsinger, et al. (1986) Nucl. Acids Res. 14:3487-499; Sawai, et al. (1984) Chem. Lett. 805; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; and Pauwels, et al. (1986) Chemica Scripta 26:141-149), phosphorothioate (Mag, et al. (1991) Nucleic Acids Res. 19:1437-441; and U.S. Patent No. 5,644,048), phosphorodithioate (Brill, et al. (1989) J. Am.

- Chem. Soc. 111:2321-2322), O-methylphosphoroamidite linkages (see Eckstein (1992) Oligonucleotides and Analogues: A Practical Approach, Oxford Univ. Press), and peptide nucleic acid backbones and linkages (see Egholm (1992) J. Am. Chem. Soc. 114:1895-1897; Meier, et al. (1992) Chem. Int. Ed. Engl. 31:1008-1010; Nielsen (1993) Nature 365:566-568; Carlsson, et al. (1996) Nature 380:207, all of which are incorporated by reference). Other analog nucleic acids include those with positive backbones (Denpcy, et al. (1995) Proc. Natl. Acad. Sci. USA 92:6097-101; non-ionic backbones (U.S. Patent Nos. 5,386,023, 5,637,684, 5,602,240, 5,216,141, and 4,469,863; Kiedrowski, et al. (1991) Angew. Chem. Intl. Ed. English 30:423-426; Letsinger, et al. (1988) J. Am. Chem. Soc. 110:4470-4471; Letsinger, et al. (1994) Nucleoside and Nucleotide 13:1597-xxx; Chapters 2 and 3 in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580; Mesmaeker, et al. (1994) Bioorganic and Medicinal Chem. Lett. 4:395-398; Jeffs, et al. (1994) J. Biomolecular NMR 34:17; Horn, et al. (1996) Tetrahedron Lett. 37:743-xxx) and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7 in Sanghvi and Cook (eds. 1994) Carbohydrate Modifications in Antisense Research ACS Symposium Series 580. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids (see Jenkins, et al. (1995) Chem. Soc. Rev. pp 169-176). Several nucleic acid analogs are described in Rawls (page 35, June 2, 1997) C&E News.
- 20 Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in at least two advantages. The PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (T_m) for mismatched versus perfectly
- 25 matched basepairs. DNA and RNA typically exhibit a 2-4° C drop in T_m for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9° C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.
- 30 The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. The depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also

provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA, or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. "Transcript" typically refers to a naturally occurring RNA, e.g., a pre-mRNA, hnRNA, or mRNA. As used herein, the term "nucleoside" includes nucleotides and nucleoside and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus, e.g., the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, physiological, chemical, or other physical means. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies, antigens, or epitope tags; and c) colored or fluorescent dyes. The labels may be incorporated into the cancer nucleic acids, proteins, and antibodies. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as ^3H , ^{14}C , ^{32}P , ^{35}S , or ^{125}I , electron-dense reagents, a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins or other entities which can be made detectable such as alkaline phosphatase, beta-galactosidase, or horseradish peroxidase. Methods are known for conjugating the antibody to the label. See, e.g., Hunter, et al. (1962) Nature 144:945; David, et al. (1974) Biochemistry 13:1014-1021; Pain, et al. (1981) J. Immunol. Meth. 40:219-230; and Nygren (1982) J. Histochem. and Cytochem. 30:407-412.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, e.g., detection moieties including radioactive compounds, fluorescent compounds, enzymes or substrates, tags such as epitope tags, toxins; activatable moieties, chemotherapeutic agents; lipases; antibiotics; or radioisotopes, e.g., emitting "hard" beta, radiation.

A "labeled nucleic acid probe or oligonucleotide" is one that is bound, e.g., covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals,

electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, methods using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

5 As used herein a "nucleic acid probe or oligonucleotide" is a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, e.g., through hydrogen bond formation. As used herein, a probe may include natural (e.g., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage
10 other than a phosphodiester bond, preferably one that does not functionally interfere with hybridization. Thus, e.g., probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. Probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled, e.g., with
15 isotopes, chromophores, lumiphores, chromogens, or indirectly labeled, e.g., with biotin to which a streptavidin complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence. Diagnosis or prognosis may be based at the genomic level, or at the level of RNA or protein expression.

 The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid,
20 protein, or vector, indicates that the cell, nucleic acid, protein, or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, e.g., recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed, or not expressed at all.
25 By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid, e.g., using polymerases and endonucleases, in a form not normally found in nature. In this manner, operably linkage of different sequences is achieved. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant
30 for the purposes of this invention. It is understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, e.g., using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such

nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, e.g., through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. The protein may be isolated or purified away from some or most of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. An isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of a skin cancer protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not normally found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences, e.g., from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein will often refer to two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is typically an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under

environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, e.g., wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second
5 sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed
10 in operable linkage to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule selectively to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

15 The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in "Overview of principles of
20 hybridization and the strategy of nucleic acid assays" in Tijssen (1993) Hybridization with Nucleic Probes (Laboratory Techniques in Biochemistry and Molecular Biology) (vol. 24) Elsevier. Generally, stringent conditions are selected to be about 5-10° C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of
25 the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m , 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01-1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30° C for short probes (e.g., about 10-50 nucleotides)
30 and at least about 60° C for long probes (e.g., greater than about 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is typically at least two times

background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42° C, or, 5x SSC, 1% SDS, incubating at 65° C, with wash in 0.2x SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C is typical for low stringency amplification, although
5 annealing temperatures may vary between about 32°-48° C depending on primer length. For high stringency PCR amplification, a temperature of about 62° C is typical, although high stringency annealing temperatures can range from about 50-65° C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90-95° C for 30-120 sec, an annealing phase lasting 30-120 sec,
10 and an extension phase of about 72° C for 1-2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis, et al. (1990) PCR Protocols: A Guide to Methods and Applications, Academic Press, NY.

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This
15 occurs, e.g., when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C, and a wash in 1X SSC at 45° C. A positive hybridization is typically at least twice background.
20 Alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous references, e.g., Ausubel, et al. (eds. 1991 and supplements) Current Protocols in Molecular Biology Wiley.

The phrase "functional effects" in the context of assays for testing compounds that
25 modulate activity of a cancer protein includes the determination of a parameter that is indirectly or directly under the influence of the cancer protein or nucleic acid, e.g., a physiological, functional, physical, or chemical effect, such as the ability to decrease cancer. It includes ligand binding activity; cell viability; cell growth on soft agar; anchorage dependence; contact inhibition and density limitation of growth; cellular proliferation; cellular transformation;
30 growth factor or serum dependence; tumor specific marker levels; invasiveness into Matrigel; tumor growth and metastasis in vivo; mRNA and protein expression in cells undergoing

metastasis; and other characteristics of cancer cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of a cancer protein sequence, e.g., physiological, functional, enzymatic, physical, or chemical effects. Such functional effects can be measured, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the cancer protein, measuring binding activity or binding assays, e.g., binding to antibodies or other ligands, and measuring growth, cellular proliferation, cell viability, cellular transformation, growth factor or serum dependence, tumor specific marker levels, invasiveness into Matrigel, tumor growth and metastasis in vivo, mRNA and protein expression, and other characteristics of cancer cells. The functional effects can be evaluated by many means, e.g., microscopy for quantitative or qualitative measures of alterations in morphological features, measurement of changes in RNA or protein levels for cancer-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP, and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

"Inhibitors", "activators," and "modulators" of cancer polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules or compounds identified using in vitro and in vivo assays of cancer polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of cancer proteins, e.g., antagonists. Antisense or inhibitory nucleic acids may seem to inhibit expression and subsequent function of the protein. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate cancer protein activity. Inhibitors, activators, or modulators also include genetically modified versions of cancer proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules, and the like. Such assays for inhibitors and activators include, e.g., expressing the cancer protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of cancer can also be identified

by incubating cancer cells with the test compound and determining increases or decreases in the expression of 1 or more cancer proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50, or more cancer proteins, such as cancer proteins encoded by the sequences set out in Tables 1-68.

Samples or assays comprising cancer proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of a cancer polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more preferably 200-500% (e.g., two to five fold higher relative to the control), more preferably 1000-3000% higher.

The phrase "changes in cell growth" refers to any change in cell growth and proliferation characteristics in vitro or in vivo, such as cell viability, formation of foci, anchorage independence, semi-solid or soft agar growth, changes in contact inhibition and density limitation of growth, loss of growth factor or serum requirements, changes in cell morphology, gaining or losing immortalization, gaining or losing tumor specific markers, ability to form or suppress tumors when injected into suitable animal hosts, and/or immortalization of the cell. See, e.g., pp. 231-241 in Freshney (1994) Culture of Animal Cells a Manual of Basic Technique (2d ed.) Wiley-Liss.

"Tumor cell" refers to precancerous, cancerous, and normal cells in a tumor.

"Cancer cells," "transformed" cells or "transformation" in tissue culture, refers to spontaneous or induced phenotypic changes that do not necessarily involve the uptake of new genetic material. Although transformation can arise from infection with a transforming virus and incorporation of new genomic DNA, or uptake of exogenous DNA, it can also arise spontaneously or following exposure to a carcinogen, thereby mutating an endogenous gene. Transformation is associated with phenotypic changes, such as immortalization of cells, aberrant growth control, nonmorphological changes, and/or malignancy. See, Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss.

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes.

Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD, and IgE, respectively. Typically, the antigen-binding region of an antibody or its functional equivalent will be most critical in specificity and affinity of binding. See Paul (ed. 5 1999) Fundamental Immunology (4th ed.) Raven.

An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen 10 recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, e.g., pepsin digests an antibody below the disulfide linkages in the hinge region to produce $F(ab)'_2$, a dimer of Fab which itself 15 is a light chain joined to V_H - C_H1 by a disulfide bond. The $F(ab)'_2$ may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the $F(ab)'_2$ dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Paul (ed. 1999) Fundamental Immunology (4th ed.) Raven. While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate 20 that such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty, et al. (1990) Nature 348:552-554).

25 For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many techniques known. See, e.g., Kohler and Milstein (1975) Nature 256:495-497; Kozbor, et al. (1983) Immunology Today 4:72; Cole, et al. (1985) pp. 77-96 in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; Coligan (1991) Current Protocols in Immunology Lippincott; Harlow and Lane (1988) Antibodies: A Laboratory Manual CSH 30 Press; and Goding (1986) Monoclonal Antibodies: Principles and Practice (2d ed.) Academic Press. Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other

organisms such as other mammals, may be used to express humanized antibodies.

Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens. See, e.g., McCafferty, et al. (1990) Nature 348:552-554; Marks, et al. (1992) Biotechnology 10:779-783.

- 5 A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced, or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function, and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a
10 portion thereof, is altered, replaced, or exchanged with a variable region having a different or altered antigen specificity.

Identification of cancer-associated sequences

- In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression
15 profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is characteristic of the state of the cell. That is, normal tissue may be distinguished from cancerous or metastatic
20 cancerous tissue, or cancer tissue or metastatic cancerous tissue can be compared with tissue from surviving cancer patients. By comparing expression profiles of tissue in known different cancer states, information regarding which genes are important (including both up-and down-regulation of genes) in each of these states is obtained. Molecular profiling may distinguish subtypes of a currently collective disease designation, e.g., different forms of a cancer.

- The identification of sequences that are differentially expressed in cancer versus non-
25 cancer tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate cancer, and thus tumor growth or recurrence, in a particular patient. Alternatively, a treatment step may induce other markers which may be used as targets to destroy tumor cells. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the
30 known expression profiles. Malignant disease may be compared to non-malignant conditions. Metastatic tissue can also be analyzed to determine the stage of cancer in the tissue, or origin of primary tumor, e.g., metastasis from a remote primary site. Furthermore, these gene expression

profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; e.g., screening can be done for drugs that suppress the cancer expression profile. This may be done by making biochips comprising sets of the important cancer genes, which can then be used in these screens. These methods can also be
5 done on the protein basis; that is, protein expression levels of the cancer proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the cancer nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the cancer proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

10 Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in cancer relative to normal tissues and/or non-malignant disease, or in different types of related diseases, herein termed "cancer sequences." As outlined below, cancer sequences include those that are up-regulated (e.g., expressed at a higher level) in cancer, as well as those that are down-regulated (e.g., expressed at a lower level). In a preferred
15 embodiment, the cancer sequences are from humans; however, cancer sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other cancer sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc.) and pets (e.g., dogs, cats, etc.). Cancer sequences from other organisms may be obtained
20 using the techniques outlined below.

Cancer sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the skin cancer sequences are recombinant nucleic acids. These nucleic acid sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; e.g., biochips
25 comprising nucleic acid probes or PCR microtiter plates with selected probes to the cancer sequences.

A cancer sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined
30 below, e.g., using homology programs or hybridization conditions.

For identifying cancer-associated sequences, the cancer screen typically includes comparing genes identified in different tissues, e.g., normal and cancerous tissues, cancer and

non-malignant conditions, non-malignant conditions and normal tissues, or tumor tissue samples from patients who have metastatic disease vs. non metastatic tissue. Other suitable tissue comparisons include comparing cancer samples with metastatic cancer samples from other cancers, such as lung, stomach, gastrointestinal cancers, etc. Samples of different stages of cancer, e.g., survivor tissue, drug resistant states, and tissue undergoing metastasis, are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated for preparation of mRNA. Suitable biochips are commercially available, e.g., from Affymetrix, Santa Clara, CA. Gene expression profiles as described herein are generated and the data analyzed.

10 In one embodiment, the genes showing changes in expression as between normal and disease states are compared to genes expressed in other normal tissues, including, and not limited to lung, heart, brain, liver, stomach, kidney, muscle, colon, small intestine, large intestine, spleen, bone, and/or placenta. In a preferred embodiment, those genes identified during the cancer screen that are expressed in a significant amount in other tissues (e.g., essential organs) are removed from the profile, although in some embodiments, this is not necessary (e.g., where organs may be dispensible, e.g., female or male specific). That is, when screening for drugs, it is usually preferable that the target expression be disease specific, to minimize possible side effects on other organs were there expression.

20 In a preferred embodiment, cancer sequences are those that are up-regulated in cancer; that is, the expression of these genes is higher in the cancer tissue as compared to non-cancer or non-malignant tissue. "Up-regulation" as used herein often means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred. Another embodiment is directed to sequences up-regulated in non-malignant conditions relative to normal. Uniformity among relevant samples is also preferred.

25 Unigene cluster identification numbers and accession numbers herein are for the GenBank sequence database and the sequences of the accession numbers are hereby expressly incorporated by reference. GenBank is available, see, e.g., Benson, et al. (1998) Nuc. Acids Res. 26:1-7; and <http://www.ncbi.nlm.nih.gov/>. Sequences are also available in other databases, e.g., European Molecular Biology Laboratory (EMBL) and DNA Database of Japan (DDBJ).
30 In some situations, the sequences may be derived from assembly of available sequences or be predicted from genomic DNA using exon prediction algorithms, such as FGENESH. See

Salamov and Solovyev (2000) Genome Res. 10:516-522. In other situations, sequences have been derived from cloning and sequencing of isolated nucleic acids.

In another preferred embodiment, cancer sequences are those that are down-regulated in the cancer; that is, the expression of these genes is lower in cancer tissue as compared to non-cancerous tissue. "Down-regulation" as used herein often means at least about a two-fold
5 change, preferably at least about a three fold change, with at least about five-fold or higher being preferred.

Informatics

The ability to identify genes that are over or under expressed in cancer can additionally
10 provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, pharmacogenetics, protein structure, biosensor development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with cancer or related diseases. See Tables 1 and 3. Or as another example, subcellular toxicological information can be generated to better direct drug
15 structure and activity correlation (see Anderson (June 11-12, 1998) Pharmaceutical Proteomics: Targets, Mechanism, and Function, paper presented at the IBC Proteomics conference, Coronado, CA). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see U.S. Patent No. 5,811,231). Similar advantages accrue from datasets
20 relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like).

Thus, in another embodiment, the present invention provides a database that includes at least one set of assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in a form in which data can be
25 maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for
30 clarity of illustration only. Similar databases can be assembled for assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample representing cancer, e.g., the identification of cancer-associated sequences described herein, provide an abundance of information which can be correlated with pathological
5 conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, data processing using high-speed computers is utilized.

An array of methods for indexing and retrieving biomolecular information is available.
10 For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to
15 association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of
20 peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multi-dimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or
25 dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures. See also Baxevanis, et al. (2001) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins Wiley; Mount (2001) Bioinformatics: Sequence and Genome Analysis CSH Press, NY; Durbin, et al. (eds. 1999) Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids Cambridge University Press; Baxevanis and Ouellette (eds. 1998) Bioinformatics: A Practical Guide to the

Analysis of Genes and Proteins (2d. ed.) Wiley-Liss; Rashidi and Buehler (1999)

Bioinformatics: Basic Applications in Biological Science and Medicine CRC Press; Setubal, et

al. (eds. 1997) Introduction to Computational Molecular Biology Brooks/Cole; Misener and

Krawetz (eds. 2000) Bioinformatics: Methods and Protocols Humana Press; Higgins and Taylor

5 (eds. 2000) Bioinformatics: Sequence, Structure, and Databanks: A Practical Approach Oxford

University Press; Brown (2001) Bioinformatics: A Biologist's Guide to Biocomputing and the

Internet Eaton Pub.; Han and Kamber (2000) Data Mining: Concepts and Techniques

Kaufmann Pub.; and Waterman (1995) Introduction to Computational Biology: Maps,

Sequences, and Genomes Chap and Hall.

10 The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

 In an exemplary embodiment, at least one of the sources of target-containing sample is
15 from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for cancer. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique
20 identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

 The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble
25 memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention
30 provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can
5 include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBM-compatible
10 (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format (e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices
15 linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal transmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit
20 pattern encoding data acquired from an assay of the invention.

The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modem, ISDN terminal adapter, DSL, cable modem, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database
25 comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute
30 the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer

program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem, an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values. See, e.g., Ewens and Grant (2001) Statistical Methods in Bioinformatics: An Introduction Springer-Verlag. Mathematical approaches can also be used to conclude whether similarities or differences in the gene expression exhibited by different samples are significant. See, e.g., Golub, et al. (1999) Science 286:531-537; Duda, et al. (2001) Pattern Classification Wiley; and Hastie, et al. (2001) The Elements of Statistical Learning: Data Mining, Inference, and Prediction Springer-Verlag. One approach to determine whether a sample is more similar to or has maximum similarity with a given condition between the sample and one or more pools representing different conditions for comparison; the pool with the smallest vector angle is then chosen as the most similar to the biological sample among the pools compared.

30 Characteristics of cancer-associated proteins

Cancer proteins of the present invention may be classified as secreted proteins, transmembrane proteins, or intracellular proteins. In one embodiment, the cancer protein is an

intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (see, e.g., Alberts, et al. (eds. 1994) Molecular Biology of the
5 Cell (3d ed.) Garland). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity, and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

10 An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more structural motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets
15 in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. These motifs can be identified on the basis of amino
20 acid sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate. One useful database is Pfam (protein families), which is a large collection of multiple sequence alignments and hidden Markov models covering many common protein domains. Versions are available via the internet from Washington University in St. Louis, the Sanger Center in
25 England, and the Karolinska Institute in Sweden. See, e.g., Bateman, et al. (2000) Nuc. Acids Res. 28:263-266; Sonnhammer, et al. (1997) Proteins 28:405-420 ; Bateman, et al. (1999) Nuc. Acids Res. 27:260-262; and Sonnhammer, et al. (1998) Nuc. Acids Res. 26:320-322.

In another embodiment, the cancer sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. They may
30 have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity

and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain
5 containing proteins.

Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous
10 transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 17 consecutive hydrophobic amino acids that may be followed by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and
15 number of transmembrane domains within the protein may be predicted (see, e.g., PSORT web site <http://psort.nibb.ac.jp/>). Important transmembrane protein receptors include, but are not limited to the insulin receptor, insulin-like growth factor receptor, human growth hormone receptor, glucose transporters, transferrin receptor, epidermal growth factor receptor, low density lipoprotein receptor, epidermal growth factor receptor, leptin receptor, and interleukin
20 receptors, e.g., IL-1 receptor, IL-2 receptor, etc.

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on
25 receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF, and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors, and the like. Extracellular domains also bind to cell-associated
30 molecules. In this respect, they may mediate cell-cell interactions. Cell-associated ligands can be tethered to the cell, e.g., via a glycosylphosphatidylinositol (GPI) anchor, or may themselves

be transmembrane proteins. Extracellular domains may also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Cancer proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein.

- 5 In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ. Alternatively, antibodies can also label intracellular proteins, in which case samples are typically permeabilized to provide access to intracellular proteins. In addition, some membrane proteins can be processed to release a soluble protein, or to expose a residual fragment.
- 10 Released soluble proteins may be useful diagnostic markers, processed residual protein fragments may be useful lung markers of disease.

- It will also be appreciated that a transmembrane protein can be made soluble by removing transmembrane sequences, e.g., through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through
- 15 recombinant means by adding an appropriate signal sequence.

- In another embodiment, the cancer proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins may have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; e.g., if circulating, they often serve to transmit signals to
- 20 various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor), an endocrine manner (acting on cells at a distance, e.g., secretion into the blood stream), or exocrine (secretion, e.g., through a duct or to adjacent epithelial surface as sweat glands, sebaceous glands, pancreatic ducts, lacrimal glands, mammary glands, wax producing glands of the ear, etc.). Thus secreted molecules often find use in modulating or
- 25 altering numerous aspects of physiology. Cancer proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood, plasma, serum, or stool tests. Those which are enzymes may be antibody or small molecule targets. Others may be useful as vaccine targets, e.g., via CTL
- 30 mechanisms.

Use of cancer nucleic acids

As described above, cancer sequence is initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the cancer sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally
5 determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

As detailed elsewhere, percent identity can be determined using an algorithm such as BLAST. A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively. Alignment
10 may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleotides than those of the nucleic acids described, the percentage of homology may be determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, e.g., homology of sequences shorter than those of the sequences identified will be determined using the number of nucleosides in the
15 shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, e.g., nucleic acids which hybridize under high stringency to a described nucleic acid, or its complement, or is also found on naturally occurring mRNAs is considered a cancer sequence. In another embodiment, less stringent hybridization conditions are used; e.g.,
20 moderate or low stringency conditions may be used; see Ausubel, supra, and Tijssen, supra.

The cancer nucleic acid sequences of the invention, e.g., the sequences in Tables 1-68, can be fragments of larger genes, e.g., they are nucleic acid segments. "Genes" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, using the sequences provided herein, extended sequences, in either direction, of
25 the cancer genes can be obtained, using techniques well known for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences corresponding to a single gene, e.g., systems such as UniGene (see, <http://www.ncbi.nlm.nih.gov/UniGene/>).

Once a cancer nucleic acid is identified, it can be cloned and, if necessary, its constituent
30 parts recombined to form the entire cancer nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant cancer nucleic acid can

be further used as a probe to identify and isolate other cancer nucleic acids, e.g., extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant cancer nucleic acids and proteins.

The cancer nucleic acids of the present invention are used in several ways. In one embodiment, nucleic acid probes to the cancer nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, e.g., for gene therapy, vaccine, RNAi, and/or antisense applications. Alternatively, cancer nucleic acids that include coding regions of cancer proteins can be put into expression vectors for the expression of cancer proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to cancer nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the cancer nucleic acids, e.g., the target sequence (either the target sequence of the sample or to other probe sequences, e.g., in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8-100 bases long, with from about 10-80 bases being preferred, and from about 30-50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a

particular target. The probes can be overlapping (e.g., have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

Nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or
5 binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic, hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, e.g., streptavidin to the support and
10 the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds, and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid
15 support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

20 The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. Often, the substrate may contain discrete individual sites appropriate for individual partitioning and identification. The number of possible substrates is very large, and include, but
25 are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, Teflon, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silica-based materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably
30 fluoresce. See WO 0055627.

Generally the substrate is planar, although other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube for flow-

through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, e.g., the biochip is
5 derivatized with a chemical functional group including, but not limited to, amino groups, carboxy groups, oxo groups, and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, e.g., using linkers; e.g., homo-or hetero-bifunctional linkers as are well known
10 (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized, and then attached to the surface of the solid support. Either the 5' or 3' terminus may be attached to the solid support, or
15 attachment may be via linkage to an internal nucleoside. In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface. For example,
20 photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affymetrix
25 GeneChip™ technology.

Often, amplification-based assays are performed to measure the expression level of cancer-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, a cancer-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative
30 amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of cancer-associated RNA. Methods of quantitative amplification are well known.

Detailed protocols for quantitative PCR are provided, e.g., in Innis, et al. (1990) PCR Protocols, A Guide to Methods and Applications Academic Press.

In some embodiments, a TaqMan based assay is used to measure expression. TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, e.g., literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see Wu and Wallace (1989) Genomics 4:560-569, Landegren, et al. (1988) Science 241:1077-1080, and Barringer, et al. (1990) Gene 89:117-122), transcription amplification (Kwoh, et al. (1989) Proc. Natl. Acad. Sci. USA 86:1173-1177), self-sustained sequence replication (Guatelli, et al. (1990) Proc. Nat. Acad. Sci. USA 87:1874-1878), dot PCR, linker adapter PCR, etc.

Expression of cancer proteins from nucleic acids

In a preferred embodiment, cancer nucleic acids, e.g., encoding cancer proteins, are used to make a variety of expression vectors to express cancer proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known (see, e.g., Ausubel, supra, and Fernandez and Hoeffler (eds. 1999) Gene Expression Systems Academic Press) to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the cancer protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are suitable for prokaryotes, e.g., include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in

the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the cancer protein. Numerous types of appropriate expression vectors and suitable regulatory sequences are known for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

Promoter sequences may be either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known, and are useful in the present invention.

An expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, e.g., in mammalian or insect cells for expression and in a prokaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector often contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are available. See, e.g., Fernandez and Hoeffler, *supra*; and Kitamura, et al. (1995) Proc. Nat'l Acad. Sci. USA 92:9146-9150.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known and will vary with the host cell used.

The cancer proteins of the present invention are usually produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding a cancer protein, under the appropriate conditions to induce or cause expression of the cancer protein. Conditions appropriate for cancer protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

Appropriate host cells include yeast, bacteria, archaeobacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are *Saccharomyces cerevisiae* and other yeasts, *E. coli*, *Bacillus subtilis*, Sf9 cells, C129 cells, 293 cells, *Neurospora*, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line), and various other human cells and cell lines.

In a preferred embodiment, the cancer proteins are expressed in mammalian cells. Mammalian expression systems may be used, and include retroviral and adenoviral systems. One expression vector system is a retroviral vector system such as is generally described in PCT/US97/01019 and PCT/US97/01048. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez and Hoeffler, *supra*). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenylation signals include those derived from SV40.

Methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, are available, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, cancer proteins are expressed in bacterial systems. Promoters from bacteriophage may also be used. In addition, synthetic promoters and hybrid promoters are also useful; e.g., the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the cancer protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin, kanamycin, neomycin, and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan, and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known, and include vectors for *Bacillus subtilis*, *E. coli*, *Streptococcus cremoris*, and *Streptococcus lividans*, among others (e.g., Fernandez and Hoeffler, supra). The bacterial expression vectors are transformed into bacterial host cells using techniques such as calcium chloride treatment, electroporation, and others.

In one embodiment, cancer proteins are produced in insect cells using, e.g., expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors.

In a preferred embodiment, a cancer protein is produced in yeast cells. Yeast expression systems are well known, and include expression vectors for *Saccharomyces cerevisiae*, *Candida albicans* and *C. maltosa*, *Hansenula polymorpha*, *Kluyveromyces fragilis* and *K. lactis*, *Pichia guillerimondii* and *P. pastoris*, *Schizosaccharomyces pombe*, and *Yarrowia lipolytica*.

The cancer protein may also be made as a fusion protein, using available techniques. Thus, e.g., for the creation of monoclonal antibodies, if the desired epitope is small, the cancer protein may be fused to a carrier protein to form an immunogen. Alternatively, the cancer protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the cancer protein is a cancer peptide, the nucleic acid encoding the peptide may

be linked to other nucleic acid for expression purposes. Fusion with detection epitope tags can be made, e.g., with FLAG, His6, myc, HA, etc.

In a preferred embodiment, the cancer protein is purified or isolated after expression. Cancer proteins may be isolated or purified in a variety of ways depending on what other components are present in the sample and the requirements for purified product, e.g., natural conformation or denatured. Standard purification methods include ammonium sulfate precipitations, electrophoretic, molecular, immunological, and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reverse-phase HPLC chromatography, and chromatofocusing. For example, the cancer protein may be purified using a standard anti-cancer protein antibody column. Ultrafiltration and diafiltration techniques, in conjunction with protein concentration, are also useful. See, e.g., Walsh (2002) Proteins: Biochemistry and Biotechnology Wiley; Hardin, et al. (eds. 2001) Cloning, Gene Expression and Protein Purification Oxford Univ. Press; Wilson, et al. (eds. 2000) Encyclopedia of Separation Science Academic Press; and Scopes (1993) Protein Purification Springer-Verlag. The degree of purification necessary will vary depending on the use of the cancer protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the cancer proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, therapeutic entities, for production of antibodies, as transcription or translation inhibitors, etc.

Variants of cancer proteins

Also included within one embodiment of cancer proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more preferably greater than about 80%, even more preferably greater than about 85%, and most preferably greater than 90%. In some embodiments the homology will be as high as about 93-95% or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques, as are outlined above for nucleic acid homologies.

Cancer proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of cancer proteins are portions or fragments of the wild type sequences herein. In addition, as

outlined above, the cancer nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence.

In one embodiment, the cancer proteins are derivative or variant cancer proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative
5 cancer peptide will often contain at least one amino acid substitution, deletion, or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion, or deletion may occur at many residue positions within the cancer peptide.

Also included within one embodiment of cancer proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes:
10 substitutional, insertional, or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the cancer protein, using cassette or PCR mutagenesis or other techniques, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant cancer protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis
15 using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the cancer protein amino acid sequence. The variants typically exhibit a similar qualitative biological activity as a naturally occurring analogue, although variants can also be selected which have modified characteristics.

20 While the site or region for introducing an amino acid sequence variation is often predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed cancer variants screened for the optimal combination of desired activity. Techniques for making substitution mutations at predetermined
25 sites in DNA having a known sequence are well known, e.g., M13 primer mutagenesis and PCR mutagenesis. Screening of mutants is often done using assays of cancer protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1-20 amino acids, although considerably larger insertions may be tolerated. Deletions generally range from about 1-20 residues, although in some cases deletions
30 may be much larger.

Substitutions, deletions, insertions, or combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the

alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the cancer protein are desired, substitutions are generally made in accordance with the amino acid substitution relationships described.

The variants typically exhibit essentially the same qualitative biological activity and will
5 elicit the same immune response as a naturally-occurring analog, although variants also are selected to modify the characteristics of cancer proteins as needed. Alternatively, the variant may be designed such that a biological activity of the cancer protein is altered. For example, glycosylation sites may be added, altered, or removed.

Substantial changes in function or immunological identity are sometimes made by
10 selecting substitutions that are less conservative than those described above. For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. Substitutions which generally are expected to produce the greatest changes in the polypeptide's
15 properties are those in which (a) a hydrophilic residue, e.g., serine or threonine is substituted for (or by) a hydrophobic residue, e.g., leucine, isoleucine, phenylalanine, valine, or alanine; (b) a cysteine or proline is substituted for (or by) another residue; (c) a residue having an electropositive side chain, e.g., lysine, arginine, or histidine, is substituted for (or by) an electronegative residue, e.g., glutamic or aspartic acid; (d) a residue having a bulky side chain,
20 e.g., phenylalanine, is substituted for (or by) one not having a side chain, e.g., glycine; or (e) a proline residue is incorporated or substituted, which changes the degree of rotational freedom of the peptidyl bond.

Variants typically exhibit a similar qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to
25 modify the characteristics of the skin cancer proteins as needed. Alternatively, the variant may be designed such that the biological activity of the cancer protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of cancer polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of
30 a cancer polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of a cancer polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking cancer polypeptides to a water-

insoluble support matrix or surface for use in a method for purifying anti-cancer polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, e.g., esters with 4-azidosalicylic acid, homobifunctional
5 imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-((p-azidophenyl)dithio)propioimide.

Other modifications include deamidation of glutamyl and asparagyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine,
10 phosphorylation of hydroxyl groups of serinyl, threonyl, or tyrosyl residues, methylation of the amino groups of the lysine, arginine, and histidine side chains (e.g., pp. 79-86, Creighton (1992) Proteins: Structure and Molecular Properties Freeman), acetylation of the N-terminal amine, and amidation of a C-terminal carboxyl group.

Another type of covalent modification of the cancer polypeptide included within the
15 scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence cancer polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence cancer polypeptide. Glycosylation patterns can be altered in many ways. Different cell types to express cancer-
20 associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to cancer polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, e.g., by the addition of, or substitution by, one or more serine or threonine residues to the native sequence cancer polypeptide (for O-linked glycosylation sites). The cancer amino acid sequence may optionally
25 be altered through changes at the DNA level, particularly by mutating the DNA encoding the cancer polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the cancer polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. See, e.g.,
30 WO 87/05330; pp. 259-306 in Aplin and Wriston (1981) CRC Crit. Rev. Biochem.

Removal of carbohydrate moieties present on the cancer polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for

amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are applicable. See, e.g., Sojar and Bahl (1987) Arch. Biochem. Biophys. 259:52-57 and Edge, et al. (1981) Anal. Biochem. 118:131-137. Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases. See, e.g., Thotakura, et al. (1987) Meth. Enzymol. 138:350-359.

Another type of covalent modification of cancer comprises linking the cancer polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192, or 4,179,337.

Cancer polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising a cancer polypeptide fused to another heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of a cancer polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl-terminus of the cancer polypeptide. The presence of such epitope-tagged forms of a cancer polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the cancer polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of a cancer polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are available. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 (Field, et al. (1988) Mol. Cell. Biol. 8:2159-2165); the c-myc tag and the 8F9, 3C7, 6E10, G4, B7, and 9E10 antibodies thereto (Evan, et al. (1985) Molecular and Cellular Biology 5:3610-3616); and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody (Paborsky, et al. (1990) Protein Engineering 3(6):547-553). Other tag polypeptides include the Flag-peptide (Hopp, et al. (1988) BioTechnology 6:1204-1210); the KT3 epitope peptide (Martin, et al. (1992) Science 255:192-194); tubulin epitope peptide (Skinner, et al. (1991) J. Biol. Chem. 266:15163-15166); and the T7 gene 10 protein peptide tag (Lutz-Freyermuth, et al. (1990) Proc. Natl. Acad. Sci. USA 87:6393-6397).

Also included are other cancer proteins of the cancer family, and cancer proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related cancer proteins from humans or other organisms. Particularly useful probe and/or PCR primer
5 sequences include the unique areas of the cancer nucleic acid sequence. Preferred PCR primers are from about 15-35 nucleotides in length, with from about 20-30 being preferred, and may contain inosine as needed. The conditions for PCR reaction have been well described (e.g., Innis, PCR Protocols, supra).

In addition, cancer proteins can be made that are longer than those encoded by the
10 nucleic acids of the Tables, e.g., by the elucidation of extended sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

Cancer proteins may also be identified as being encoded by cancer nucleic acids. Thus, cancer proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

15 Antibodies to cancer proteins

In a preferred embodiment, when the cancer protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the cancer protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell
20 receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller cancer protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from a protein sequence set out in the tables.

25 Methods of preparing polyclonal antibodies exist (e.g., Coligan, supra; and Harlow and Lane, supra). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of Tables 1-68 or
30 fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum

albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). Various immunization protocols may be used.

- 5 The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein (1975) Nature 256:495. In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent.
- 10 Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of the tables or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line
- 15 using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell (e.g., pp. 59-103 in Goding (1986) Monoclonal Antibodies: Principles and Practice Academic Press). Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine, or human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or
- 20 more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.
- 25 In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid of the tables or a fragment thereof, the other one is for another antigen, and
- 30 preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to cancer protein are capable of reducing or eliminating a biological function of a cancer protein, in a naked form or conjugated to an effector moiety, as is described below. That is, the addition of anti-cancer protein antibodies (either polyclonal or preferably monoclonal) to cancer tissue (or cells containing cancer) may
5 reduce or eliminate the cancer. Generally, at least a 25% decrease in activity, growth, size, or the like is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

In a preferred embodiment the antibodies to the cancer proteins are humanized antibodies (e.g., Xenerex Biosciences, Medarex, Inc., Abgenix, Inc., Protein Design Labs, Inc.)
10 Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')₂ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the
15 recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat, or rabbit having the desired specificity, affinity, and capacity. In some instances, Fv framework residues of a human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized
20 antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will typically comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human
25 immunoglobulin (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-329; and Presta (1992) Curr. Op. Struct. Biol. 2:593-596). Humanization can be essentially performed following the method of Winter and co-workers (Jones, et al. (1986) Nature 321:522-525; Riechmann, et al. (1988) Nature 332:323-327; Verhoeyen, et al. (1988) Science 239:1534-1536), by substituting rodent CDRs or CDR sequences for corresponding
30 sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by corresponding sequence from a non-human species.

Human antibodies can also be produced using phage display libraries (Hoogenboom and Winter (1992) J. Mol. Biol. 227:381-388; Marks, et al. (1991) J. Mol. Biol. 222:581-597) or human monoclonal antibodies (e.g., p. 77, Cole, et al. in Reisfeld and Sell (1985) Monoclonal Antibodies and Cancer Therapy Liss; and Boerner, et al. (1991) J. Immunol. 147:86-95).

5 Similarly, human antibodies can be made by introducing human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in nearly all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, e.g., in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the
10 following scientific publications: Marks, et al. (1992) Bio/Technology 10:779-783; Lonberg, et al. (1994) Nature 368:856-859; Morrison (1994) Nature 368:812-13; Fishwild, et al. (1996) Nature Biotechnology 14:845-851; Neuberger (1996) Nature Biotechnology 14:826; and Lonberg and Huszar (1995) Intern. Rev. Immunol. 13:65-93.

15 By immunotherapy is meant treatment of cancer with an antibody raised against cancer proteins. As used herein, immunotherapy can be passive or active. Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient (patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are
20 raised. The antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the cancer proteins against which antibodies are raised are
25 secreted proteins as described above. Without being bound by theory, antibodies used for treatment may bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted cancer protein, e.g., in autocrine signaling.

In another preferred embodiment, the cancer protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment may
30 bind the extracellular domain of the cancer protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The antibody may cause down-regulation of the transmembrane cancer protein. The antibody may be a competitive, non-

competitive or uncompetitive inhibitor of protein binding to the extracellular domain of the cancer protein. The antibody may also be an antagonist of the cancer protein. Further, the antibody may prevent activation of the transmembrane cancer protein, or may induce or suppress a particular cellular pathway. In one aspect, when the antibody prevents the binding of other molecules to the cancer protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF- α , TNF- β , IL-1, INF- γ , and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody may belong to a sub-type that activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, cancer may be treated by administering to a patient antibodies directed against the transmembrane cancer protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated to an effector moiety. The effector moiety can be various molecules, including labeling moieties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In one aspect the therapeutic moiety is a small molecule that modulates the activity of a cancer protein. In another aspect the therapeutic moiety may modulate the activity of molecules associated with or in close proximity to a cancer protein. The therapeutic moiety may inhibit enzymatic or signaling activity such as protease or collagenase or protein kinase activity associated with cancer, or be an attractant of other cells, such as NK cells.

In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to cancer tissue or cells results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with cancer. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin, saporin, auristatin, and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against cancer proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane cancer proteins not only serves to increase the local

concentration of therapeutic moiety in the cancer afflicted area, but also serves to reduce deleterious side effects that may be associated with the untargeted therapeutic moiety.

In another preferred embodiment, the cancer protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the cancer protein can be targeted within a cell, e.g., the nucleus, an antibody thereto may contain a signal for that target localization, e.g., a nuclear localization signal.

The cancer antibodies of the invention specifically bind to cancer proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μ M, preferably at least about 0.1 μ M or better, and most preferably, 0.01 μ M or better. Selectivity of binding to the specific target and not to related sequences is often also important.

Detection of cancer sequence for diagnostic and therapeutic applications

In one aspect, the RNA expression levels of genes are determined for different cellular states in the cancer phenotype. Expression levels of genes in normal tissue (e.g., not undergoing cancer) and in cancer tissue (and in some cases, for varying severities of cancer that relate to prognosis, as outlined below), or in non-malignant disease are evaluated to provide expression profiles. A gene expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state of the cell. While two states may have a particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or cancerous tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus cancer tissue. Genes may be turned on or turned off in a particular state, relative to another state thus

permitting comparison of two or more states. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that expression is increased or decreased; e.g., gene
5 expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChip™ expression arrays. See, Lockhart (1996) Nature Biotechnology 14:1675-1680. Other techniques include, but are not limited to,
10 quantitative reverse transcriptase PCR, northern analysis, and RNase protection. As outlined above, preferably the change in expression (e.g., upregulation or downregulation) is at least about 50%, more preferably at least about 100%, more preferably at least about 150%, more preferably at least about 200%, with from 300 to at least 1000% being especially preferred.

Evaluation may be at the gene transcript or the protein level. The amount of gene
15 expression may be monitored using nucleic acid probes to the RNA or DNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the cancer protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to cancer genes, e.g., those identified as
20 being important in a cancer or disease phenotype, can be evaluated in a cancer diagnostic test. In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed as well.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell. The assays
25 are further described below in the example. PCR techniques can be used to provide greater sensitivity.

In a preferred embodiment nucleic acids encoding the cancer protein are detected. Although DNA or RNA encoding the cancer protein may be detected, of particular interest are methods wherein an mRNA encoding a cancer protein is detected. Probes to detect mRNA can
30 be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA, or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after

immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is detected. In another method, detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably
5 labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxigenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding a cancer protein is detected by binding the digoxigenin with an anti-digoxigenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl
10 phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane, or intracellular proteins) are used in diagnostic assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in diagnostic assays. This can be performed on an individual gene or
15 corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

As described and defined herein, cancer proteins, including intracellular, transmembrane, or secreted proteins, find use as markers of cancer, e.g., for prognostic or
20 diagnostic purposes. Detection of these proteins in putative cancer tissue allows for detection, prognosis, or diagnosis of cancer or similar disease, and for selection of therapeutic strategy. In one embodiment, antibodies are used to detect cancer proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following
25 separation of proteins, the cancer protein is detected, e.g., by immunoblotting with antibodies raised against the cancer protein.

In another preferred method, antibodies to the cancer protein find use in in situ imaging techniques, e.g., in histology. See, e.g., Asai, et al. (eds. 1993) Methods in Cell Biology: Antibodies in Cell Biology (vol. 37) Academic Press. In this method, cells are contacted with
30 from one to many antibodies to the cancer protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a

detectable label. In another method the primary antibody to the cancer protein(s) contains a detectable label, e.g., an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and detectable label. This method finds particular use in simultaneous screening for a plurality of cancer proteins.

5 Many other histological imaging techniques are also provided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

10 In another preferred embodiment, antibodies find use in diagnosing cancer from blood, serum, plasma, stool, and other samples. Such samples, therefore, are useful as samples to be probed or tested for the presence of cancer proteins. Antibodies can be used to detect a cancer protein by previously described immunoassay techniques including ELISA, immunoblotting (western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous cancer protein.

15 In a preferred embodiment, in situ hybridization of labeled cancer nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including cancer tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, a diagnosis, a prognosis, or a prediction may be based on the findings. It is further understood that the genes
20 which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in prognosis assays. As above, gene
25 expression profiles can be generated that correlate to cancer, clinical, pathological, or other information, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. Single or multiple genes may be useful in various combinations. As above, cancer probes may be attached to biochips for the detection and quantification of cancer sequences in a tissue or patient. The assays proceed as outlined
30 above for diagnosis. PCR method may provide more sensitive and accurate quantification.

Assays for therapeutic compounds

In a preferred embodiment, the proteins, nucleic acids, and antibodies as described herein are used in drug screening assays. The cancer proteins, antibodies, nucleic acids, modified proteins, and cells containing cancer sequences are used in drug screening assays or
5 by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al. (1998) Science 279:84-88; Heid (1996) Genome Res. 6:986-994.

10 In a preferred embodiment, the cancer proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified cancer proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the cancer phenotype or an identified physiological function of a cancer protein. As above, this can be done on an individual gene level or by evaluating the effect of
15 drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques, to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokarnik, supra.

Having identified the differentially expressed genes herein, a variety of assays may be
20 performed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in cancer, test compounds can be screened for the ability to modulate gene expression or for binding to the cancer protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal
25 versus tissue undergoing cancer, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in cancer tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in cancer tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

30 The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be

monitored, e.g., through the use of antibodies to the cancer protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entities, e.g., an expression profile, is monitored simultaneously. Such profiles will typically
5 involve a plurality of those entities described herein.

In this embodiment, the cancer nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of cancer sequences in a particular cell.

Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for
10 each well.

Modulators of cancer

Expression monitoring can be performed to identify compounds that modify the expression of one or more cancer-associated sequences, e.g., a polynucleotide sequence set out
15 in the tables. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate cancer, modulate cancer proteins, bind to a cancer protein, or interfere with the binding of a cancer protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical
20 equivalents as used herein describes a molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the cancer phenotype or the expression of a cancer sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator
25 suppresses a cancer phenotype, e.g., to a normal or non-malignant tissue fingerprint. In another embodiment, a modulator induced a cancer phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, e.g., at zero concentration or below the level of detection.

30 Drug candidates encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 100 and less than about 2,500 daltons. Preferred small molecules are less than 2000, or

less than 1500, or less than 1000, or less than 500 D. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise cyclical carbon or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups. Candidate agents are also found among biomolecules including peptides, saccharides, fatty acids, steroids, purines, pyrimidines, derivatives, structural analogs, or combinations thereof. Particularly preferred are peptides.

In one aspect, a modulator will neutralize the effect of a cancer protein. By "neutralize" is meant that activity of a protein is inhibited or blocked and the consequent effect on the cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to a cancer polypeptide or to modulate activity. Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis. See, e.g., Janzen (2002) High Throughput Screening: Methods and Protocols Humana; Devlin (ed. 1997) High Throughput Screening: The Discovery of Bioactive Substances Dekker; and Mei and Czarnik (eds. 2002) Integrated Drug Discovery Techniques Dekker.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (e.g., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be

synthesized through such combinatorial mixing of chemical building blocks (Gallop, et al. (1994) J. Med. Chem. 37:1233-1251).

Preparation and screening of combinatorial chemical libraries is well known. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5,010,175, Furka (1991) Pept. Prot. Res. 37:487-493, Houghton, et al. (1991) Nature 354:84-88), peptoids (PCT Publication No WO 91/19735), encoded peptides (PCT Publication WO 93/20242), random bio-oligomers (PCT Publication WO 92/00091), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs, et al. (1993) Proc. Nat. Acad. Sci. USA 90:6909-6913, vinylogous polypeptides (Hagihara, et al. (1992) J. Amer. Chem. Soc. 114:6568-570), nonpeptidal peptidomimetics with a Beta-D-Glucose scaffolding (Hirschmann, et al. (1992) J. Amer. Chem. Soc. 114:9217-9218), analogous organic syntheses of small compound libraries (Chen, et al. (1994) J. Amer. Chem. Soc. 116:2661-662), oligocarbamates (Cho, et al. (1993) Science 261:1303-1305), and/or peptidyl phosphonates (Campbell, et al. (1994) J. Org. Chem. 59:658-xxx). See, generally, Gordon, et al. (1994) J. Med. Chem. 37:1385-1401, nucleic acid libraries (see, e.g., Stratagene, Corp.), peptide nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn, et al. (1996) Nature Biotechnology 14(3):309-314, and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang, et al. (1996) Science 274:1520-1522, and U.S. Patent No. 5,593,853), and small organic molecule libraries (see, e.g., benzodiazepines, page 33 Baum (Jan 18, 1993) C&EN; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. The above devices are suitable for use with the present invention. The nature and

implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of cancer gene transcription, inhibition, or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known. Similarly, binding assays and reporter gene assays are similarly well known. Thus, e.g., U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (e.g., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments, Inc. Fullerton, CA; Precision Systems, Inc., Natick, MA, etc.). These systems typically automate entire procedures, including sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, e.g., Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Particularly useful test

compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

In a preferred embodiment, modulators are peptides of from about 5-30 amino acids, with from about 5-20 amino acids being preferred, and from about 7-15 being particularly preferred. The peptides may be digests of naturally occurring proteins, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate a nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized candidate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, e.g., of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking, prolines for SH-3 domains, serines, threonines, tyrosines, or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of cancer can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of prokaryotic or eukaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical moieties, a wide variety of which are available in the literature.

After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an in

vitro transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, e.g., a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

These assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246, and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate, and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration, pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g., albumin, detergents, etc. which may be used

to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

5 The assay data are analyzed to determine the expression levels, and changes in expression levels as between states of individual genes, forming a gene expression profile.

 Screens are performed to identify modulators of the cancer phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another
10 embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens
15 are performed to identify agents that bind and/or modulate the biological activity of the gene product.

 In addition, screens can be done for genes that are induced in response to a candidate agent or treatment process. After identifying a modulator based upon its ability to suppress a cancer expression pattern leading to a normal expression pattern (or its converse), or to
20 modulate a single cancer gene expression profile so as to mimic the expression of the gene from normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated cancer tissue reveals genes that are not expressed in normal tissue or cancer tissue, but are expressed in agent treated tissue. These agent-specific sequences can be
25 identified and used by methods described herein for cancer genes or proteins. In particular, these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated cancer tissue sample.

 Thus, in one embodiment, a test compound is administered to a population of cancer
30 cells that have an associated cancer expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell

surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (e.g., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used.

5 Once a test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

 Thus, e.g., cancer or non-malignant tissue may be screened for agents that modulate, e.g., induce or suppress a cancer phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on cancer activity. By defining such a signature for the cancer phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein
15 need to change.

 In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "cancer proteins" or a "cancer modulatory protein". The cancer modulatory protein may be a fragment, or alternatively, be the full length protein to the fragment encoded by the nucleic acids of the Tables. Preferably, the cancer modulatory protein is a fragment. In a preferred embodiment, the cancer amino acid sequence which is used to determine sequence identity or similarity is encoded by a nucleic acid of the Tables. In another
20 embodiment, the sequences are naturally occurring allelic variants of a protein encoded by a nucleic acid of the Tables. In another embodiment, the sequences are sequence variants as further described herein.

 Preferably, the cancer modulatory protein is a fragment of about 14-24 amino acids long. More preferably the fragment is a soluble fragment. Preferably, the fragment includes a non-transmembrane region. In a preferred embodiment, the fragment has an N-terminal Cys to aid in solubility. In one embodiment, the C-terminus of the fragment is kept as a free acid and the N-terminus is a free amine to aid in coupling, e.g., to cysteine.
30

In one embodiment the cancer proteins are conjugated to an immunogenic agent as discussed herein. In one embodiment the cancer protein is conjugated to BSA.

Measurements of cancer polypeptide activity, or of cancer or the cancer phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the cancer polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention. When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of cancer associated with tumors, tumor growth, tumor metastasis, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian cancer polypeptide is typically used, e.g., mouse, preferably human.

Assays to identify compounds with modulating activity can be performed in vitro. For example, a cancer polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5–48 hours. In one embodiment, the cancer polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is typically measured using immunoassays such as western blotting, ELISA, and the like with an antibody that selectively binds to the cancer polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNase protection, dot blotting, are preferred. The level of protein or mRNA is typically detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

Alternatively, a reporter gene system can be devised using a cancer protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or

the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "cancer proteins." The cancer protein may be a fragment, or alternatively, the full length protein to a fragment shown herein.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate structure activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the cancer proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining a cancer protein and a candidate compound, and determining the binding of the compound to the cancer protein. Preferred embodiments utilize the human cancer protein, although other mammalian proteins may also be used, e.g., for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative cancer proteins may be used.

Generally, in a preferred embodiment of the methods herein, the cancer protein or the candidate agent is non-diffusably bound to an insoluble support, preferably having isolated sample receiving areas (e.g., a microtiter plate, an array, etc.). The insoluble supports may be made of a composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of a convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes, and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflon™, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is typically not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition, and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not

sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked
5 through incubation with bovine serum albumin (BSA), casein, or other innocuous protein or other moiety.

In a preferred embodiment, the cancer protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the cancer protein is added. Novel binding agents include specific antibodies, non-natural
10 binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding, functional assays (phosphorylation assays, etc.), and the like.

15 The determination of the binding of the test modulating compound to the cancer protein may be done in a number of ways. In a preferred embodiment, the compound is labeled, and binding determined directly, e.g., by attaching all or a portion of the cancer protein to a solid support, adding a labeled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and
20 washing steps may be utilized as appropriate.

In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., ^{125}I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

25 In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor may be a binding moiety known to bind to the target molecule (e.g., a cancer protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test
30 compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between about 4-40° C. Incubation

periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1-1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

5 In a preferred embodiment, the competitor is added first, followed by a test compound. Displacement of the competitor is an indication that the test compound is binding to the cancer protein and thus is capable of binding to, and potentially modulating, the activity of the cancer protein. In this embodiment, either component can be labeled. Thus, e.g., if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent.

10 Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the cancer protein with a higher affinity. Thus, if the test
15 compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the cancer protein.

In a preferred embodiment, the methods comprise differential screening to identity agents that are capable of modulating the activity of the cancer proteins. In one embodiment, the methods comprise combining a cancer protein and a competitor in a first sample. A second
20 sample comprises a test compound, a cancer protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the cancer protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the cancer protein.

25 Alternatively, differential screening is used to identify drug candidates that bind to the native cancer protein, but cannot bind to modified cancer proteins. The structure of the cancer protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of a cancer protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

30 Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein.

Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

5 A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g., albumin, detergents, etc., which may be used to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may
10 be added in an order that provides for the requisite binding.

 In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of a cancer protein. The methods comprise adding a test compound, as defined above, to a cell comprising cancer proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes a
15 cancer protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

 In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, e.g., hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including
20 chemotherapeutics, radiation, carcinogenics, or other cells (e.g., cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

 In this way, compounds that modulate cancer agents are identified. Compounds with pharmacological activity are able to enhance or interfere with the activity of the cancer protein. Once identified, similar structures are evaluated to identify critical structural feature of the
25 compound.

 In one embodiment, a method of inhibiting cancer cell division is provided. The method comprises administration of a cancer inhibitor. In another embodiment, a method of inhibiting cancer is provided. The method may comprise administration of a cancer inhibitor. In a further embodiment, methods of treating cells or individuals with cancer are provided, e.g., comprising
30 administration of a cancer inhibitor.

 In one embodiment, a cancer inhibitor is an antibody as discussed above. In another embodiment, the cancer inhibitor is an antisense molecule.

A variety of cell growth, proliferation, viability, and metastasis assays are available, as described below.

Soft agar growth or colony formation in suspension

Normal cells require a solid substrate to attach and grow. When the cells are transformed, they lose this phenotype and grow detached from the substrate. For example, transformed cells can grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft agar. The transformed cells, when transfected with tumor suppressor genes, regenerate normal phenotype and require a solid substrate to attach and grow. Soft agar growth or colony formation in suspension assays can be used to identify modulators of cancer sequences, which when expressed in host cells, inhibit abnormal cellular proliferation and transformation. A therapeutic compound would reduce or eliminate the host cells' ability to grow in stirred suspension culture or suspended in semi-solid media, such as semi-solid or soft.

Techniques for soft agar growth or colony formation in suspension assays are described, e.g., in Freshney (1998) Culture of Animal Cells: A Manual of Basic Technique (3d ed.) Wiley-Liss; Freshney (2000) Culture of Animal Cells: A Manual of Basic Technique (4th ed.) Wiley-Liss; and Garkavtsev, et al. (1996) Nature Genet. 14:415-20.

Contact inhibition and density limitation of growth

Normal cells typically grow in a flat and organized pattern in a petri dish until they touch other cells. When the cells touch one another, they are contact inhibited and stop growing. When cells are transformed, however, the cells are not contact inhibited and continue to grow to high densities in disorganized foci. Thus, the transformed cells grow to a higher saturation density than normal cells. This can be detected morphologically by the formation of a disoriented monolayer of cells or rounded cells in foci within the regular pattern of normal surrounding cells. Alternatively, labeling index with (³H)-thymidine at saturation density can be used to measure density limitation of growth. See Freshney (2000), supra. The transformed cells, when transfected with tumor suppressor genes, regenerate a normal phenotype and become contact inhibited and would grow to a lower density.

In this assay, labeling index with (³H)-thymidine at saturation density is a preferred method of measuring density limitation of growth. Transformed host cells are transfected with a cancer-associated sequence and are grown for 24 hours at saturation density in non-limiting medium conditions. The percentage of cells labeling with (³H)-thymidine is determined autoradiographically. See, Freshney (1998), supra.

Growth factor or serum dependence

Transformed cells typically have a lower serum dependence than their normal counterparts (see, e.g., Temin (1966) J. Natl. Cancer Inst. 37:167-175; Eagle, et al. (1970) J. Exp. Med. 131:836-879); Freshney, supra. This is in part due to release of various growth factors by the transformed cells. Growth factor or serum dependence of transformed host cells can be compared with that of control.

Tumor specific markers levels

Tumor cells release an increased amount of certain factors (hereinafter "tumor specific markers") than their normal counterparts. For example, plasminogen activator (PA) is released from human glioma at a higher level than from normal brain cells (see, e.g., Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum. Similarly, tumor angiogenesis factor (TAF) is released at a higher level in tumor cells than their normal counterparts. See, e.g., Folkman (1992) Sem. Cancer Biol. 3:89-96.

Various techniques which measure the release of these factors are described in Freshney (1998), supra. Also, see, Unkeless, et al. (1974) J. Biol. Chem. 249:4295-4305; Strickland and Beers (1976) J. Biol. Chem. 251:5694-5702; Whur, et al. (1980) Br. J. Cancer 42:305-312; Gullino "Angiogenesis, tumor vascularization, and potential interference with tumor growth" pp. 178-184 in Mihich (ed. 1985) Biological Responses in Cancer Plenum; Freshney (1985) Anticancer Res. 5:111-130.

Invasiveness into Matrigel

The degree of invasiveness into Matrigel or some other extracellular matrix constituent can be used as an assay to identify compounds that modulate cancer-associated sequences. Tumor cells exhibit a good correlation between malignancy and invasiveness of cells into Matrigel or some other extracellular matrix constituent. In this assay, tumorigenic cells are typically used as host cells. Expression of a tumor suppressor gene in these host cells would decrease invasiveness of the host cells.

Techniques described in Freshney (1994), supra, can be used. Briefly, the level of invasion of host cells can be measured by using filters coated with Matrigel or some other extracellular matrix constituent. Penetration into the gel, or through to the distal side of the filter, is rated as invasiveness, and rated histologically by number of cells and distance moved,

or by prelabeling the cells with ^{125}I and counting the radioactivity on the distal side of the filter or bottom of the dish. See, e.g., Freshney (1984), supra.

Tumor growth in vivo

Effects of cancer-associated sequences on cell growth can be tested in transgenic or immune-suppressed mice. Knock-out transgenic mice can be made, in which the cancer gene is disrupted or in which a cancer gene is inserted. Knock-out transgenic mice can be made by insertion of a marker gene or other heterologous gene into the endogenous cancer gene site in the mouse genome via homologous recombination. Such mice can also be made by substituting the endogenous cancer gene with a mutated version of the cancer gene, or by mutating the endogenous cancer gene, e.g., by exposure to carcinogens.

A DNA construct is introduced into the nuclei of embryonic stem cells. Cells containing the newly engineered genetic lesion are injected into a host mouse embryo, which is re-implanted into a recipient female. Some of these embryos develop into chimeric mice that possess germ cells partially derived from the mutant cell line. Therefore, by breeding the chimeric mice it is possible to obtain a new line of mice containing the introduced genetic lesion (see, e.g., Capecchi, et al. (1989) Science 244:1288-1292). Chimeric targeted mice can be derived according to Hogan, et al. (1988) Manipulating the Mouse Embryo: A Laboratory Manual CSH Press; and Robertson (ed. 1987) Teratocarcinomas and Embryonic Stem Cells: A Practical Approach IRL Press, Washington, D.C.

Alternatively, various immune-suppressed or immune-deficient host animals can be used. For example, genetically athymic "nude" mouse (see, e.g., Giovanella, et al. (1974) J. Natl. Cancer Inst. 52:921-930), a SCID mouse, a thymectomized mouse, or an irradiated mouse (see, e.g., Bradley, et al. (1978) Br. J. Cancer 38:263-272; Selby, et al. (1980) Br. J. Cancer 41:52-61) can be used as a host. Transplantable tumor cells (typically about 10^6 cells) injected into isogenic hosts will produce invasive tumors in a high proportions of cases, while normal cells of similar origin will not. In hosts which developed invasive tumors, cells expressing a cancer-associated sequences are injected subcutaneously. After a suitable length of time, preferably 4-8 weeks, tumor growth is measured (e.g., by volume or by its two largest dimensions) and compared to the control. Tumors that have statistically significant reduction (using, e.g., Student's T test) are said to have inhibited growth.

Polynucleotide modulators of cancer

Antisense and RNAi Polynucleotides

In certain embodiments, the activity of a cancer-associated protein is down-regulated, or entirely inhibited, by the use of an inhibitory or antisense polynucleotide, e.g., a nucleic acid
5 complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., a cancer protein mRNA, or a subsequence thereof. Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their
10 close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species. Analogs are comprehended by this invention so long as they function effectively to hybridize with the cancer protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Sequitor, Inc., Natick, MA.

15 Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known.

Antisense molecules as used herein include antisense or sense oligonucleotides. Sense
20 oligonucleotides can, e.g., be employed to block transcription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for cancer molecules. A preferred antisense molecule is for a cancer sequences in the Tables, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to
25 the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14-30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, e.g., Stein and Cohen (1988) Cancer Res. 48:2659-2668; and van der Krol, et al. (1988) BioTechniques 6:958-976.

RNA interference is a mechanism to suppress gene expression in a sequence specific
30 manner. See, e.g., Brumelkamp, et al. (2002) Sciencexpress (21March2002); Sharp (1999) Genes Dev. 13:139-141; and Cathew (2001) Curr. Op. Cell Biol. 13:244-248. In mammalian cells, short, e.g., 21 nt, double stranded small interfering RNAs (siRNA) have been shown to be

effective at inducing an RNAi response. See, e.g., Elbashir, et al. (2001) Nature 411:494-498. The mechanism may be used to downregulate expression levels of identified genes, e.g., treatment of or validation of relevance to disease.

Ribozymes

5 In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of cancer-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto, et al. (1994) Adv. in Pharmacology 25: 289-317 for a general
10 review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel, et al. (1990) Nucl. Acids Res. 18:299-304; European Patent Publication No. 0 360 257; U.S. Patent No. 5,254,678. Methods of preparation are described in, e.g., WO 94/26877; Ojwang, et al. (1993) Proc. Natl. Acad. Sci. USA 90:6340-6344; Yamada, et al. (1994) Human Gene Therapy 1:39-
15 45; Leavitt, et al. (1995) Proc. Natl. Acad. Sci. USA 92:699-703; Leavitt, et al. (1994) Human Gene Therapy 5:1151-120; and Yamada, et al. (1994) Virology 205: 121-126.

Polynucleotide modulators of cancer may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface
20 receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of cancer may be introduced into a cell containing the
25 target nucleic acid sequence, e.g., by formation of a polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating cancer in cells or organisms are
30 provided. In one embodiment, the methods comprise administering to a cell an anti-cancer antibody that reduces or eliminates the biological activity of an endogenous cancer protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic

acid encoding a cancer protein. This may be accomplished in any number of ways. In a preferred embodiment, e.g., when the cancer sequence is down-regulated in cancer, such state may be reversed by increasing the amount of cancer gene product in the cell. This can be accomplished, e.g., by overexpressing the endogenous cancer gene or administering a gene
5 encoding the cancer sequence, using known gene-therapy techniques. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), e.g., as described in PCT/US93/0386. Alternatively, e.g., when the cancer sequence is up-regulated in cancer, the activity of the endogenous cancer gene is decreased, e.g., by the administration of a cancer antisense or other
10 inhibitor, e.g., RNAi.

In one embodiment, the cancer proteins of the present invention may be used to generate polyclonal and monoclonal antibodies to cancer proteins. Similarly, the cancer proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify cancer antibodies useful for production, diagnostic, or therapeutic
15 purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a cancer protein; that is, the antibodies show little or no cross-reactivity to other proteins. The cancer antibodies may be coupled to standard affinity chromatography columns and used to purify cancer proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the cancer protein.

20 Methods of identifying variant cancer-associated sequences

Without being bound by theory, expression of various cancer sequences is correlated with cancer. Accordingly, disorders based on mutant or variant cancer genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant cancer genes, e.g., determining all or part of the sequence of at least one
25 endogenous cancer gene in a cell. In a preferred embodiment, the invention provides methods of identifying the cancer genotype of an individual, e.g., determining all or part of the sequence of at least one cancer gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced cancer gene to
30 a known cancer gene, e.g., a wild-type gene.

The sequence of all or part of the cancer gene can then be compared to the sequence of a known cancer gene to determine if any differences exist. This can be done using known

homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a difference in the sequence between the cancer gene of the patient and the known cancer gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the cancer genes are used as probes to determine the number
5 of copies of the cancer gene in the genome.

In another preferred embodiment, the cancer genes are used as probes to determine the chromosomal localization of the cancer genes. Information such as chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the cancer gene locus.

10 Administration of pharmaceutical and vaccine compositions

In one embodiment, a therapeutically effective dose of a cancer protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable using known techniques. See, e.g., Ansel, et al. (1999)
15 Pharmaceutical Dosage Forms and Drug Delivery Lippincott; Lieberman (1992) Pharmaceutical Dosage Forms (vols. 1-3) Dekker, ISBN 0824770846, 082476918X, 0824712692, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding Amer. Pharmaceut. Assn.; and Pickar (1998) Dosage Calculations Thomson. Adjustments for cancer degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as
20 the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary. U.S. Patent Application No. 09/687,576, further discloses the use of compositions and methods of diagnosis and treatment in cancer.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and
25 veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the cancer proteins and modulators thereof of the present invention can be done in a variety of ways, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intraperitoneally, intramuscularly, intrapulmonary,
30 vaginally, rectally, or intraocularly. In some instances, e.g., in the treatment of wounds and inflammation, the cancer proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise a cancer protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid, and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid, and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts, and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine.

The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that cancer protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are available.

The compositions for administration will commonly comprise a cancer protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by
5 conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents, and the like, e.g., sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate, and the like. The concentration of active agent in these formulations can vary widely, and will be
10 selected primarily based on fluid volumes, viscosities, body weight, and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., (1980) Remington's Pharmaceutical Science (18th ed.) Mack, and Hardman and Limbird (eds. 2001) Goodman and Gilman: The Pharmacological Basis of Therapeutics (10th ed.) McGraw-Hill.

Thus, a typical pharmaceutical composition for intravenous administration would be
15 about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent.

20 The compositions containing modulators of cancer proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend
25 upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a
30 mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender,

administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer based, at least in part, upon gene expression profiles. Vaccine strategies may be used, in either a DNA vaccine form, or protein vaccine.

It will be appreciated that the present cancer protein-modulating compounds can be administered alone or in combination with additional cancer modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments.

In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in the Tables, such as RNAi, antisense polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of cancer-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors, and other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA, or other foreign genetic material into a host cell (see, e.g., Berger and Kimmel (1987) Guide to Molecular Cloning Techniques from Methods in Enzymology (vol. 152) Academic Press; Ausubel, et al. (eds. 1999 and supplements) Current Protocols Lippincott; and Sambrook, et al. (2001) Molecular Cloning: A Laboratory Manual (3d ed., Vol. 1-3) CSH Press.

In a preferred embodiment, cancer proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, cancer genes (including both the full-length sequence, partial sequences, or regulatory sequences of the cancer coding regions) can be administered in a gene therapy application. These cancer genes can include inhibitory applications, e.g., as inhibitory RNA, gene therapy (e.g., for incorporation into the genome), or antisense compositions.

Cancer polypeptides and polynucleotides can also be administered as vaccine compositions to stimulate HTL, CTL, and antibody responses. Such vaccine compositions can

include, e.g., lipidated peptides (see, e.g., Vitiello, et al. (1995) J. Clin. Invest. 95:341-349), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, et al. (1991) Molec. Immunol. 28:287-294.; Alonso, et al. (1994) Vaccine 12:299-306; Jones, et al. (1995) Vaccine 13:675-681), peptide compositions contained in
 5 immune stimulating complexes (ISCOMS) (see, e.g., Takahashi, et al. (1990) Nature 344:873-875; Hu, et al. (1998) Clin Exp Immunol. 113:235-243), multiple antigen peptide systems (MAPs) (see, e.g., Tam (1988) Proc. Natl. Acad. Sci. USA 85:5409-5413; Tam (1996) J. Immunol. Methods 196:17-32), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, et al., p.
 10 379, in Kaufmann (ed. 1996) Concepts in Vaccine Development de Gruyter; Chakrabarti, et al. (1986) Nature 320:535-537; Hu, et al. (1986) Nature 320:537-540; Kieny, et al. (1986) Bio/Technology 4:790-795; Top, et al. (1971) J. Infect. Dis. 124:148-154; Chanda, et al. (1990) Virology 175:535-547), particles of viral or synthetic origin (see, e.g., Kofler, et al. (1996) J. Immunol. Methods 192:25-35; Eldridge, et al. (1993) Sem. Hematol. 30:16-24; Falo, et al.
 15 (1995) Nature Med. 1:649-653), adjuvants (Warren, et al. (1986) Annu. Rev. Immunol. 4:369-388; Gupta, et al. (1993) Vaccine 11:293-306), liposomes (Reddy, et al. (1992) J. Immunol. 148:1585-1589; Rock (1996) Immunol. Today 17:131-137), or, naked or particle absorbed cDNA (Ulmer, et al. (1993) Science 259:1745-1749; Robinson, et al. (1993) Vaccine 11:957-960; Shiver, et al., p 423, in Kaufmann (ed. 1996) Concepts in Vaccine Development de
 20 Gruyter; Cease and Berzofsky (1994) Annu. Rev. Immunol. 12:923-989; and Eldridge, et al. (1993) Sem. Hematol. 30:16-24). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

Vaccine compositions often include adjuvants. Many adjuvants contain a substance
 25 designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bordetella pertussis, or Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, e.g., Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham,
 30 Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron, or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes;

biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient.

5 This approach is described, for instance, in Wolff et. al. (1990) Science 247:1465-1468, as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivacaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S.
10 Patent No. 5,922,687).

For therapeutic or prophylactic immunization purposes, the peptides of the invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, e.g., as a vector to express nucleotide sequences that encode cancer polypeptides or polypeptide
15 fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover, et al. (1991) Nature 351:456-460. A wide variety of other vectors are available for therapeutic
20 administration or immunization, e.g., adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the like. See, e.g., Shata, et al. (2000) Mol Med Today 6:66-71; Shedlock, et al. (2000) J. Leukoc. Biol. 68:793-806; Hipp, et al. (2000) In Vivo 14:571-85.

Methods for the use of genes as DNA vaccines are well known, and include placing a
25 cancer gene or portion of a cancer gene under the control of a regulatable promoter or a tissue-specific promoter for expression in a cancer patient. The cancer gene used for DNA vaccines can encode full-length cancer proteins, but more preferably encodes portions of the cancer proteins including peptides derived from the cancer protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from a
30 cancer gene. For example, cancer-associated genes or sequence encoding subfragments of a cancer protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure

provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the cancer polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment, cancer genes find use in generating animal models of cancer. When the cancer gene identified is repressed or diminished in cancer tissue, gene therapy technology, e.g., wherein inhibitory or antisense RNA directed to the cancer gene will also diminish or repress expression of the gene. Animal models of cancer find use in screening for modulators of a cancer-associated sequence or modulators of cancer. Similarly, transgenic animal technology, including gene knockout technology, e.g., as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the cancer protein. When desired, tissue-specific expression or knockout of the cancer protein may be necessary.

It is also possible that the cancer protein is overexpressed in cancer. As such, transgenic animals can be generated that overexpress the cancer protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods will find use as animal models of cancer and are additionally useful in screening for modulators to treat cancer.

Kits for Use in Diagnostic and/or Prognostic Applications

For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In diagnostic and research applications, such kits may include at least one of the following: assay reagents, buffers, cancer-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, dominant negative cancer polypeptides or polynucleotides, small molecule inhibitors of cancer-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing instructions (e.g., protocols) for the practice of the methods of this invention. While the instructional materials

typically comprise written or printed materials, they are not limited to such. A medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to, electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may
5 include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of cancer-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: a cancer-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing cancer-associated
10 activity. Optionally, the kit contains biologically active cancer protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will typically be selected based on correlations with important parameters in disease which may be identified in historical or
15 outcome data.

EXAMPLES

Example 1: Gene Chip Analysis

Molecular profiles of various normal and cancerous tissues were determined and
20 analyzed using gene chips. RNA was isolated and gene chip analysis was performed as described (Glynne, et al. (2000) Nature 403:672-676; Zhao, et al. (2000) Genes Dev. 14:981-993).

Table 1 lists medical conditions, abnormalities, or organs affected by disease, referred to in Tables 2A-68, for which markers have been identified, and other related medical conditions (including various stages and/or metastases) in which those markers will also be useful, e.g., in therapeutic, diagnostic, prognostic, subsetting, vaccine, and other uses.

- 5 blood vessels/angiogenesis: hemangiomas, lymphangiomas, wound healing, tissue remodeling, psoriasis, ischemic heart disease, inflammatory diseases (e.g., arthritis, asthma, chronic bronchitis), atherosclerosis, endometriosis, presumed ocular histoplasmosis syndrome, hypoxia, solid tumors, lymphomas, autoimmune diseases (e.g., RA, SLE, juvenile chronic arthritis, pigmented villonodular synovitis, etc.), retinal neovascularization syndromes (e.g., diabetic retinopathy, macular degeneration, presumed ocular histoplasmosis syndrome, etc.), scleritis/conjunctivitis, hypertrophic scars (keloid), birth control, uterine fibroids
- 10 bladder: carcinoma in situ, papillary carcinomas, transitional cell carcinoma
bone marrow: Ewing sarcoma, sarcomas arising from skeletal and extraskelatal connective tissues, including the peripheral nervous system
brain: glioblastoma, oligodendroglioma, anaplastic astrocytoma, meningioma, medulloblastoma, neuroblastoma, ependymoma, schwannoma, craniopharyngioma, pineoblastoma, pineocytoma
breast: ductal carcinoma in situ, lobular carcinoma in situ
cervix: cancer of the cervix, vagina, or vulva
15 colon/rectum: precancerous colorectal disease (e.g., neoplastic polyps (adenomas), familial adenomatous polyposis, ulcerative colitis), colon cancer, e.g., epithelial tumor (e.g., adenocarcinoma, mucinous adenocarcinoma, signet-ring cell adenocarcinoma, squamous cell carcinoma, adenosquamous carcinoma, undifferentiated carcinoma, unclassified carcinoma), carcinoid tumor (e.g., argentaffin, nonargentaffin, composite), non-epithelial tumor (e.g., leiomyosarcoma, others), inflammatory bowel disease (e.g., ulcerative colitis, Crohn's disease (granulomatous colitis), dysplasia), rectal cancer, cancer of the anal region (e.g., squamous cell carcinoma, transitional carcinoma, adenocarcinoma, carcinoma, papillary villous carcinoma, mucinous adenocarcinoma, melanoma)
20 esophagus: premalignant or predisposing conditions (e.g., esophagitis), squamous cell cancers (e.g., cancers of the head and neck, lung, or cervix), gastrointestinal carcinomas (e.g., cancers of the stomach, colon, or rectum)
fibrosis: lung fibrosis (idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, interstitial pneumonitis, nonspecific idiopathic pneumonitis), chronic obstructive pulmonary disease (e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, cirrhosis (liver fibrosis), renal fibrosis, scleroderma, wound healing
head and neck: tumors of the nasal cavity, paranasal sinuses, nasopharynx, oral cavity, oral pharynx, lip, larynx, hypopharynx, salivary glands, paragangliomas, esophagus
25 kidney: clear cell (nonpapillary) carcinoma, papillary carcinoma, chromophobe renal carcinoma, hypernephroma, adenocarcinoma, sporadic renal carcinomas, hereditary renal carcinomas (von Hippel-Lindau disease), carcinoma of the renal pelvis, ureteral carcinoma, fibroma, papillary adenoma, angiosarcoma, oncocytoma
leukocytes: acute lymphoblastic leukemia/lymphoma, malignant transformation of immature, precursor B (pre-B) or precursor T (pre-T) lymphocytes, or lymphoblasts, arthritis, inflammation, wound healing
liver: hepatitis (e.g., types A, B, C), benign epithelial tumors and tumor bile conditions, primary malignant epithelial tumors, primary malignant mesenchymal tumors, tumors of the gallbladder or bile duct
30 lung: lung cancer, small cell lung carcinoma (oat cell carcinoma), non-small cell carcinomas (e.g., squamous cell carcinoma, adenocarcinoma, large cell lung carcinoma, carcinoid, granulomatous), fibrosis (idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, interstitial pneumonitis, nonspecific idiopathic pneumonitis), chronic obstructive pulmonary disease (e.g., emphysema, chronic bronchitis), asthma, bronchiectasis, esophageal cancer
ovary: ovarian carcinoma (e.g., epithelial (serous tumors, mucinous tumors, endometrioid tumors), germ cell (e.g., teratomas, choriocarcinomas, polyembryomas, embryonal carcinoma, endodermal sinus tumor, dysgerminoma, gonadoblastoma), stromal carcinomas (e.g., granulosa stromal cell tumors)), fallopian tube carcinoma, peritoneal carcinoma, leiomyoma
35 pancreas: adenocarcinoma, ductal adenocarcinoma, mucinous cyst adenocarcinoma, acinar cell carcinoma, unclassified large cell carcinoma, small cell carcinoma, pancreatoblastoma, duct-ectatic mucin-hypersecreting tumor, mucinous cyst adenoma, papillary cystic neoplasm, serous cyst adenoma, diabetes mellitus, chronic pancreatitis
prostate: epithelial neoplasms (e.g., adenocarcinoma, small cell tumors, transitional cell carcinoma, carcinoma in situ, and basal cell carcinoma), carcinosarcoma, non-epithelial neoplasms (e.g., mesenchymal and lymphoma), germ cell tumors, prostatic intraepithelial neoplasia (PIN), hormone independent prostate cancer, benign prostate hyperplasia, prostatitis
40 skin/melanoma: melanoma, lentigo (common benign localized hyperplasia of melanocytes), nevocellular nevi (congenital or acquired neoplasm of melanocytes), actinic keratosis (overgrowth of outer layers of skin), basal cell carcinoma, Merkel cell carcinoma, benign fibrous histiocytoma (dermal neoplasms of fibroblasts and histiocytes), dermatofibrosarcoma protuberans (well differentiated fibrosarcoma of the skin), xanthomas (tumor-like collections of foamy histiocytes within the dermis), dermal vascular tumors, seborrheic keratoses (benign tumor), acanthosis nigricans (benign or malignant hyperplasia and hyperpigmentation of skin), and squamous cell carcinomas of the skin, lung, cervix, esophagus, uterus, head, neck, or bladder
45 stomach: adenocarcinoma, squamous cell carcinoma, adenocanthoma, carcinoid, leiomyosarcoma, gastritis (chronic atrophic, H. pylori associated), hyperplastic polyps, lipoma, leiomyoma, esophageal adenocarcinomas
testicles: germ cell tumors (including seminomas, embryonal carcinomas, teratomas, choriocarcinomas, yolk sac tumors), sex chord stromal tumors (including Leydig cell tumors, Sertoli cell tumors, and Granulosa cell tumors), germ cell and gonadal stromal elements (e.g., gonadoblastomas), adnexal and paratesticular tumors (e.g., mesotheliomas, soft tissue sarcomas, and adnexal of the rete testes), miscellaneous neoplasms (including carcinoid, lymphoma, and cysts)
50 uterus: epithelial tumors (e.g., endometrioid, papillary endometrioid, papillary serous, clear cell, mucinous), mesenchymal tumors (e.g., endometrial stromal sarcoma, leiomyosarcoma, nonspecific sarcomas), mixed tumors (e.g., malignant mixed müllerian tumors, adenosarcoma)

55 Tables 2B-66C list accession numbers for Pkeys lacking UnigenelD's for Tables 2A-66C, respectively. For each probeset is listed gene cluster number from which oligonucleotides were designed. Gene clusters were compiled using sequences derived from Genbank ESTs and mRNAs. These sequences were clustered based on sequence similarity using Clustering and Alignment Tools (DoubleTwist, Oakland California). Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

60 Tables 2C-66C list genomic positioning for Pkeys lacking UnigenelD's and accession numbers in Tables 2A-66C, respectively. For each predicted exon is listed genomic sequence source used for prediction. Nucleotide locations of each predicted exon are also listed.

TABLE 2A: ABOUT 1031 GENES UP-REGULATED IN ACUTE LYMPHOCYTIC LEUKEMIA (ALL)

Table 2A lists about 1031 genes up-regulated in acute lymphocytic leukemia (ALL) compared to normal adult tissues. These were selected from 35403 probesets on the Affymetrix/Eos Hu01 GeneChip array such that the ratio of "average" leukemia to "average" normal adult tissues was greater than or equal to 1.7. The "average" leukemia level was set to the 75th percentile amongst various ALL samples. The "average" normal adult tissue level was set to the 85th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 7.5th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
70 UnigenelD: Unigenel number
Unigenel Title: Unigenel gene title
R1: Ratio of leukemia to normal body tissue

| Pkey | ExAcc | UnigenelD | Unigenel Title | R1 |
|--------|-----------|-----------|--|------|
| 100458 | S74019 | Hs.247979 | pre-B lymphocyte gene 1 | 46.8 |
| 113089 | T40707 | Hs.270862 | ESTs | 20.4 |
| 105956 | R06428 | Hs.226351 | ESTs | 15.8 |
| 101447 | M21305 | | gb:Human alpha satellite and satellite 3 | 13.8 |
| 113009 | T23699 | Hs.7246 | ESTs | 12.5 |
| 126947 | Z40778 | Hs.191837 | ESTs | 11.4 |
| 100893 | BE245294 | Hs.180789 | S164 protein | 11.1 |
| 101050 | AU077324 | Hs.1832 | neuropeptide Y | 11.0 |
| 132114 | NM_006152 | Hs.40202 | lymphoid-restricted membrane protein | 10.7 |

| | | | | | |
|----|--------|----------|-----------|---|------|
| 5 | 101304 | AA001021 | Hs.6685 | thyroid hormone receptor interactor 8 | 10.4 |
| | 105667 | AA767526 | Hs.22030 | paired box gene 5 (B-cell lineage specif | 9.1 |
| | 112727 | T91029 | Hs.15069 | ESTs | 9.0 |
| | 109788 | T79971 | Hs.12432 | Homo sapiens clone 24407 mRNA sequence | 8.7 |
| | 113374 | T79925 | Hs.269165 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 7.8 |
| 10 | 130466 | W19744 | Hs.180059 | Homo sapiens cDNA FLJ20553 fs, clone KA | 7.7 |
| | 109384 | AA219172 | Hs.86849 | ESTs | 7.6 |
| | 112602 | AW004045 | Hs.203365 | ESTs | 6.6 |
| | 125278 | A1218439 | Hs.129998 | enhancer of polycomb 1 | 6.5 |
| | 112167 | N99591 | Hs.25587 | ESTs, Weakly similar to T00329 hypothe | 6.4 |
| 15 | 116355 | AA789133 | Hs.88650 | ESTs | 5.8 |
| | 123440 | A1733692 | Hs.112488 | ESTs | 5.5 |
| | 100918 | AK001335 | Hs.31137 | protein tyrosine phosphatase, receptor t | 5.4 |
| | 101879 | AA176374 | Hs.243886 | nuclear autoantigenic sperm protein (his | 5.4 |
| | 109260 | AW978515 | Hs.131915 | KIAA0863 protein | 5.4 |
| 20 | 129213 | A1146494 | Hs.109525 | ESTs, Weakly similar to IROX2_HUMAN IROQU | 5.4 |
| | 120809 | AA346495 | | gb:EST52657 Fetal heart II Homo sapiens | 5.4 |
| | 105498 | H68279 | Hs.24937 | transformer-2 alpha (htra-2 alpha) | 5.1 |
| | 114840 | AA447591 | Hs.87359 | ESTs, Highly similar to RB18_HUMAN RAS-R | 5.0 |
| | 103304 | BE561801 | Hs.2484 | T-cell leukemia/lymphoma 1A | 4.9 |
| 25 | 113983 | W87415 | Hs.55296 | HLA-B associated transcript-1 | 4.8 |
| | 115844 | A1373062 | Hs.332938 | hypothetical protein MGC5370 | 4.8 |
| | 120712 | AF193339 | Hs.102506 | eukaryotic translation initiation factor | 4.8 |
| | 107794 | AA019255 | | gb:ze56e10.s1 Soares retina N2b4HR Homo | 4.7 |
| | 135101 | U82275 | Hs.94498 | leukocyte immunoglobulin-like receptor, | 4.6 |
| 30 | 129898 | A1672731 | Hs.13256 | ESTs | 4.6 |
| | 113494 | T91451 | Hs.86538 | ESTs | 4.6 |
| | 115004 | AA329340 | Hs.4867 | mannosyl (alpha-1,3)-glycoprotein beta- | 4.5 |
| | 113074 | AK001335 | Hs.31137 | protein tyrosine phosphatase, receptor t | 4.5 |
| | 112326 | R55822 | Hs.4268 | ESTs | 4.4 |
| 35 | 105169 | BE245294 | Hs.180789 | S164 protein | 4.4 |
| | 117048 | H89732 | Hs.230113 | EST | 4.3 |
| | 123133 | AA487264 | Hs.154974 | Homo sapiens mRNA; cDNA DKFZp667N064 (fr | 4.3 |
| | 111394 | AA412227 | Hs.16131 | hypothetical protein FLJ12876 | 4.3 |
| | 106112 | AL117518 | Hs.3686 | KIAA0978 protein | 4.2 |
| 40 | 114414 | AW152166 | Hs.182113 | ESTs | 4.2 |
| | 125219 | A1804331 | Hs.99423 | ATP-dependent RNA helicase | 4.2 |
| | 114995 | AA769266 | Hs.193657 | ESTs | 4.2 |
| | 123338 | AA504249 | Hs.187585 | ESTs | 4.1 |
| | 126666 | AA648886 | Hs.151999 | ESTs | 4.1 |
| 45 | 112908 | BE281000 | Hs.3530 | TLS-associated serine-arginine protein 2 | 4.1 |
| | 116640 | X89984 | Hs.211563 | B-cell CLL/lymphoma 7A | 4.0 |
| | 108292 | AW975746 | Hs.188662 | KIAA1702 protein | 4.0 |
| | 131724 | AK001335 | Hs.31137 | protein tyrosine phosphatase, receptor t | 4.0 |
| | 119772 | AJ250839 | Hs.58241 | gene for serine/threonine protein kinase | 4.0 |
| 50 | 134453 | A1272141 | Hs.83484 | SRV (sex determining region Y)-box 4 | 4.0 |
| | 123562 | AA177088 | Hs.190065 | ESTs | 4.0 |
| | 103226 | X75042 | Hs.44313 | v-rel avian reticuloendotheliosis viral | 3.9 |
| | 127610 | AA960867 | Hs.150271 | ESTs, Highly similar to unnamed protein | 3.9 |
| | 119873 | A1660149 | Hs.44865 | lymphoid enhancer-binding factor 1 | 3.9 |
| 55 | 115553 | AJ275986 | Hs.71414 | transcription factor (SMIF gene) | 3.9 |
| | 131844 | A1419294 | Hs.324342 | ESTs | 3.8 |
| | 123360 | AA532718 | Hs.178604 | ESTs | 3.8 |
| | 111180 | A1798851 | Hs.283108 | hemoglobin, gamma G | 3.8 |
| | 129426 | AF077953 | Hs.111323 | Protein inhibitor of activated STAT X | 3.8 |
| 60 | 105434 | AA252111 | Hs.15200 | ESTs | 3.8 |
| | 119073 | BE245360 | Hs.279477 | ESTs | 3.8 |
| | 127003 | AW816515 | Hs.173540 | ATPase, Class V, type 10D | 3.7 |
| | 119325 | T51136 | Hs.90489 | ESTs | 3.7 |
| | 115998 | AA448488 | Hs.336629 | ribosomal protein L44 | 3.7 |
| 65 | 119830 | AW054922 | Hs.53478 | Homo sapiens cDNA FLJ12366 fs, clone MA | 3.7 |
| | 104584 | AA704538 | Hs.193777 | ESTs | 3.6 |
| | 105212 | AA205334 | Hs.324278 | Homo sapiens mRNA; cDNA DKFZp566M063 (f | 3.6 |
| | 109223 | AW000714 | Hs.65818 | ESTs | 3.6 |
| | 112605 | R79374 | Hs.29852 | ESTs | 3.5 |
| 70 | 105733 | AA767669 | Hs.10242 | ESTs | 3.5 |
| | 120562 | BE244580 | Hs.302267 | hypothetical protein FLJ10330 | 3.5 |
| | 112268 | W39609 | Hs.22003 | solute carrier family 6 (neurotransmitte | 3.5 |
| | 127834 | AW301022 | Hs.337631 | EST | 3.5 |
| | 115147 | AA745781 | Hs.38399 | hypothetical protein MGC2454 | 3.5 |
| 75 | 115185 | BE299677 | Hs.105461 | hypothetical protein FLJ20357 | 3.5 |
| | 113921 | AW978530 | Hs.28355 | hypothetical protein FLJ22402 | 3.5 |
| | 115835 | AA521410 | Hs.41371 | ESTs | 3.5 |
| | 123503 | AW975051 | Hs.293156 | ESTs, Weakly similar to I78885 serine/th | 3.5 |
| | 128527 | AA504583 | Hs.101047 | transcription factor 3 (E2A immunoglobul | 3.4 |
| 80 | 128743 | R44284 | Hs.2730 | heterogeneous nuclear ribonucleoprotein | 3.4 |
| | 117031 | H88353 | | gb:yy21a02.s1 Morton Fetal Cochlea Homo | 3.4 |
| | 123149 | A1734179 | Hs.105676 | ESTs | 3.4 |
| | 102581 | AU077228 | Hs.77256 | enhancer of zeste (Drosophila) homolog 2 | 3.4 |
| | 103158 | BE242587 | Hs.118651 | hematopoietically expressed homeobox | 3.4 |
| | 107599 | AW664072 | Hs.60136 | ESTs | 3.4 |
| | 125556 | AB033064 | Hs.334806 | KIAA1238 protein | 3.4 |
| | 103331 | A1825463 | Hs.147996 | protein kinase, X-linked | 3.4 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 114387 | AI655141 | Hs.107720 | ESTs, Weakly similar to A54295 inter | 3.4 |
| | 119040 | R02394 | Hs.269436 | ESTs, Moderately similar to PC4259 ferri | 3.4 |
| | 100305 | NM_004941 | Hs.171872 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypep | 3.4 |
| 5 | 129818 | T71092 | Hs.172572 | hypothetical protein FLJ20093 | 3.3 |
| | 133445 | AC005262 | Hs.73797 | guanine nucleotide binding protein (G pr | 3.3 |
| | 132111 | AW500857 | Hs.40137 | anaphase-promoting complex 1; meiotic ch | 3.3 |
| | 105292 | AF128542 | Hs.166846 | polymerase (DNA directed), epsilon | 3.3 |
| | 118397 | BE139479 | Hs.161492 | ESTs | 3.3 |
| 10 | 118922 | AW205193 | Hs.91065 | hypothetical protein DKFZp761B2423 | 3.2 |
| | 132344 | AW977189 | Hs.45719 | KIAA0823 protein | 3.2 |
| | 129889 | AA810932 | Hs.131899 | ESTs, Weakly similar to T00370 hypothe | 3.2 |
| | 123670 | AI189844 | Hs.112708 | ESTs, Moderately similar to ZN91_HUMAN Z | 3.2 |
| | 116291 | AW410377 | Hs.41502 | hypothetical protein FLJ21276 | 3.2 |
| 15 | 105289 | AB020638 | Hs.103000 | KIAA0831 protein | 3.2 |
| | 105583 | AA278907 | Hs.3530 | TLS-associated serine-arginine protein | 3.2 |
| | 104796 | BE620712 | Hs.33026 | hypothetical protein PP2447 | 3.2 |
| | 111657 | R07364 | Hs.268667 | ESTs, Weakly similar to ALU1_HUMAN ALU | 3.2 |
| | 134174 | AF283770 | Hs.79530 | CD79A antigen (immunoglobulin-associated | 3.2 |
| 20 | 126077 | M78772 | Hs.210836 | ESTs | 3.1 |
| | 133733 | AK000476 | Hs.75798 | hypothetical protein | 3.1 |
| | 124847 | W07701 | Hs.304177 | Homo sapiens clone FLB8503 PRO2286 mRNA, | 3.1 |
| | 127879 | AA768098 | Hs.189079 | ESTs | 3.1 |
| | 113108 | AW516695 | Hs.8438 | ESTs | 3.1 |
| 25 | 110343 | AW136703 | Hs.17268 | ESTs | 3.1 |
| | 102935 | BE561850 | Hs.80506 | small nuclear ribonucleoprotein polypept | 3.1 |
| | 111676 | AB040882 | Hs.109778 | KIAA1449 protein | 3.1 |
| | 127311 | AA492582 | Hs.322404 | hypothetical protein MGC4175 | 3.1 |
| | 108830 | AA131743 | Hs.193352 | ESTs | 3.1 |
| 30 | 111330 | BE247767 | Hs.18166 | KIAA0870 protein | 3.1 |
| | 104246 | AF016032 | Hs.201377 | lysosomal apyrase-like 1 | 3.1 |
| | 126568 | AA011616 | Hs.269877 | ESTs | 3.1 |
| | 124724 | H20816 | Hs.112423 | Homo sapiens mRNA; cDNA DKFZp586i1420 (f | 3.1 |
| | 114794 | AI751157 | Hs.101395 | hypothetical protein MGC11352 | 3.1 |
| 35 | 134599 | X99226 | Hs.284153 | Fanconi anemia, complementation group A | 3.0 |
| | 130314 | NM_014674 | Hs.154332 | KIAA0212 gene product | 3.0 |
| | 100265 | O38521 | Hs.112396 | KIAA0077 protein | 3.0 |
| | 115005 | AI760825 | Hs.111339 | ESTs | 3.0 |
| | 123433 | AW450922 | Hs.112478 | ESTs | 3.0 |
| 40 | 127798 | AA737068 | Hs.294078 | ESTs | 3.0 |
| | 117403 | H84455 | Hs.40639 | ESTs | 3.0 |
| | 107111 | AI298448 | Hs.22670 | chromodomain helicase DNA binding protei | 3.0 |
| | 105898 | AW957300 | Hs.294142 | ESTs, Weakly similar to C55663 oligodend | 3.0 |
| | 108358 | M81933 | Hs.1634 | cell division cycle 25A | 3.0 |
| 45 | 132066 | AI929392 | Hs.181195 | DnaJ (Hsp40) homolog, subfamily B, membe | 2.9 |
| | 130303 | BE245294 | Hs.180789 | S164 protein | 2.9 |
| | 104596 | AF067804 | Hs.15423 | hypothetical protein HDCMC04P | 2.9 |
| | 112197 | NM_003655 | Hs.5637 | ESTs | 2.9 |
| | 132809 | AF036144 | Hs.5734 | meningioma expressed antigen 5 (hyaluron | 2.9 |
| 50 | 100877 | X80821 | Hs.27973 | KIAA0874 protein | 2.9 |
| | 108147 | AI972094 | Hs.286221 | Homo sapiens cDNA FLJ13741 fis, clone PL | 2.9 |
| | 133674 | AW851121 | Hs.75497 | Homo sapiens cDNA: FLJ22139 fis, clone H | 2.9 |
| | 129001 | AA443323 | Hs.107812 | BPOZ protein | 2.9 |
| | 131920 | BE002320 | Hs.287864 | Homo sapiens cDNA FLJ14030 fis, clone HE | 2.9 |
| 55 | 134709 | NM_006290 | Hs.211600 | tumor necrosis factor, alpha-induced pro | 2.8 |
| | 113577 | AI300699 | Hs.278937 | PRO0470 protein | 2.8 |
| | 115839 | BE300266 | Hs.28935 | transducin-like enhancer of split 1, hom | 2.8 |
| | 129969 | N57818 | Hs.103315 | gb:yy59d07.s1 Soares fetal liver spleen | 2.8 |
| | 128659 | AW630087 | Hs.103315 | trinucleotide repeat containing 1 | 2.8 |
| 60 | 105011 | BE091926 | Hs.16244 | mitotic spindle coiled-coil related prot | 2.8 |
| | 129294 | AF172940 | Hs.184542 | CGI-127 protein | 2.8 |
| | 104518 | H20816 | Hs.112423 | Homo sapiens mRNA; cDNA DKFZp586i1420 (f | 2.7 |
| | 107796 | AA058848 | Hs.60797 | ESTs | 2.7 |
| | 106331 | AB037742 | Hs.24336 | KIAA1321 protein | 2.7 |
| | 127692 | AI021912 | Hs.187983 | ESTs | 2.7 |
| 65 | 131916 | AA025976 | Hs.34569 | ESTs | 2.7 |
| | 124971 | T23900 | Hs.151001 | hypothetical protein FLJ14728 | 2.7 |
| | 129428 | AA256906 | Hs.111364 | ESTs, Weakly similar to ubiquitous TPR m | 2.7 |
| | 118348 | AW408586 | Hs.91052 | ESTs, Moderately similar to ALU5_HUMAN A | 2.7 |
| 70 | 113219 | T59257 | Hs.269528 | ESTs, Moderately similar to ALU8_HUMAN A | 2.7 |
| | 131720 | Z68128 | Hs.3109 | Rho GTPase activating protein 4 | 2.7 |
| | 109593 | AW196801 | Hs.6685 | thyroid hormone receptor interactor 8 | 2.7 |
| | 135359 | AF043722 | Hs.99491 | RAS guanyl releasing protein 2 (calcium | 2.7 |
| | 131689 | AB012124 | Hs.30696 | transcription factor-like 5 (basic helix | 2.7 |
| 75 | 117457 | N29682 | Hs.44071 | ESTs, Weakly similar to ALU5_HUMAN ALU | 2.7 |
| | 121073 | H46199 | Hs.112184 | DKFZP586J0619 protein | 2.7 |
| | 125069 | H81306 | Hs.194485 | ESTs | 2.7 |
| | 116456 | AI381911 | Hs.334859 | KIAA1814 protein | 2.7 |
| 80 | 124271 | AW293223 | Hs.8928 | hypothetical protein FLJ20291 | 2.7 |
| | 112369 | AW966243 | Hs.4243 | hypothetical protein FLJ12650 | 2.7 |
| | 115866 | AW062629 | Hs.52081 | KIAA0867 protein | 2.7 |
| | 132543 | BE568452 | Hs.5101 | protein regulator of cytokinesis 1 | 2.7 |
| | 124494 | N54831 | Hs.271381 | ESTs, Weakly similar to I380222 hypothet | 2.7 |
| | 104799 | AA029703 | | gb:ze95h08.s1 Soares_fetal_heart_NbHH19w | 2.7 |

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|----|--------|-----------|-----------|--|-----|
| | 120510 | AI796395 | Hs.111377 | ESTs | 2.6 |
| | 129781 | AA306090 | Hs.124707 | ESTs | 2.6 |
| | 122698 | AA456112 | Hs.99410 | ESTs | 2.6 |
| 5 | 106995 | AB023139 | Hs.37892 | KIAA0922 protein | 2.6 |
| | 105502 | BE464016 | Hs.238956 | ESTs | 2.6 |
| | 128671 | AI885045 | Hs.211586 | phosphoinositide-3-kinase, regulatory s | 2.6 |
| | 107059 | BE614410 | Hs.23044 | RAD51 (S. cerevisiae) homolog (E coli Re | 2.6 |
| 10 | 126502 | T10077 | Hs.13453 | hypothetical protein FLJ14753 | 2.6 |
| | 129703 | BE388665 | Hs.179999 | Homo sapiens, clone IMAGE:3457003, mRNA | 2.6 |
| | 111219 | N68836 | Hs.19247 | ESTs, Moderately similar to ALUC_HUMAN | 2.6 |
| | 133529 | W45623 | Hs.74571 | ADP-ribosylation factor 1 | 2.6 |
| | 125626 | AI038854 | Hs.180789 | S164 protein | 2.6 |
| | 111189 | N67603 | Hs.272130 | ESTs, Weakly similar to S65824 reverse | 2.6 |
| 15 | 113146 | BE151985 | Hs.5722 | hypothetical protein FLJ23316 | 2.6 |
| | 125562 | AI494372 | Hs.98958 | hypothetical protein FLJ23058 | 2.6 |
| | 102263 | U29171 | Hs.75852 | casein kinase 1, delta | 2.6 |
| | 118835 | AA535246 | Hs.50852 | ESTs | 2.6 |
| | 103141 | X66113 | Hs.75584 | polymyositis/scleroderma autoantigen 2 (| 2.6 |
| 20 | 109598 | R40515 | Hs.21248 | ESTs | 2.6 |
| | 127262 | AA828125 | | gb:cd71a09.s1 NCL_CGAP_Ov2 Homo sapiens | 2.6 |
| | 129620 | D79338 | Hs.239720 | CCR4-NOT transcription complex, subunit | 2.6 |
| | 125905 | AI678638 | Hs.6456 | chaperonin containing TCP1, subunit 2 (b | 2.6 |
| | 123255 | AA830335 | Hs.105273 | ESTs | 2.6 |
| 25 | 133160 | N54968 | Hs.66309 | hypothetical protein MGC11061 | 2.6 |
| | 109638 | AW977747 | Hs.119120 | E3 ubiquitin ligase SMURF1 | 2.6 |
| | 119896 | AA731836 | Hs.137319 | ESTs | 2.6 |
| | 134770 | M89957 | Hs.89575 | CD79B antigen (immunoglobulin-associated | 2.6 |
| | 119403 | AL117554 | Hs.119908 | nucleolar protein NOP5/NOP58 | 2.6 |
| 30 | 129563 | AF119664 | Hs.27299 | transcriptional regulator protein | 2.6 |
| | 111719 | AI655806 | Hs.179262 | ESTs | 2.6 |
| | 103982 | AA218558 | Hs.7905 | sorting nexin 9 | 2.6 |
| | 125032 | T74884 | | gb:yc58d02.s1 Stratagene liver (937224) | 2.5 |
| 35 | 131426 | AL122045 | Hs.26703 | CCR4-NOT transcription complex, subunit | 2.5 |
| | 131938 | AF176085 | Hs.34956 | neural polypyrimidine tract binding prot | 2.5 |
| | 102450 | U48251 | Hs.75871 | protein kinase C binding protein 1 | 2.5 |
| | 133761 | AF041430 | Hs.75922 | brain protein I3 | 2.5 |
| | 126339 | AA152106 | Hs.4859 | cyclin L ania-6a | 2.5 |
| | 118967 | AI668670 | Hs.216756 | ESTs | 2.5 |
| 40 | 123110 | AA486256 | Hs.193510 | EST | 2.5 |
| | 114092 | H81213 | Hs.14825 | ESTs, Weakly similar to KIAA1503 protein | 2.5 |
| | 113247 | T63856 | Hs.193430 | ESTs, Weakly similar to 2109260A B cell | 2.5 |
| | 122024 | AA431296 | Hs.139433 | ESTs | 2.5 |
| | 106657 | AW854339 | Hs.33476 | hypothetical protein FLJ11937 | 2.5 |
| 45 | 126127 | N95428 | | gb:zb80d09.s1 Soares_senescent_fibroblas | 2.5 |
| | 111836 | R58394 | Hs.25119 | ESTs, Weakly similar to YEX0_YEAST HYPOT | 2.5 |
| | 121470 | AA558958 | Hs.324751 | ESTs | 2.5 |
| | 120132 | W57554 | Hs.125019 | ESTs | 2.5 |
| | 107731 | AA016086 | Hs.272106 | ESTs, Weakly similar to I38022 hypothe | 2.5 |
| | 118122 | AI186671 | Hs.48008 | ESTs | 2.5 |
| 50 | 106589 | AK000933 | Hs.28561 | Homo sapiens cDNA FLJ10071 fis, clone HE | 2.5 |
| | 129948 | AI537162 | Hs.263988 | ESTs | 2.5 |
| | 115652 | BE093589 | Hs.38178 | hypothetical protein FLJ23468 | 2.5 |
| | 103076 | NM_001034 | Hs.75319 | ribonucleotide reductase M2 polypeptide | 2.5 |
| 55 | 131019 | W28614 | Hs.306155 | chorionic somatomammotropin hormone 1 (p | 2.5 |
| | 100512 | D13317 | Hs.78915 | GA-binding protein transcription factor, | 2.5 |
| | 105393 | AF167570 | Hs.256583 | interleukin enhancer binding factor 3, 9 | 2.5 |
| | 100571 | L14561 | Hs.78546 | ATPase, Ca++ transporting, plasma membra | 2.5 |
| | 106890 | AA489245 | Hs.88500 | mitogen-activated protein kinase 8 inte | 2.5 |
| 60 | 104276 | AW965275 | Hs.284288 | hsp0256 protein | 2.5 |
| | 113283 | T66813 | Hs.12947 | EST | 2.5 |
| | 118078 | N54321 | Hs.47790 | EST | 2.5 |
| | 120796 | AI247356 | Hs.96820 | ESTs | 2.5 |
| | 106265 | AA412176 | Hs.236463 | Homo sapiens mRNA; cDNA DKFZp586l0521 (f | 2.5 |
| 65 | 102507 | U52154 | Hs.193044 | potassium inwardly-rectifying channel, s | 2.5 |
| | 106508 | AI205785 | Hs.30348 | ESTs | 2.5 |
| | 104568 | AW629981 | Hs.172182 | poly(A)-binding protein, cytoplasmic 1 | 2.5 |
| | 103698 | AA001021 | Hs.6685 | thyroid hormone receptor interactor 8 | 2.5 |
| | 113947 | W84768 | | gb:zh53d03.s1 Soares_fetal_liver_spleen_ | 2.5 |
| 70 | 132112 | AL021938 | Hs.40154 | jumonji (mouse) homolog | 2.5 |
| | 129052 | BE275031 | Hs.158210 | hypothetical protein MGC2555 | 2.4 |
| | 117265 | AA451966 | Hs.43005 | RAB9-like protein | 2.4 |
| | 107834 | AA253162 | Hs.40838 | ESTs | 2.4 |
| | 113119 | T47910 | | gb:yb18b11.s1 Stratagene fetal spleen (9 | 2.4 |
| 75 | 133726 | AI803188 | Hs.252716 | oxysterol-binding protein-related protei | 2.4 |
| | 120548 | AA280356 | Hs.187634 | ESTs | 2.4 |
| | 121545 | AA412442 | Hs.98132 | ESTs | 2.4 |
| | 131136 | AB033099 | Hs.23413 | KIAA1273 protein | 2.4 |
| | 126589 | AW027809 | Hs.187698 | Homo sapiens cytomegalovirus partial fus | 2.4 |
| 80 | 115475 | AB033085 | Hs.40193 | hypothetical protein KIAA1259 | 2.4 |
| | 103760 | AA642973 | Hs.183842 | ubiquitin B | 2.4 |
| | 127889 | AI147408 | Hs.144941 | ESTs | 2.4 |
| | 124457 | AK000680 | Hs.265175 | phosphoprotein associated with GEMs | 2.4 |
| | 113721 | AF143885 | Hs.18190 | EST | 2.4 |

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|----|--------|-----------|-----------|---|-----|
| | 129079 | AK000157 | Hs.108502 | hypothetical protein FLJ20150 | 2.4 |
| | 123530 | AA608705 | Hs.187772 | ESTs | 2.4 |
| | 123592 | AA805331 | Hs.112637 | ESTs | 2.4 |
| 5 | 113474 | R50752 | Hs.23856 | hypothetical protein MGC5297 | 2.4 |
| | 116728 | F13687 | Hs.227976 | EST | 2.4 |
| | 101759 | M80244 | Hs.184601 | solute carrier family 7 (cationic amino | 2.4 |
| | 131686 | NM_012296 | Hs.30687 | GRB2-associated binding protein 2 | 2.4 |
| | 127841 | AW136558 | Hs.125246 | ESTs | 2.4 |
| 10 | 102737 | R51790 | Hs.239483 | Human clone 23933 mRNA sequence | 2.4 |
| | 129573 | D38552 | Hs.1191 | KIAA0073 protein | 2.4 |
| | 133095 | BE046490 | Hs.180677 | zinc finger protein 162 | 2.4 |
| | 124540 | N63232 | | gb:yz39a12.s1 Morton Fetal Cochlea Homo | 2.4 |
| | 113609 | T93263 | Hs.16875 | ESTs, Weakly similar to S23650 retrovir | 2.4 |
| 15 | 128826 | Z40313 | Hs.106330 | Homo sapiens clone IMAGE:23371, mRNA seq | 2.4 |
| | 129059 | AW069534 | Hs.279583 | CGI-81 protein | 2.4 |
| | 134092 | AA218558 | Hs.7905 | sorting nexin 9 | 2.4 |
| | 132317 | BE262438 | Hs.44592 | beta-1,4 mannosyltransferase | 2.4 |
| | 135278 | AA399542 | Hs.229671 | EST, Moderately similar to PEPTIDYL-PROL | 2.4 |
| 20 | 128468 | T23625 | Hs.150580 | putative translation initiation factor | 2.4 |
| | 127407 | AW089514 | Hs.279681 | heterogeneous nuclear ribonucleoprotein | 2.4 |
| | 132342 | AW162758 | Hs.45232 | ESTs, Weakly similar to ALU5_HUMAN ALU S | 2.4 |
| | 113518 | AW367788 | Hs.323954 | postmeiotic segregation increased 2-lik | 2.4 |
| | 100330 | AW410976 | Hs.77152 | minichromosome maintenance deficient (S. | 2.4 |
| 25 | 116046 | BE395293 | Hs.94491 | hypothetical protein FLJ20297 | 2.4 |
| | 123910 | AA621262 | Hs.179923 | ESTs, Weakly similar to S65657 alpha-1C- | 2.4 |
| | 101651 | AL037111 | Hs.75641 | galactose-1-phosphate uridylyltransferase | 2.4 |
| | 100114 | X02308 | Hs.82962 | thymidylate synthetase | 2.4 |
| | 125038 | AA812234 | Hs.270134 | hypothetical protein FLJ20280 | 2.4 |
| 30 | 135191 | X16866 | Hs.301086 | cytochrome P450, subfamily IID (debrisoq | 2.4 |
| | 123258 | AA490929 | Hs.105274 | ESTs, Weakly similar to RMS1_HUMAN REGUL | 2.4 |
| | 132380 | AW373665 | Hs.46853 | ESTs | 2.4 |
| | 114046 | BE018658 | Hs.141003 | Homo sapiens cDNA: FLJ21691 fis, clone C | 2.3 |
| | 133582 | BE391579 | Hs.75087 | Fas-activated serine/threonine kinase | 2.3 |
| 35 | 134839 | D63479 | Hs.115907 | diacylglycerol kinase, delta (130kD) | 2.3 |
| | 105734 | AI952797 | Hs.10888 | hypothetical protein FLJ21709 | 2.3 |
| | 101086 | AA382524 | Hs.250959 | histatin 1 | 2.3 |
| | 118349 | N63786 | Hs.94149 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.3 |
| | 101194 | L20971 | Hs.188 | phosphodiesterase 4B, cAMP-specific (dun | 2.3 |
| 40 | 130588 | AL030996 | Hs.16411 | hypothetical protein LOC57187 | 2.3 |
| | 101875 | BE241753 | Hs.74592 | special AT-rich sequence binding protein | 2.3 |
| | 118751 | N74210 | Hs.50454 | ESTs | 2.3 |
| | 125174 | W51835 | Hs.231082 | EST | 2.3 |
| | 105966 | AA142984 | Hs.5344 | adaptor-related protein complex 1, gamma | 2.3 |
| 45 | 104624 | AA353125 | Hs.184721 | ESTs | 2.3 |
| | 131263 | AU077002 | Hs.24950 | regulator of G-protein signalling 5 | 2.3 |
| | 105014 | AA121123 | Hs.269267 | ESTs, Weakly similar to AF161361 1 HSPC | 2.3 |
| | 123423 | AA598484 | | gb:ae3804.s1 Gessler Wilms tumor Homo s | 2.3 |
| | 128531 | H03721 | Hs.2953 | ribosomal protein S15a | 2.3 |
| 50 | 108876 | AI733860 | Hs.191453 | ESTs | 2.3 |
| | 130216 | BE301883 | Hs.152707 | glioblastoma amplified sequence | 2.3 |
| | 132232 | AI522273 | Hs.42640 | ESTs | 2.3 |
| | 132664 | AI740461 | Hs.54542 | ESTs | 2.3 |
| 55 | 105991 | AA215701 | Hs.186541 | ESTs, Weakly similar to I38022 hypotheti | 2.3 |
| | 100253 | D38024 | Hs.157425 | double homeobox, 2 | 2.3 |
| | 105574 | AA045281 | Hs.266175 | phosphoprotein associated with GEMs | 2.3 |
| | 100780 | BE561958 | Hs.302063 | immunoglobulin heavy constant mu | 2.3 |
| | 134964 | AI803516 | Hs.272891 | hippocalcin-like protein 4 | 2.3 |
| | 132786 | BE083422 | Hs.56851 | hypothetical protein MGC2668 | 2.3 |
| 60 | 104952 | AW076098 | Hs.74316 | desmoplakin (DPI, DPII) | 2.3 |
| | 119127 | AA708035 | Hs.12248 | ESTs | 2.3 |
| | 104857 | AI920902 | Hs.19058 | ESTs, Moderately similar to S65657 alpha | 2.3 |
| | 107592 | AA694264 | Hs.60049 | ESTs | 2.3 |
| | 113378 | T80738 | Hs.14757 | ESTs | 2.3 |
| 65 | 129228 | U40714 | Hs.239307 | tyrosyl-tRNA synthetase | 2.3 |
| | 106898 | AA490069 | Hs.305676 | Homo sapiens cDNA FLJ14302 fis, clone PL | 2.3 |
| | 130734 | AW137091 | Hs.18624 | KIAA1052 protein | 2.3 |
| | 125728 | AW954565 | Hs.57987 | B-cell CLL/lymphoma 11B (zinc finger pro | 2.3 |
| | 113697 | T97183 | Hs.17992 | Homo sapiens mRNA; cDNA DKFZp434J1726 (f | 2.3 |
| 70 | 107104 | AU076640 | Hs.15243 | nucleolar protein 1 (120kD) | 2.3 |
| | 134267 | AI174596 | Hs.196209 | RAE1 (RNA export 1, S.pombe) homolog | 2.3 |
| | 105777 | R42755 | Hs.23096 | ESTs | 2.3 |
| | 115306 | AA280288 | Hs.88746 | ESTs | 2.3 |
| | 133363 | AI866286 | Hs.71962 | ESTs, Weakly similar to B36298 proline-r | 2.3 |
| 75 | 129535 | AA397972 | Hs.169965 | chimerin (chimaerin) 1 | 2.3 |
| | 121520 | AA412163 | Hs.164785 | ESTs | 2.3 |
| | 123808 | AA620552 | | gb:ae58g11.s1 Stratagene lung carcinoma | 2.3 |
| | 105700 | AW580830 | Hs.35254 | hypothetical protein FLB6421 | 2.3 |
| | 120820 | AA347417 | Hs.96869 | EST | 2.3 |
| 80 | 128721 | AW403911 | Hs.266175 | phosphoprotein associated with GEMs | 2.3 |
| | 107711 | W96141 | Hs.220687 | ESTs | 2.3 |
| | 102564 | U59423 | Hs.79067 | MAD (mothers against decapentaplegic, Dr | 2.3 |
| | 131868 | AW408296 | Hs.33532 | zinc finger protein 151 (pHZ-67) | 2.3 |
| | 122333 | AA625872 | Hs.98977 | ESTs, Moderately similar to T34561 hypot | 2.3 |

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|----|--------|-----------|-----------|--|-----|
| | 118865 | AA736405 | Hs.54530 | ESTs | 2.3 |
| | 128952 | AL043463 | Hs.6755 | RaP2 interacting protein 8 | 2.3 |
| | 133772 | BE379867 | Hs.76038 | isopentenyl-diphosphate delta isomerase | 2.3 |
| 5 | 111795 | AI435437 | Hs.24567 | ESTs, Weakly similar to KBF3_HUMAN NUCL | 2.3 |
| | 103437 | AV655598 | Hs.184211 | peptidase (mitochondrial processing) bet | 2.3 |
| | 123060 | AA482027 | Hs.142569 | ESTs, Weakly similar to I38022 hypothe | 2.3 |
| | 125466 | R08234 | Hs.180461 | ESTs | 2.3 |
| | 100892 | BE245294 | Hs.180789 | S164 protein | 2.3 |
| 10 | 121613 | AA416879 | Hs.193195 | ESTs, Weakly similar to 2109260A B cell | 2.3 |
| | 133665 | AL036883 | Hs.75450 | della sleep inducing peptide, immunoreac | 2.2 |
| | 129248 | W04606 | Hs.171637 | hypothetical protein MGC2628 | 2.2 |
| | 126153 | H85692 | Hs.40730 | ESTs | 2.2 |
| | 125590 | R23858 | Hs.143375 | Homo sapiens, clone IMAGE:3840937, mRNA, | 2.2 |
| 15 | 104960 | AA558677 | Hs.8928 | hypothetical protein FLJ20291 | 2.2 |
| | 113941 | AA531016 | Hs.22399 | hypothetical protein FLJ14824 | 2.2 |
| | 112540 | R69751 | | gb:yl40a10.s1 Soares placenta Nb2HP Homo | 2.2 |
| | 105322 | T87179 | Hs.16346 | ESTs, Weakly similar to S57447 HPBRIL-7 | 2.2 |
| | 112003 | AW978731 | Hs.301824 | hypothetical protein PRO1331 | 2.2 |
| 20 | 134733 | N87353 | Hs.89421 | CBF1 interacting corepressor | 2.2 |
| | 114620 | AA642974 | | gb:nr60h01.s1 NCL_CGAP_Tym3 Homo sapiens | 2.2 |
| | 123451 | AI793211 | Hs.165372 | ESTs, Moderately similar to ALU1_HUMAN A | 2.2 |
| | 130850 | AB040922 | Hs.20237 | DKFZP566C134 protein | 2.2 |
| | 105561 | AA262881 | Hs.323836 | ESTs, Weakly similar to alternatively s | 2.2 |
| 25 | 125957 | H41694 | | gb:yo06b06.r1 Soares adult brain N2b5HB5 | 2.2 |
| | 130362 | BE513050 | Hs.279681 | heterogeneous nuclear ribonucleoprotein | 2.2 |
| | 122682 | AA984531 | Hs.159293 | ESTs | 2.2 |
| | 124250 | AA350256 | Hs.323875 | EST, Weakly similar to 2109260A B cell | 2.2 |
| | 131392 | AA235153 | Hs.26320 | TRABID protein | 2.2 |
| 30 | 128845 | AW503976 | Hs.10649 | basement membrane-induced gene | 2.2 |
| | 130453 | U80735 | Hs.173854 | PAX transcription activation domain inte | 2.2 |
| | 126973 | W46653 | Hs.251928 | nuclear pore complex interacting protein | 2.2 |
| | 103156 | BE259039 | Hs.129953 | Ewing sarcoma breakpoint region 1 | 2.2 |
| | 103163 | AIJ077018 | Hs.3235 | keratin 4 | 2.2 |
| 35 | 109252 | BE440157 | Hs.85944 | ESTs | 2.2 |
| | 131163 | AA099524 | Hs.23754 | ESTs | 2.2 |
| | 115292 | AA279956 | Hs.88672 | ESTs | 2.2 |
| | 122591 | AI188219 | Hs.99311 | ESTs, Weakly similar to H5J2_HUMAN DNAB | 2.2 |
| | 124977 | F04819 | Hs.190452 | KIAA0365 gene product | 2.2 |
| 40 | 103319 | X83492 | Hs.82359 | tumor necrosis factor receptor superfam | 2.2 |
| | 100370 | D79989 | Hs.184884 | KIAA0167 gene product | 2.2 |
| | 128992 | H04150 | Hs.107708 | ESTs | 2.2 |
| | 129928 | AI338993 | Hs.134535 | ESTs | 2.2 |
| | 108451 | AA079195 | | gb:zm92h12.s1 Stratagene ovarian cancer | 2.2 |
| 45 | 133910 | AW835281 | Hs.77500 | ubiquitin specific protease 4 (proto-onc | 2.2 |
| | 106288 | AB037742 | Hs.24336 | KIAA1321 protein | 2.2 |
| | 134125 | NM_014781 | Hs.50421 | KIAA0203 gene product | 2.2 |
| | 101379 | X02994 | Hs.1217 | adenosine deaminase | 2.2 |
| | 112276 | R53442 | Hs.26038 | ESTs, Weakly similar to I38022 hypothe | 2.2 |
| 50 | 106251 | R12607 | Hs.35101 | proline-rich Gla (G-carboxyglutamic acid | 2.2 |
| | 125394 | BE178502 | Hs.173772 | ESTs, Weakly similar to I78885 serine/th | 2.2 |
| | 103392 | X94563 | | gb:H.sapiens dbi/acbp gene exon 1 & 2 | 2.2 |
| | 112853 | T02843 | | gb:FB11H5 Fetal brain, Stratagene Homo s | 2.2 |
| | 133195 | AI434760 | Hs.279949 | KIAA1007 protein | 2.2 |
| 55 | 135060 | AK001887 | Hs.259842 | protein kinase, AMP-activated, gamma 2 n | 2.2 |
| | 131381 | M92642 | Hs.26208 | collagen, type XVI, alpha 1 | 2.2 |
| | 134104 | L35253 | Hs.79107 | mitogen-activated protein kinase 14 | 2.2 |
| | 105225 | AA211777 | | gb:zn57d02.s1 Stratagene muscle 937209 H | 2.2 |
| | 131320 | AA505691 | Hs.145696 | splicing factor (CC1.3) | 2.2 |
| 60 | 114419 | AI248013 | Hs.106532 | ESTs, Weakly similar to I38588 reverse t | 2.2 |
| | 103634 | BE541733 | Hs.180877 | H3 histone, family 3B (H3.3B) | 2.2 |
| | 134624 | AF035119 | Hs.8700 | deleted in liver cancer 1 | 2.2 |
| | 126524 | Z45455 | Hs.182447 | heterogeneous nuclear ribonucleoprotein | 2.2 |
| | 115556 | AL031778 | Hs.797 | nuclear transcription factor Y, alpha | 2.2 |
| 65 | 111898 | R38944 | Hs.183475 | Homo sapiens clone 25061 mRNA sequence | 2.2 |
| | 100415 | D86970 | Hs.75822 | TGFB1-induced anti-apoptotic factor 1 | 2.2 |
| | 103898 | AA248884 | | gb:k3517.seq.F Human fetal heart, Lambda | 2.2 |
| | 129501 | AI631811 | Hs.180403 | STRIN protein | 2.2 |
| | 127251 | AA936428 | Hs.128638 | ESTs | 2.2 |
| 70 | 100613 | X52078 | Hs.101047 | transcription factor 3 (E2A immunoglobul | 2.2 |
| | 116332 | AA491208 | Hs.62620 | chromosome 6 open reading frame 1 | 2.2 |
| | 128897 | AW979134 | Hs.10700 | hypothetical protein | 2.2 |
| | 111777 | AK001100 | Hs.41690 | desmocolin 3 | 2.2 |
| | 128804 | AI879099 | Hs.102397 | GIOT-3 for gonadotropin inducible transc | 2.2 |
| 75 | 125585 | AW298113 | Hs.92909 | SON DNA binding protein | 2.2 |
| | 129584 | AV656017 | Hs.184325 | CGI-76 protein | 2.2 |
| | 114461 | AA531187 | Hs.125705 | ESTs | 2.2 |
| | 121387 | AA405854 | | gb:zu66g08.s1 Soares_testis_NHT Homo sap | 2.2 |
| | 109339 | AA314554 | Hs.27774 | ESTs, Highly similar to AF161349 1 HSPC0 | 2.2 |
| 80 | 129179 | AW969025 | Hs.109154 | ESTs | 2.2 |
| | 106711 | BE390125 | Hs.143187 | hypothetical protein | 2.2 |
| | 106424 | H61005 | Hs.37902 | ESTs | 2.2 |
| | 123949 | AA621665 | Hs.208957 | EST | 2.2 |
| | 127256 | AI738610 | Hs.267957 | ESTs, Moderately similar to ALU8_HUMAN | 2.2 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 104868 | AF173867 | Hs.28906 | glucocorticoid modulatory element bindin | 2.2 |
| | 132984 | BE539199 | Hs.62112 | zinc finger protein 207 | 2.2 |
| | 126383 | AB032977 | Hs.6298 | KIAA1151 protein | 2.2 |
| 5 | 130557 | H51825 | Hs.268911 | ESTs, Weakly similar to S65824 reverse | 2.2 |
| | 119232 | AI655226 | Hs.117659 | ESTs, Weakly similar to T46481 hypotheti | 2.2 |
| | 105715 | BE621800 | Hs.29444 | putative small membrane protein NID67 | 2.2 |
| | 124691 | R05835 | Hs.110153 | ESTs | 2.2 |
| | 113649 | N94768 | Hs.16400 | ESTs, Weakly similar to KIAA1435 protein | 2.2 |
| 10 | 117040 | AW970600 | Hs.303261 | ESTs | 2.2 |
| | 128767 | M85169 | Hs.1050 | pleckstrin homology, Sec7 and coiled/coi | 2.2 |
| | 120602 | AA808018 | Hs.109302 | ESTs | 2.2 |
| | 107182 | AI311782 | Hs.20013 | GCIIP-interacting protein p29 | 2.2 |
| | 107357 | U63973 | Hs.103501 | rhodopsin kinase | 2.2 |
| 15 | 125499 | H10543 | | gb:ym04c06.r1 Soares infant brain 1NIB H | 2.1 |
| | 126872 | AW450979 | | gb:UH-H-813-ata-a-12-0-UI.s1 NCL CGAP_Su | 2.1 |
| | 113233 | T61955 | Hs.279867 | CGI-59 protein | 2.1 |
| | 128367 | AW611791 | Hs.150742 | ESTs | 2.1 |
| | 127432 | AW067708 | Hs.170311 | heterogeneous nuclear ribonucleoprotein | 2.1 |
| 20 | 114021 | AW235215 | Hs.16145 | ESTs | 2.1 |
| | 104455 | AL110261 | Hs.157211 | DKFZP586B0621 protein | 2.1 |
| | 134966 | AW402389 | Hs.920 | modulator recognition factor I | 2.1 |
| | 129765 | M86933 | Hs.1238 | amelogenin (Y chromosome) | 2.1 |
| | 133461 | NM_000762 | Hs.334345 | cytochrome P450, subfamily IIA (phenobar | 2.1 |
| 25 | 109639 | AA082650 | Hs.6217 | Homo sapiens cDNA FLJ12521 fis, clone NT | 2.1 |
| | 129794 | AF161399 | Hs.23259 | hypothetical protein FLJ13433 | 2.1 |
| | 134869 | AL157518 | Hs.90421 | PRO2463 protein | 2.1 |
| | 110256 | H63947 | Hs.237955 | RAB7, member RAS oncogene family | 2.1 |
| | 128817 | BE395776 | Hs.168640 | ankylosis, progressive (mouse) homolog | 2.1 |
| 30 | 120906 | NM_000734 | Hs.97087 | CD3Z antigen, zeta polypeptide (TIT3 com | 2.1 |
| | 134354 | M90391 | Hs.82127 | interleukin 16 (lymphocyte chemoattracta | 2.1 |
| | 106048 | AW883367 | Hs.301732 | hypothetical protein MGC5306 | 2.1 |
| | 128352 | AW137413 | Hs.169942 | ESTs | 2.1 |
| | 115348 | AA281562 | Hs.292100 | ESTs | 2.1 |
| 35 | 123474 | AA599209 | | gb:ag34b11.s1 Jia bone marrow stroma Hom | 2.1 |
| | 107121 | AB015427 | Hs.250493 | zinc finger protein 219 | 2.1 |
| | 118509 | N22617 | Hs.43228 | Homo sapiens cDNA FLJ11835 fis, clone HE | 2.1 |
| | 135051 | AI272141 | Hs.83484 | SRY (sex determining region Y)-box 4 | 2.1 |
| | 109442 | AW296134 | Hs.86999 | ESTs, Weakly similar to S65657 alpha-1C- | 2.1 |
| 40 | 126661 | AA009835 | Hs.269521 | ESTs | 2.1 |
| | 129270 | AA357185 | Hs.109918 | ras homolog gene family, member H | 2.1 |
| | 125568 | AW615396 | Hs.105613 | ESTs | 2.1 |
| | 132867 | AF226667 | Hs.58553 | CTP synthase II | 2.1 |
| | 124656 | AW297702 | Hs.102915 | ESTs | 2.1 |
| 45 | 128954 | AA346839 | Hs.209100 | DKFZP434C171 protein | 2.1 |
| | 132985 | AL045579 | Hs.62113 | KIAA0717 protein | 2.1 |
| | 119247 | BE269047 | Hs.65234 | hypothetical protein FLJ20596 | 2.1 |
| | 105686 | N66397 | Hs.334825 | Homo sapiens cDNA FLJ14752 fis, clone NT | 2.1 |
| | 131009 | AF169802 | Hs.22142 | cytochrome b5 reductase b5R.2 | 2.1 |
| 50 | 112170 | BE246743 | Hs.288529 | hypothetical protein FLJ22635 | 2.1 |
| | 130755 | BE293520 | Hs.18910 | prostate cancer overexpressed gene 1 | 2.1 |
| | 117357 | N24829 | | gb:yx98h12.s1 Soares melanocyte 2NbHM Ho | 2.1 |
| | 101613 | M24283 | Hs.168383 | intercellular adhesion molecule 1 (CD54) | 2.1 |
| | 127644 | N88858 | Hs.155101 | ATP synthase, H+ transporting, mitochond | 2.1 |
| 55 | 101183 | AA442324 | Hs.795 | H2A histone family, member O | 2.1 |
| | 100420 | D86983 | Hs.118893 | Melanoma associated gene | 2.1 |
| | 129879 | AK001698 | Hs.13109 | Ran binding protein 11 | 2.1 |
| | 122311 | NM_014913 | Hs.131915 | KIAA0863 protein | 2.1 |
| | 130666 | R85474 | Hs.16073 | ESTs | 2.1 |
| 60 | 113517 | AI874223 | Hs.293560 | ESTs | 2.1 |
| | 115810 | AA426026 | Hs.187615 | ESTs | 2.1 |
| | 108743 | AI580150 | Hs.71074 | ESTs | 2.1 |
| | 129255 | AI961727 | Hs.109804 | H1 histone family, member X | 2.1 |
| | 120766 | AA764879 | Hs.12570 | tubulin-specific chaperone d | 2.1 |
| 65 | 126893 | AJ252060 | Hs.26320 | TRABID protein | 2.1 |
| | 115254 | AA279024 | Hs.269316 | ESTs, Weakly similar to S65657 alpha-1C | 2.1 |
| | 105865 | BE279383 | Hs.26557 | plakophilin 3 | 2.1 |
| | 120999 | AI972375 | Hs.29626 | hypothetical brain protein my038 | 2.1 |
| | 125636 | H12382 | Hs.25119 | ESTs, Weakly similar to YEX0_YEAST HYPOT | 2.1 |
| 70 | 117997 | N52090 | Hs.47420 | EST | 2.1 |
| | 104333 | D82418 | Hs.29626 | hypothetical brain protein my038 | 2.1 |
| | 134315 | AA291183 | Hs.81648 | hypothetical protein FLJ11021 similar to | 2.1 |
| | 135332 | AW393883 | Hs.98968 | hypothetical protein FLJ23058 | 2.1 |
| | 107279 | S57296 | Hs.323910 | v-erb-b2 avian erythroblastic leukemia | 2.1 |
| | 133097 | W03512 | Hs.6479 | hypothetical protein MGC13272 | 2.1 |
| 75 | 112563 | AW961220 | Hs.29282 | mitogen-activated protein kinase kinase | 2.1 |
| | 121782 | AW452957 | Hs.334698 | Homo sapiens, clone MGC:15203, mRNA, com | 2.1 |
| | 111567 | F12628 | Hs.334786 | hypothetical protein MGC16040 | 2.1 |
| | 133912 | H42679 | Hs.77522 | major histocompatibility complex, class | 2.1 |
| 80 | 134076 | AF086215 | | gb:Homo sapiens full length insert cDNA | 2.1 |
| | 116665 | F04405 | | gb:HSC2S8082 normalized infant brain cDN | 2.1 |
| | 133562 | M60721 | Hs.74870 | H2.0 (Drosophila)-like homeo box 1 | 2.1 |
| | 129092 | O56365 | Hs.63525 | poly(rC)-binding protein 2 | 2.1 |
| | 106869 | AW975362 | Hs.292679 | ESTs | 2.1 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| 5 | 130820 | AL353934 | Hs.288798 | hypothetical protein FLJ21012 | 2.1 |
| | 126277 | AB037847 | Hs.15441 | Crm (Cramped Drosophila)-like | 2.1 |
| | 106392 | BE350058 | Hs.36787 | chromodomain helicase DNA binding protei | 2.1 |
| | 131902 | AA180145 | Hs.34348 | Homo sapiens mRNA; cDNA DKFZp434P0235 (f | 2.1 |
| | 120734 | AA299948 | | gb:EST12544 Uterus tumor I Homo sapiens | 2.1 |
| 10 | 113070 | AB032977 | Hs.6298 | KIAA1151 protein | 2.1 |
| | 116031 | AA452239 | Hs.103329 | KIAA0970 protein | 2.1 |
| | 123869 | AA620824 | Hs.112923 | EST | 2.1 |
| | 106145 | AA424791 | Hs.5734 | meningioma expressed antigen 5 (hyaluron | 2.1 |
| | 109061 | AA160896 | | gb:zo79c07.s1 Stralagene pancreas (93720 | 2.1 |
| 15 | 126348 | T16243 | Hs.6473 | Homo sapiens cDNA FLJ13992 fis, clone Y7 | 2.1 |
| | 133231 | AK000517 | Hs.6844 | hypothetical protein FLJ20510 | 2.1 |
| | 123132 | AI061582 | Hs.324179 | Homo sapiens cDNA FLJ12371 fis, clone MA | 2.1 |
| | 117452 | N34687 | Hs.44054 | ninein (GSK3B interacting protein) | 2.1 |
| | 128538 | R44214 | Hs.101189 | ESTs | 2.1 |
| 20 | 111945 | R40663 | Hs.124944 | ESTs | 2.1 |
| | 119155 | R61715 | Hs.310598 | ESTs, Moderately similar to ALU1_HUMAN | 2.1 |
| | 124362 | AL046405 | Hs.103483 | KIAA1798 protein | 2.1 |
| | 129198 | N57532 | Hs.109315 | KIAA1415 protein | 2.1 |
| | 122059 | AA431737 | Hs.98749 | EST, Moderately similar to T42671 hypoth | 2.1 |
| 25 | 115643 | AA404276 | Hs.123253 | hypothetical protein FLJ22009 | 2.0 |
| | 112558 | AK001621 | Hs.15921 | hypothetical protein FLJ10759 | 2.0 |
| | 115355 | AA262292 | Hs.88445 | ESTs | 2.0 |
| | 130724 | AK001507 | Hs.306084 | Homo sapiens clone FLB6914 PRO1821 mRNA, | 2.0 |
| | 125360 | AW898892 | Hs.189741 | ESTs | 2.0 |
| 30 | 104926 | BE298808 | Hs.33363 | DKFZP434N093 protein | 2.0 |
| | 119468 | AI911535 | Hs.6657 | hypothetical protein bK1048E9.5 | 2.0 |
| | 132891 | BE267143 | Hs.59271 | U2(RNU2) small nuclear RNA auxiliary fac | 2.0 |
| | 100237 | D30715 | Hs.306333 | Human PAP (pancreatitis-associated prot | 2.0 |
| | 105335 | AW291165 | Hs.25447 | ESTs | 2.0 |
| 35 | 106727 | AA357001 | Hs.34045 | hypothetical protein FLJ20764 | 2.0 |
| | 126053 | H64450 | | gb:yu62d01.r1 Weizmann Olfactory Epithel | 2.0 |
| | 115084 | BE383668 | Hs.42484 | hypothetical protein FLJ10618 | 2.0 |
| | 128408 | AI183407 | Hs.143704 | EST | 2.0 |
| | 132311 | AI765559 | Hs.20072 | myosin regulatory light chain interactin | 2.0 |
| 40 | 113626 | T94318 | Hs.17359 | ESTs, Moderately similar to RL44_HUMAN 6 | 2.0 |
| | 116379 | AA448588 | Hs.71252 | hypothetical protein DKFZp761C169 | 2.0 |
| | 105474 | AL134843 | Hs.219614 | f-box and leucine-rich repeat protein 11 | 2.0 |
| | 108922 | AA115268 | Hs.269263 | ESTs | 2.0 |
| | 123720 | AA609734 | Hs.112755 | EST | 2.0 |
| 45 | 128902 | AA036637 | Hs.107052 | ESTs | 2.0 |
| | 113226 | AI821008 | Hs.10697 | ESTs | 2.0 |
| | 105798 | BE252749 | Hs.20558 | hypothetical protein FLJ20345 | 2.0 |
| | 106665 | BE090009 | Hs.323164 | hypothetical protein MGC2217 | 2.0 |
| | 105952 | AI767152 | Hs.181400 | ESTs, Weakly similar to I78885 serine/th | 2.0 |
| 50 | 127248 | AA364195 | | gb:EST75015 Pineal gland II Homo sapiens | 2.0 |
| | 112972 | AI684745 | Hs.165983 | hypothetical C2H2 zinc finger protein FL | 2.0 |
| | 128148 | AA918175 | Hs.126637 | ESTs | 2.0 |
| | 116176 | AA311152 | Hs.288708 | hypothetical protein FLJ21562 | 2.0 |
| | 126457 | AA007489 | Hs.50382 | ESTs | 2.0 |
| 55 | 112610 | AW500106 | Hs.23643 | serine/threonine protein kinase MASK | 2.0 |
| | 109249 | AA194730 | Hs.268189 | hypothetical protein FLJ20436 | 2.0 |
| | 121292 | AA401807 | | gb:zv65f11.s1 Soares_totai_fetus_Nb2HF8_ | 2.0 |
| | 128605 | AW058113 | Hs.102402 | Mad4 homolog | 2.0 |
| | 127705 | AJ003322 | | gb:AJ003322 Selected chromosome 21 cDNA | 2.0 |
| 60 | 134674 | AF219139 | Hs.87726 | KIAA0154 protein; ADP-ribosylation facto | 2.0 |
| | 107529 | BE515065 | Hs.296585 | nucleolar protein (KKE/D repeat) | 2.0 |
| | 116411 | AA608897 | Hs.321618 | hypothetical protein FLJ12525 | 2.0 |
| | 111576 | T88827 | Hs.15489 | ESTs | 2.0 |
| | 127002 | AL353940 | Hs.24979 | hypothetical protein DKFZp761P1010 | 2.0 |
| 65 | 112662 | R85436 | Hs.268814 | ESTs | 2.0 |
| | 126250 | AL050391 | Hs.321247 | Homo sapiens mRNA; cDNA DKFZp586A181 (f | 2.0 |
| | 101045 | J05614 | | gb:Human proliferating cell nuclear anti | 2.0 |
| | 117186 | H98988 | Hs.42612 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.0 |
| | 122110 | AI123000 | Hs.301240 | melanocortin 1 receptor (alpha melanocyt | 2.0 |
| 70 | 119849 | AI074585 | Hs.58440 | ESTs | 2.0 |
| | 124395 | N29963 | Hs.272095 | ESTs, Weakly similar to I38022 hypotheti | 2.0 |
| | 131600 | NM_004377 | Hs.29331 | camiline palmitoyltransferase I, muscle | 2.0 |
| | 112774 | R95770 | Hs.35455 | ESTs | 2.0 |
| | 109751 | AB033492 | Hs.6679 | hHDC for homolog of Drosophila headcase | 2.0 |
| 75 | 102377 | U40343 | Hs.29656 | cyclin-dependent kinase inhibitor 2D (p1 | 2.0 |
| | 115197 | R18656 | Hs.6749 | ESTs | 2.0 |
| | 102808 | BE242818 | Hs.179606 | nuclear RNA helicase, DECD variant of DE | 2.0 |
| | 128869 | AA768242 | Hs.80518 | hypothetical protein | 2.0 |
| | 111229 | AW389845 | Hs.110855 | ESTs | 2.0 |
| 80 | 129330 | AL079310 | Hs.92260 | high-mobility group protein 2-like 1 | 2.0 |
| | 105448 | NM_001186 | Hs.154276 | BTB and CNC homology 1, basic leucine zi | 2.0 |
| | 127391 | AW380893 | Hs.11039 | hypothetical protein MGC2722 | 2.0 |
| | 102337 | AI814663 | Hs.170133 | forkhead box O1A (rhabdomyosarcoma) | 2.0 |
| | 121897 | AA427419 | Hs.229162 | EST, Weakly similar to ZN91_HUMAN ZINC | 2.0 |
| | 107902 | AA026627 | Hs.61358 | ESTs | 2.0 |
| | 129340 | H75334 | Hs.11050 | F-box only protein 9 | 2.0 |
| | 101097 | BE245301 | Hs.89414 | chemokine (C-X-C motif), receptor 4 (fus | 2.0 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| 5 | 124864 | AW970168 | Hs.185706 | ESTs | 2.0 |
| | 118485 | AA508515 | Hs.291049 | ESTs | 2.0 |
| | 116715 | AL117440 | Hs.170263 | tumor protein p53-binding protein, 1 | 2.0 |
| | 130743 | AL049266 | Hs.18724 | Homo sapiens mRNA; cDNA DKFZp564F093 (fr | 2.0 |
| | 118677 | AW971146 | Hs.293187 | ESTs | 2.0 |
| 10 | 100020 | | | | 2.0 |
| | 123252 | AW968776 | Hs.287585 | Homo sapiens cDNA FLJ13648 fis, clone PL | 2.0 |
| | 134977 | AL044963 | Hs.306121 | leukocyte receptor cluster (LRC) encoded | 2.0 |
| | 115334 | AA702972 | Hs.65300 | ESTs | 2.0 |
| | 111790 | AW769683 | Hs.6734 | ESTs, Weakly similar to S26650 DNA-bindin | 2.0 |
| 15 | 129101 | NM_013403 | Hs.108665 | zinedin | 2.0 |
| | 132676 | N92589 | Hs.261038 | ESTs, Weakly similar to t38022 hypothet | 2.0 |
| | 111018 | AI287912 | Hs.3628 | mitogen-activated protein kinase kinase | 2.0 |
| | 105933 | AF078544 | Hs.194686 | solute carrier family 25 (mitochondrial | 2.0 |
| | 110679 | AA004798 | Hs.108311 | ESTs, Weakly similar to T00351 hypotheti | 2.0 |
| 20 | 120861 | AA350394 | Hs.95952 | ESTs | 2.0 |
| | 132430 | AW973652 | Hs.283105 | ESTs | 2.0 |
| | 115026 | AA251972 | Hs.188718 | ESTs | 2.0 |
| | 128660 | AA011597 | Hs.177398 | ESTs | 2.0 |
| | 134554 | AI184316 | Hs.85273 | retinoblastoma-binding protein 6 | 2.0 |
| 25 | 109592 | AI198059 | Hs.26370 | ESTs | 2.0 |
| | 123636 | AA609263 | | gb:af13c08.s1 Soares_testis_NHT Homo sap | 2.0 |
| | 132610 | AA160511 | Hs.5326 | amino acid system N transporter 2; porcu | 2.0 |
| | 122652 | AA454641 | | gb:zx99d05.s1 Soares_NhHMPu_S1 Homo sapi | 2.0 |
| | 120467 | AW292562 | Hs.187628 | ESTs | 2.0 |
| 30 | 126046 | AA804957 | Hs.119840 | ESTs | 2.0 |
| | 128179 | AW293689 | Hs.127116 | ESTs | 2.0 |
| | 123349 | AB033042 | Hs.29679 | cofactor required for Sp1 transcriptiona | 2.0 |
| | 106208 | AK001674 | Hs.22630 | cofactor required for Sp1 transcriptiona | 2.0 |
| | 125832 | AA628600 | Hs.117587 | ESTs | 2.0 |
| 35 | 133317 | AC005258 | Hs.70830 | U6 snRNA-associated Sm-like protein LSM7 | 2.0 |
| | 132886 | AW978168 | Hs.5912 | F-box only protein 7 | 2.0 |
| | 127447 | AA386192 | Hs.193482 | Homo sapiens cDNA FLJ11903 fis, clone HE | 2.0 |
| | 133149 | AA370045 | Hs.6607 | AXIN1 up-regulated | 2.0 |
| | 120468 | AW967675 | Hs.96487 | ESTs, Highly similar to S08228 ribosomal | 2.0 |
| 40 | 106487 | AI697340 | Hs.135265 | Homo sapiens clone FLB8436 PRO2277 mRNA, | 2.0 |
| | 126770 | AI292320 | Hs.81361 | heterogeneous nuclear ribonucleoprotein | 2.0 |
| | 120592 | AA830664 | Hs.143974 | ESTs | 2.0 |
| | 100944 | L07518 | Hs.159593 | mucin 6, gastric | 2.0 |
| | 101887 | AW967413 | Hs.83958 | transducin-like enhancer of split 4, hom | 2.0 |
| 45 | 125324 | R07785 | | gb:yf15c06.r1 Soares fetal liver spleen | 2.0 |
| | 133906 | BE386038 | Hs.77492 | heterogeneous nuclear ribonucleoprotein | 2.0 |
| | 113408 | NM_005908 | Hs.115945 | mannosidase, beta A, lysosomal | 2.0 |
| | 115613 | AW136951 | Hs.173946 | hypothetical protein FLJ10486 | 2.0 |
| | 107468 | AA740979 | Hs.91389 | ESTs | 2.0 |
| 50 | 100554 | M95923 | | gb:Human 12-lipoxygenase mRNA, partial c | 2.0 |
| | 120476 | NM_014922 | Hs.104305 | death effector filament-forming Ced-4-l | 2.0 |
| | 117160 | AA322302 | Hs.183302 | PCTAIRE protein kinase 2 | 2.0 |
| | 115582 | AW245047 | Hs.136164 | cutaneous T-cell lymphoma-associated tu | 2.0 |
| | 125536 | F08266 | Hs.77948 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.0 |
| 55 | 100842 | U05597 | | gb:Human anion exchanger 3 cardiac isofo | 2.0 |
| | 133207 | AI561173 | Hs.67688 | ESTs | 2.0 |
| | 122053 | AI637498 | Hs.98745 | ESTs | 2.0 |
| | 121080 | AA617830 | Hs.28310 | ESTs | 2.0 |
| | 113316 | T70318 | Hs.268581 | ESTs | 2.0 |
| 60 | 113137 | AW952129 | Hs.293225 | ESTs, Weakly similar to FLDED-1 [H.sapie | 1.9 |
| | 100416 | AW505086 | Hs.196914 | minor histocompatibility antigen HA-1 | 1.9 |
| | 133975 | C18356 | Hs.295944 | tissue factor pathway inhibitor 2 | 1.9 |
| | 103872 | AI816078 | Hs.21756 | translation factor su1 homolog | 1.9 |
| | 132439 | AK001942 | Hs.4863 | hypothetical protein DKFZp566A1524 | 1.9 |
| 65 | 126082 | H81188 | Hs.269571 | ESTs | 1.9 |
| | 124677 | R01073 | | gb:ye84c03.s1 Soares fetal liver spleen | 1.9 |
| | 123385 | BE149685 | Hs.17767 | KIAA1554 protein | 1.9 |
| | 103138 | X65965 | | gb:H.sapiens SOD-2 gene for manganese su | 1.9 |
| | 104867 | AA278898 | Hs.225979 | hypothetical protein similar to small G | 1.9 |
| 70 | 128668 | AI754363 | Hs.103422 | Homo sapiens cDNA FLJ14630 fis, clone NT | 1.9 |
| | 125826 | M20681 | Hs.7594 | solute carrier family 2 (facilitated glu | 1.9 |
| | 113701 | T97301 | Hs.18026 | ESTs | 1.9 |
| | 134447 | M58603 | Hs.83428 | nuclear factor of kappa light polypeptid | 1.9 |
| | 128895 | AW467000 | Hs.106985 | ESTs | 1.9 |
| 75 | 112719 | AI200957 | Hs.19301 | Homo sapiens, Similar to Nedd-4-like ubi | 1.9 |
| | 102552 | NM_005426 | Hs.44585 | tumor protein p53-binding protein, 2 | 1.9 |
| | 131186 | Z70200 | Hs.246112 | KIAA0788 protein | 1.9 |
| | 133347 | BE257758 | Hs.71475 | acid cluster protein 33 | 1.9 |
| | 133388 | AW245631 | Hs.182447 | heterogeneous nuclear ribonucleoprotein | 1.9 |
| 80 | 112266 | AI652534 | Hs.25934 | ESTs, Weakly similar to HSHU11 histone H | 1.9 |
| | 100336 | I76101 | Hs.8127 | KIAA0144 gene product | 1.9 |
| | 113479 | AI023133 | Hs.10739 | ESTs | 1.9 |
| | 135231 | BE613615 | Hs.74280 | hypothetical protein FLJ22237 | 1.9 |
| | 123783 | AA610112 | | gb:af19g05.s1 Soares_total_fetus_Nb2HFB_ | 1.9 |
| | 113016 | NM_014007 | Hs.127649 | KIAA0414 protein | 1.9 |
| | 132761 | AI815537 | Hs.323502 | nuclear RNA export factor 1 | 1.9 |
| | 128536 | AW955085 | Hs.101150 | Homo sapiens, clone IMAGE:4054156, mRNA, | 1.9 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 126663 | AW518478 | Hs.181297 | ESTs | 1.9 |
| | 103973 | AA305729 | Hs.18272 | amino acid transporter system A1 | 1.9 |
| | 106742 | AW591428 | Hs.27556 | hypothetical protein FLJ22405 | 1.9 |
| 5 | 129793 | AW207000 | Hs.126857 | Homo sapiens cDNA FLJ12936 fis, clone NT | 1.9 |
| | 105888 | AW970672 | Hs.9247 | protein kinase, AMP-activated, alpha 1 c | 1.9 |
| | 101892 | AI825838 | Hs.75206 | protein phosphatase 3 (formerly 2B), cat | 1.9 |
| | 125511 | AJ271379 | Hs.76194 | ribosomal protein S5 | 1.9 |
| | 126751 | AI378328 | Hs.77256 | enhancer of zeste (Drosophila) homolog 2 | 1.9 |
| 10 | 129111 | AL080155 | Hs.226372 | DKFZP434J154 protein | 1.9 |
| | 128750 | T80270 | Hs.104788 | hypothetical protein LOC55565 | 1.9 |
| | 133531 | BE276738 | Hs.74578 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypep | 1.9 |
| | 125704 | R55094 | Hs.26239 | Human DNA sequence from clone RP11-438B2 | 1.9 |
| | 100157 | D14661 | Hs.119 | Wilms' tumour 1-associated protein | 1.9 |
| 15 | 125845 | AK001440 | Hs.131840 | hypothetical protein FLJ10578 | 1.9 |
| | 134682 | AW882645 | Hs.88044 | sprouty (Drosophila) homolog 1 (antagoni | 1.9 |
| | 106565 | NM_014892 | Hs.227602 | KIAA1116 protein | 1.9 |
| | 106706 | AB037810 | Hs.18760 | KIAA1389 protein | 1.9 |
| | 125761 | R68351 | | gb:yh99b03.r1 Soares placenta Nb2HP Homo | 1.9 |
| 20 | 116470 | AI272141 | Hs.83484 | SRY (sex determining region Y)-box 4 | 1.9 |
| | 123264 | AI681270 | Hs.99824 | BCE-1 protein | 1.9 |
| | 126096 | F08208 | Hs.283844 | similar to rat tricarboxylate carrier-li | 1.9 |
| | 104995 | AK001690 | Hs.16390 | hypothetical protein FLJ10035 | 1.9 |
| | 133424 | AA350994 | Hs.20281 | KIAA1700 | 1.9 |
| 25 | 132450 | AA100012 | Hs.48827 | hypothetical protein FLJ12085 | 1.9 |
| | 131803 | U73737 | Hs.284289 | vitiligo-associated protein VIT-1 | 1.9 |
| | 116548 | D20433 | | gb:HUMGS01407 Human promyelocyte Homo sa | 1.9 |
| | 113815 | AA386192 | Hs.193482 | Homo sapiens cDNA FLJ11903 fis, clone HE | 1.9 |
| | 100245 | AL039248 | Hs.3094 | KIAA0063 gene product | 1.9 |
| 30 | 113677 | Z70200 | Hs.246112 | KIAA0788 protein | 1.9 |
| | 134470 | X54942 | Hs.83758 | CDC28 protein kinase 2 | 1.9 |
| | 134937 | AI251449 | Hs.171939 | ESTs | 1.9 |
| | 134506 | AW247364 | Hs.84285 | ubiquitin-conjugating enzyme E2I (homolo | 1.9 |
| | 126469 | BE384361 | Hs.182885 | ESTs, Weakly similar to JC5024 UDP-galac | 1.9 |
| 35 | 115261 | AA938293 | Hs.60088 | hypothetical protein MGC11314 | 1.9 |
| | 125198 | W69474 | Hs.323140 | ESTs | 1.9 |
| | 115317 | AA303799 | Hs.300141 | ribosomal protein L39 | 1.9 |
| | 112342 | AW410273 | Hs.92614 | longevity assurance (LAG1, S. cerevisiae) | 1.9 |
| | 117329 | AA524065 | Hs.93670 | Homo sapiens cDNA: FLJ22664 fis, clone H | 1.9 |
| 40 | 116353 | AB032966 | Hs.131728 | KIAA1140 protein | 1.9 |
| | 114459 | AW445217 | Hs.103362 | ESTs | 1.9 |
| | 133903 | X63692 | Hs.77462 | DNA (cytosine-5-)-methyltransferase 1 | 1.9 |
| | 116083 | AA455706 | Hs.44581 | heat shock protein hsp70-related protein | 1.9 |
| | 130037 | AI498631 | Hs.111334 | ferritin, light polypeptide | 1.9 |
| 45 | 102273 | BE391815 | Hs.75981 | ubiquitin specific protease 14 (IRNA-gua | 1.9 |
| | 120452 | AL022328 | Hs.104335 | hypothetical protein IMAGE3510317 | 1.9 |
| | 116432 | BE271922 | Hs.71243 | ESTs, Weakly similar to zinc finger prot | 1.9 |
| | 115916 | AI052731 | Hs.91910 | ESTs | 1.9 |
| | 120827 | AA382525 | Hs.132967 | Human EST clone 122887 mariner transpos | 1.9 |
| 50 | 129602 | AI282193 | Hs.198298 | v-src avian sarcoma (Schmidt-Ruppin A-2) | 1.9 |
| | 105693 | BE250951 | Hs.181368 | U5 snRNP-specific protein (220 kD), orth | 1.9 |
| | 102316 | U34301 | | gb:Human nonmuscle myosin heavy chain II | 1.9 |
| | 131422 | AW607731 | Hs.26670 | Human PAC clone RP3-515N1 from Zq11.2-q | 1.9 |
| | 128434 | AI190914 | Hs.143880 | ESTs | 1.9 |
| 55 | 117086 | AA581602 | Hs.41840 | ESTs | 1.9 |
| | 102006 | AL048967 | Hs.172207 | non-POU-domain-containing, octamer-bindi | 1.9 |
| | 121335 | AA404418 | | gb:zw37e02.s1 Soares_total_fetus_Nb2HF8_ | 1.9 |
| | 105905 | AA401533 | Hs.19440 | ESTs | 1.9 |
| | 125165 | W45350 | | gb:zc81h08.s1 Pancreatic Islet Homo sapi | 1.9 |
| 60 | 109875 | H03260 | Hs.30385 | ESTs | 1.9 |
| | 109152 | AW380723 | Hs.73451 | ESTs, Weakly similar to S55024 nebulin, | 1.9 |
| | 126203 | AK001035 | Hs.130881 | B-cell CLL/lymphoma 11A (zinc finger pro | 1.9 |
| | 122530 | AW959741 | Hs.40368 | adaptor-related protein complex 1, sigma | 1.9 |
| | 124506 | BE273688 | Hs.182447 | heterogeneous nuclear ribonucleoprotein | 1.9 |
| 65 | 130525 | AA361850 | Hs.322149 | Human clone 137308 mRNA, partial cds | 1.9 |
| | 127226 | AL036559 | Hs.3463 | ribosomal protein S23 | 1.9 |
| | 106465 | AA971576 | Hs.225951 | topoisomerase-related function protein 4 | 1.9 |
| | 106970 | AA521368 | Hs.24252 | ESTs | 1.9 |
| | 134275 | AI878910 | Hs.3688 | cisplatin resistance-associated overexpr | 1.9 |
| 70 | 126825 | AA100230 | | gb:z81c01.s1 Stratagene colon (937204) | 1.9 |
| | 132443 | AW246148 | Hs.268371 | hypothetical protein FLJ20274 | 1.8 |
| | 104631 | AA002064 | Hs.18920 | ESTs | 1.8 |
| | 111468 | H62647 | Hs.205481 | ESTs | 1.8 |
| | 114317 | AA524839 | Hs.469 | succinate dehydrogenase complex, subunit | 1.8 |
| 75 | 126158 | N55989 | Hs.16390 | hypothetical protein FLJ10035 | 1.8 |
| | 113782 | AK001567 | Hs.311002 | Homo sapiens cDNA FLJ10705 fis, clone NT | 1.8 |
| | 119229 | T03229 | | gb:FB5C2 Fetal brain, Stratagene Homo sa | 1.8 |
| | 105930 | AF016371 | Hs.9880 | peptidyl prolyl isomerase H (cyclophilin | 1.8 |
| | 127245 | AA323958 | | gb:EST26810 Cerebellum II Homo sapiens c | 1.8 |
| 80 | 100967 | BE011845 | Hs.251064 | high-mobility group (nonhistone chromoso | 1.8 |
| | 105149 | BE089288 | Hs.8958 | Homo sapiens cDNA FLJ12024 fis, clone HE | 1.8 |
| | 104542 | R29657 | | gb:F1-1179D 22 week old human fetal live | 1.8 |
| | 124236 | AF086006 | | gb:Homo sapiens full length insert cDNA | 1.8 |
| | 127155 | AA284993 | | gb:z123e10.r1 Soares ovary tumor NbHOT H | 1.8 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 126854 | AJ275986 | Hs.71414 | transcription factor (SMIF gene) | 1.8 |
| | 107021 | AK001342 | Hs.14570 | hypothetical protein FLJ22530 | 1.8 |
| | 110023 | AW294701 | Hs.31040 | ESTs | 1.8 |
| 5 | 114899 | AK000342 | Hs.77646 | Homo sapiens mRNA; cDNA DKFZp761M0223 (f | 1.8 |
| | 127315 | AF116522 | | gb:Homo sapiens clone FLB4217 mRNA seque | 1.8 |
| | 110384 | H45282 | Hs.268798 | ESTs | 1.8 |
| | 132693 | BE244200 | Hs.55075 | KIAA0410 gene product | 1.8 |
| | 127684 | AA668631 | Hs.32556 | KIAA0379 protein | 1.8 |
| 10 | 127297 | AW629485 | Hs.140720 | GSK-3 binding protein FRAT2 | 1.8 |
| | 104249 | AF004231 | Hs.22405 | leukocyte immunoglobulin-like receptor, | 1.8 |
| | 112652 | BE269699 | Hs.235782 | solute carrier family 21 (organic anion | 1.8 |
| | 110312 | BE256986 | Hs.11896 | hypothetical protein FLJ12089 | 1.8 |
| | 100417 | NM_014003 | Hs.78054 | pre-mRNA splicing factor similar to S. c | 1.8 |
| | 120532 | AA262354 | Hs.186648 | ESTs, Weakly similar to I38022 hypotheti | 1.8 |
| 15 | 127629 | AA293279 | Hs.29173 | hypothetical protein FLJ20515 | 1.8 |
| | 100739 | M59287 | Hs.2083 | CDC-like kinase 1 | 1.8 |
| | 110636 | H72868 | Hs.19110 | ESTs | 1.8 |
| | 132957 | BE244044 | Hs.61469 | hypothetical protein | 1.8 |
| 20 | 115467 | AI366784 | Hs.48820 | TATA box binding protein (TBP)-associate | 1.8 |
| | 132161 | W31634 | Hs.180799 | hypothetical protein FLJ22561 | 1.8 |
| | 129510 | AW968504 | Hs.123073 | CDC2-related protein kinase 7 | 1.8 |
| | 126805 | F32658 | Hs.101359 | chromosome 6 open reading frame 32 | 1.8 |
| | 129295 | U63127 | Hs.110121 | SEC7 homolog | 1.8 |
| 25 | 127823 | AW972893 | Hs.78869 | transcription elongation factor A (SII), | 1.8 |
| | 104590 | AW373062 | Hs.83623 | nuclear receptor subfamily 1, group I, m | 1.8 |
| | 111959 | R40978 | Hs.271498 | ESTs, Moderately similar to ALU1_HUMAN A | 1.8 |
| | 109303 | AA199857 | Hs.269291 | ESTs | 1.8 |
| | 112501 | AA972447 | Hs.288833 | Homo sapiens mRNA; cDNA DKFZp434K087 (fr | 1.8 |
| 30 | 127303 | AA366951 | | gb:EST77963 Pancreas tumor III Homo sapi | 1.8 |
| | 115982 | W92113 | | gb:zh48e01.r1 Soares_fetal_liver_spleen_ | 1.8 |
| | 123331 | AA497013 | | gb:ae32g02.s1 Gessler Wilms tumor Homo s | 1.8 |
| | 111598 | R11505 | Hs.268912 | ESTs | 1.8 |
| | 121643 | AA640987 | Hs.193767 | ESTs | 1.8 |
| 35 | 105012 | AF098158 | Hs.9329 | chromosome 20 open reading frame 1 | 1.8 |
| | 118761 | AW799109 | Hs.226755 | ESTs | 1.8 |
| | 128765 | AF073310 | Hs.143648 | insulin receptor substrate 2 | 1.8 |
| | 118103 | AA401733 | Hs.184134 | ESTs | 1.8 |
| | 134595 | NM_002401 | Hs.29282 | mitogen-activated protein kinase kinase | 1.8 |
| 40 | 134212 | AA654353 | Hs.17719 | EBP50-PDZ interactor of 64 kD | 1.8 |
| | 128033 | AI248705 | Hs.149321 | ESTs | 1.8 |
| | 126972 | NM_016255 | Hs.95260 | Autosomal Highly Conserved Protein | 1.8 |
| | 111122 | N63753 | Hs.16492 | DKFZP564G2022 protein | 1.8 |
| | 114798 | AA159181 | Hs.54900 | serologically defined colon cancer anti | 1.8 |
| 45 | 106349 | AW954310 | Hs.127270 | KIAA1545 protein | 1.8 |
| | 135358 | BE622827 | Hs.99486 | hypothetical protein FLJ13044 | 1.8 |
| | 116223 | AF045458 | Hs.47061 | unc-51 (C. elegans)-like kinase 1 | 1.8 |
| | 116654 | Z26324 | Hs.79204 | ESTs, Weakly similar to I38022 hypotheti | 1.8 |
| | 124554 | N65961 | | gb:za27d03.s1 Soares fetal liver spleen | 1.8 |
| 50 | 120259 | AW014786 | Hs.192742 | hypothetical protein FLJ12785 | 1.8 |
| | 123044 | AK001035 | Hs.130881 | B-cell CLL/lymphoma 11A (zinc finger pro | 1.8 |
| | 125261 | W90351 | Hs.110134 | ESTs, Highly similar to CREB-binding pro | 1.8 |
| | 135026 | N92165 | Hs.93231 | ESTs | 1.8 |
| | 129951 | AL110282 | Hs.268024 | Homo sapiens, clone IMAGE:3873720, mRNA | 1.8 |
| 55 | 125768 | AI557486 | Hs.119122 | ribosomal protein L13a | 1.8 |
| | 114122 | R46128 | Hs.12751 | ESTs | 1.8 |
| | 133047 | AA310600 | Hs.63657 | peptide:N-glycanase similar to yeast PNG | 1.8 |
| | 133589 | L37368 | Hs.75104 | RNA-binding protein S1, serine-rich doma | 1.8 |
| | 130872 | U61084 | Hs.226307 | phorbolins (similar to apolipoprotein B m | 1.8 |
| 60 | 133498 | BE299587 | Hs.85301 | calcium binding protein P22 | 1.8 |
| | 131144 | AA305255 | Hs.23528 | HSPC038 protein | 1.8 |
| | 104261 | AW248364 | Hs.5409 | RNA polymerase I subunit | 1.8 |
| | 115507 | AI083668 | Hs.50601 | hypothetical protein MGC10986 | 1.8 |
| | 109073 | T05003 | Hs.10056 | hypothetical protein FLJ14621 | 1.8 |
| 65 | 115363 | AA214618 | Hs.152759 | activator of S phase kinase | 1.8 |
| | 112657 | AW844878 | Hs.19769 | hypothetical protein MGC4174 | 1.8 |
| | 102960 | AI904738 | Hs.76053 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypep | 1.8 |
| | 125549 | R20215 | | gb:yg18b09.r1 Soares infant brain 1N18 H | 1.8 |
| | 133797 | AL133921 | Hs.76272 | retinoblastoma-binding protein 2 | 1.8 |
| 70 | 125048 | AW440068 | Hs.59425 | hypothetical protein FLJ23323 | 1.8 |
| | 103403 | X95406 | | gb:H.sapiens cyclin E gene. | 1.8 |
| | 123546 | AA608817 | Hs.112597 | EST | 1.8 |
| | 124694 | R06108 | | gb:ye94h05.s1 Soares fetal liver spleen | 1.8 |
| | 102406 | U43177 | | (NONE) | 1.8 |
| 75 | 130695 | T97205 | Hs.17998 | ESTs, Weakly similar to 2109260A B cell | 1.8 |
| | 123951 | AB012922 | Hs.173043 | metastasis-associated 1-like 1 | 1.8 |
| | 118533 | N71861 | Hs.49413 | ESTs | 1.8 |
| | 123197 | AA489250 | | gb:aa57h12.s1 NCI_CGAP_GCB1 Homo sapiens | 1.8 |
| | 125656 | AW516428 | Hs.78687 | neutral sphingomyelinase (N-SMase) activ | 1.8 |
| 80 | 100154 | H60720 | Hs.81892 | KIAA0101 gene product | 1.8 |
| | 106876 | N52821 | Hs.269412 | ESTs, Moderately similar to ALU7_HUMAN A | 1.8 |
| | 128339 | AL121087 | Hs.296406 | KIAA0685 gene product | 1.8 |
| | 105939 | AL137728 | Hs.12258 | Homo sapiens mRNA; cDNA DKFZp434B0920 (f | 1.8 |
| | 102495 | NM_006762 | Hs.79356 | Lysosomal-associated multispanning membr | 1.8 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| 5 | 100221 | D28383 | | gb:Human mRNA for ATP synthase B chain, | 1.8 |
| | 101741 | NM_003199 | Hs.326198 | transcription factor 4 | 1.8 |
| | 101701 | NM_002436 | Hs.1861 | membrane protein, palmitoylated 1 (55kD) | 1.8 |
| | 107119 | AI375499 | Hs.27379 | ESTs | 1.8 |
| | 134362 | U47742 | Hs.82210 | zinc finger protein 220 | 1.8 |
| 10 | 127964 | F05298 | | gb:HSC13F081 normalized infant brain cDN | 1.8 |
| | 101437 | M20681 | Hs.7594 | solute carrier family 2 (facilitated glu | 1.8 |
| | 106204 | AA188734 | Hs.21479 | ubiquitin 1 | 1.8 |
| | 112716 | AW590680 | Hs.110802 | von Willebrand factor | 1.8 |
| | 109779 | AB029396 | Hs.3353 | beta-1,3-glucuronyltransferase 1 (glucur | 1.8 |
| 15 | 111369 | AA535740 | Hs.170263 | tumor protein p53-binding protein, 1 | 1.8 |
| | 135204 | AF067515 | Hs.183418 | cell division cycle 2-like 1 (PITSLRE pr | 1.8 |
| | 105788 | AB009598 | Hs.23965 | solute carrier family 22 (organic anion | 1.8 |
| | 110997 | AW862823 | Hs.168052 | KIAA0421 protein | 1.8 |
| | 111620 | R14853 | Hs.307478 | EST, Weakly similar to I39058 hypotheti | 1.8 |
| 20 | 115618 | H11695 | Hs.322901 | disrupter of silencing 10 | 1.8 |
| | 115904 | AI167560 | Hs.61297 | ESTs | 1.8 |
| | 107510 | BE613332 | Hs.132055 | ESTs, Weakly similar to GNMSLL retroviru | 1.8 |
| | 116435 | AA186761 | Hs.334812 | hypothetical protein DKFZp586K0717 | 1.8 |
| | 112399 | R60920 | Hs.296770 | KIAA1719 protein | 1.8 |
| 25 | 127426 | AA854756 | Hs.124076 | ESTs | 1.8 |
| | 125175 | W52355 | Hs.303030 | EST | 1.8 |
| | 132972 | AA034365 | Hs.288924 | Homo sapiens cDNA FLJ11392 fis, clone HE | 1.8 |
| | 125982 | R98091 | | gb:yr30e11.1 r1 Soares fetal liver spleen | 1.8 |
| | 115620 | AA399997 | Hs.211610 | CUG triplet repeat, RNA-binding protein | 1.8 |
| 30 | 128115 | AI435590 | Hs.130168 | ESTs | 1.8 |
| | 106880 | AI493206 | Hs.32425 | ESTs | 1.7 |
| | 101199 | L22075 | Hs.1666 | guanine nucleotide binding protein (G pr | 1.7 |
| | 104159 | BE386983 | Hs.283685 | hypothetical protein FLJ20396 | 1.7 |
| | 101368 | M13058 | Hs.73952 | proline-rich protein HaellI subfamily 2 | 1.7 |
| 35 | 103646 | AW248439 | Hs.2340 | junction plakoglobin | 1.7 |
| | 130717 | AA334274 | Hs.18368 | DKFZP564B0769 protein | 1.7 |
| | 124981 | N25485 | Hs.330310 | maternal G10 transcript | 1.7 |
| | 124770 | AA984414 | Hs.120429 | ESTs | 1.7 |
| | 126926 | AA179472 | Hs.832 | ESTs, Highly similar to A41029 Integrin | 1.7 |
| 40 | 101636 | BE392781 | Hs.89474 | ADP-ribosylation factor 6 | 1.7 |
| | 123553 | AI494291 | Hs.111977 | ESTs | 1.7 |
| | 127172 | AA292208 | Hs.251278 | KIAA1201 protein | 1.7 |
| | 130621 | AW513087 | Hs.16803 | LUC7 (S. cerevisiae)-like | 1.7 |
| | 116925 | H73110 | Hs.260603 | ESTs, Moderately similar to A47582 B-ce | 1.7 |
| 45 | 108845 | AW362901 | Hs.68864 | ESTs, Weakly similar to phosphatidylseri | 1.7 |
| | 128092 | AA904517 | Hs.166229 | ESTs | 1.7 |
| | 128193 | AJ224442 | Hs.155020 | putative methyltransferase | 1.7 |
| | 113965 | AL268666 | Hs.19631 | ESTs, Weakly similar to I38022 hypotheti | 1.7 |
| | 106620 | D52562 | Hs.296317 | KIAA1789 protein | 1.7 |
| 50 | 102926 | W28363 | Hs.239752 | nuclear receptor subfamily 2, group F, m | 1.7 |
| | 114964 | BE085271 | Hs.8834 | ring finger protein 3 | 1.7 |
| | 101800 | NM_006433 | Hs.105806 | granulysin | 1.7 |
| | 130094 | NM_001471 | Hs.167017 | gamma-aminobutyric acid (GABA) B recepto | 1.7 |
| | 120112 | AA180240 | Hs.6083 | Homo sapiens cDNA: FLJ21028 fis, clone C | 1.7 |
| 55 | 109978 | H09356 | Hs.22528 | ESTs | 1.7 |
| | 121252 | AA393907 | Hs.97179 | ESTs | 1.7 |
| | 127768 | AW085002 | Hs.156187 | ESTs | 1.7 |
| | 125445 | AI452722 | Hs.7709 | WW domain binding protein 1 | 1.7 |
| | 100052 | | | | 1.7 |
| 60 | 119863 | AA081218 | Hs.58608 | Homo sapiens cDNA FLJ14206 fis, clone NT | 1.7 |
| | 134333 | AW888411 | Hs.81915 | leukemia-associated phosphoprotein p18 (| 1.7 |
| | 123541 | AW976511 | Hs.112592 | ESTs | 1.7 |
| | 134191 | W26632 | Hs.7979 | KIAA0736 gene product | 1.7 |
| | 103305 | X82279 | | gb:H.sapiens Fas, Apo-1 gene (promoter a | 1.7 |
| 65 | 112411 | R43090 | Hs.271510 | ESTs, Moderately similar to ALU1_HUMAN A | 1.7 |
| | 100598 | AL121734 | Hs.146409 | cell division cycle 42 (GTP-binding prot | 1.7 |
| | 113610 | T93279 | | gb:ye2501.s1 Stratagene lung (937210) H | 1.7 |
| | 105593 | AA279341 | Hs.174151 | aldehyde oxidase 1 | 1.7 |
| | 125317 | Z99348 | Hs.112461 | ESTs, Weakly similar to I38022 hypotheti | 1.7 |
| 70 | 125956 | AK000214 | Hs.129014 | hypothetical protein FLJ20207 | 1.7 |
| | 105105 | R61532 | Hs.87016 | hypothetical protein FLJ22938 | 1.7 |
| | 132791 | AB029551 | Hs.7910 | RING1 and YY1 binding protein | 1.7 |
| | 116996 | H83935 | Hs.40535 | ESTs | 1.7 |
| | 133335 | BE251012 | Hs.263812 | nuclear distribution gene C (Anidulans) | 1.7 |
| 75 | 120959 | BE247692 | Hs.102469 | putative nuclear protein | 1.7 |
| | 105621 | AL040058 | Hs.6375 | uncharacterized hypothalamus protein HT0 | 1.7 |
| | 106181 | AI803651 | Hs.191608 | ESTs | 1.7 |
| | 125661 | AA491830 | Hs.25689 | ESTs | 1.7 |
| | 127585 | AA604144 | Hs.190632 | ESTs | 1.7 |
| 80 | 112035 | AI955289 | Hs.300759 | ribosomal protein L36 | 1.7 |
| | 102870 | M64437 | Hs.234799 | breakpoint cluster region | 1.7 |
| | 108039 | AA280319 | Hs.288840 | PRO1575 protein | 1.7 |
| | 125898 | AK001823 | Hs.92287 | Homo sapiens mRNA; cDNA DKFZp564C2478 (f | 1.7 |
| | 114740 | N70103 | | gb:za53e10.s1 Soares fetal liver spleen | 1.7 |
| | 120304 | AA192469 | Hs.271838 | ESTs | 1.7 |
| | 103433 | X98001 | Hs.78948 | Rab geranylgeranyltransferase, beta subu | 1.7 |
| | 116180 | AA463902 | Hs.13522 | ESTs, Weakly similar to I38022 hypothet | 1.7 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 105269 | AF174499 | Hs.6764 | histone deacetylase 6 | 1.7 |
| | 125431 | AW851639 | Hs.75584 | polymyositis/scleroderma autoantigen 2 (| 1.7 |
| | 133579 | X75346 | Hs.75074 | mitogen-activated protein kinase-activat | 1.7 |
| 5 | 105355 | AL031447 | Hs.26938 | Homo sapiens, clone IMAGE:4053044, mRNA, | 1.7 |
| | 129601 | AB032964 | Hs.115726 | KIAA1138 protein | 1.7 |
| | 113739 | AA356599 | Hs.173904 | ESTs | 1.7 |
| | 100840 | U04816 | Hs.183418 | cell division cycle 2-like 1 (PITSLRE pr | 1.7 |
| | 122878 | AA847744 | Hs.99640 | ESTs | 1.7 |
| 10 | 119495 | BE144608 | Hs.55533 | ESTs | 1.7 |
| | 125669 | R51308 | Hs.333256 | ESTs, Weakly similar to ALU8_HUMAN ALU | 1.7 |
| | 109891 | H04757 | Hs.323176 | ESTs | 1.7 |
| | 126884 | U49436 | Hs.286236 | KIAA1856 protein | 1.7 |
| | 132977 | AA093322 | Hs.301404 | RNA binding motif protein 3 | 1.7 |
| 15 | 101396 | BE267931 | Hs.78996 | proliferating cell nuclear antigen | 1.7 |
| | 104730 | AW139789 | Hs.16370 | Homo sapiens cDNA FLJ11652 fis, clone HE | 1.7 |
| | 102205 | BE242291 | Hs.197540 | hypoxia-inducible factor 1, alpha subunit | 1.7 |
| | 112945 | AW138458 | Hs.20787 | Homo sapiens cDNA: FLJ21688 fis, clone C | 1.7 |
| | 129902 | AA076278 | Hs.13277 | hypothetical protein FLJ22054 | 1.7 |
| 20 | 107157 | AW853745 | Hs.286035 | hypothetical protein FLJ22686 | 1.7 |
| | 133229 | AL137480 | Hs.6834 | KIAA1014 protein | 1.7 |
| | 129912 | AF155096 | Hs.107213 | hypothetical protein FLJ20585 | 1.7 |
| | 119811 | AW137640 | Hs.231444 | Homo sapiens, Similar to hypothetical pr | 1.7 |
| | 126323 | N77584 | Hs.68644 | Homo sapiens microsomal signal peptidase | 1.7 |
| 25 | 133134 | AF198620 | Hs.65648 | RNA binding motif protein 8A | 1.7 |
| | 115278 | AK002163 | Hs.301724 | hypothetical protein FLJ11301 | 1.7 |
| | 133817 | AW578716 | Hs.7644 | H1 histone family, member 2 | 1.7 |
| | 130753 | AA205223 | Hs.189 | phosphodiesterase 4C, cAMP-specific (dun | 1.7 |
| | 107463 | AW952022 | Hs.315164 | hypothetical protein similar to actin re | 1.7 |
| 30 | 121009 | NM_001533 | Hs.2730 | heterogeneous nuclear ribonucleoprotein | 1.7 |
| | 125546 | H09950 | | gb:ym01d12.r1 Soares infant brain 1N1B H | 1.7 |
| | 129991 | R28386 | Hs.179925 | ESTs, Weakly similar to ALU8_HUMAN ALU | 1.7 |
| | 119015 | N95490 | Hs.29700 | hypothetical protein FLJ20094 | 1.7 |
| | 100058 | | | | 1.7 |
| 35 | 116655 | AF271732 | Hs.68090 | bridging integrator-3 | 1.7 |
| | 119898 | R93325 | Hs.58690 | ESTs | 1.7 |
| | 105021 | H07960 | Hs.306044 | CGI-05 protein | 1.7 |
| | 102098 | N25485 | Hs.330310 | maternal G10 transcript | 1.7 |
| | 126730 | AA442429 | | gb:zv70g02.r1 Soares_total_fetus_Nb2HF8_ | 1.7 |
| 40 | 113427 | T85105 | Hs.15471 | ESTs | 1.7 |
| | 122317 | T85253 | Hs.290874 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 1.7 |
| | 130503 | BE208491 | Hs.295112 | KIAA0618 gene product | 1.7 |
| | 117348 | N24157 | | gb:yx96b12.s1 Soares melanocyte 2NbHM Ho | 1.7 |
| | 127033 | AF169301 | Hs.9098 | sulfate transporter 1 | 1.7 |
| 45 | 128554 | AW972147 | Hs.101395 | hypothetical protein MGC11352 | 1.7 |
| | 124733 | R20547 | Hs.100830 | ESTs | 1.7 |
| | 106310 | R98185 | Hs.17240 | ESTs | 1.7 |
| | 122638 | AL137476 | Hs.123609 | Homo sapiens mRNA; cDNA DKFZp434i0623 (f | 1.7 |
| | 101075 | L03532 | Hs.79024 | heterogeneous nuclear ribonucleoprotein | 1.7 |
| 50 | 126659 | T16245 | | gb:N1B1005R Normalized infant brain, Ben | 1.7 |
| | 127717 | F12209 | Hs.173380 | CK2 interacting protein 1; HQ0024c prote | 1.7 |
| | 105441 | N28522 | Hs.8935 | quinolinate phosphoribosyltransferase (n | 1.7 |
| | 104188 | AA478423 | Hs.300870 | Homo sapiens mRNA; cDNA DKFZp547M072 (fr | 1.7 |
| | 134750 | L25073 | Hs.11139 | cold shock domain protein A | 1.7 |
| 55 | 106826 | BE253927 | Hs.24983 | hypothetical protein from EUROIMAGE 2021 | 1.7 |
| | 113511 | T89578 | Hs.189740 | ESTs | 1.7 |
| | 111070 | NM_006201 | Hs.171834 | PCTAIRE protein kinase 1 | 1.7 |
| | 129091 | AA056483 | Hs.301463 | Human Chromosome 16 BAC clone CIT987SK-A | 1.7 |
| | 129710 | AJ277841 | Hs.120963 | ELG protein | 1.7 |
| 60 | 132833 | U78525 | Hs.57783 | eukaryotic translation initiation factor | 1.7 |
| | 125775 | AW514585 | Hs.29205 | alpha integrin binding protein 63 | 1.7 |
| | 113675 | T81034 | Hs.14841 | ESTs | 1.7 |
| | 100487 | AJ076640 | Hs.15243 | nucleolar protein 1 (120kD) | 1.7 |
| | 119302 | T25725 | | gb:ESTDIR152 CD34+DIRECTIONAL Homo sapie | 1.7 |
| 65 | 128245 | AA993101 | Hs.170486 | ESTs | 1.7 |
| | 130322 | NM_014247 | Hs.154545 | PDZ domain containing guanine nucleotide | 1.7 |
| | 135363 | AW589601 | Hs.119 | Wilms' tumour 1-associating protein | 1.7 |
| | 125181 | R40815 | Hs.12396 | ESTs, Weakly similar to 2004399A chromos | 1.7 |
| | 132347 | BE271016 | Hs.169850 | ESTs, Weakly similar to T21554 hypotheti | 1.7 |
| 70 | 127206 | AW816490 | Hs.337508 | ESTs | 1.7 |
| | 121880 | AW946155 | Hs.7750 | hypothetical protein AL133206 | 1.7 |
| | 125797 | H03117 | Hs.111497 | similar to mouse neuronal protein 15.6 | 1.7 |
| | 114601 | AA075566 | | gb:zm8806.s1 Stratagene ovarian cancer | 1.7 |
| | 126278 | AA417302 | Hs.63042 | DKFZp554J157 protein | 1.7 |
| 75 | 120964 | AA398085 | Hs.142390 | ESTs | 1.7 |
| | 133634 | AL035071 | Hs.234279 | microtubule-associated protein, RP/EB fa | 1.7 |
| | 107025 | AA825523 | Hs.21255 | ESTs, Weakly similar to T38022 hypotheti | 1.7 |
| | 105638 | AA493453 | Hs.247817 | H2B histone family, member A | 1.7 |
| | 135398 | M16029 | Hs.287270 | ret proto-oncogene (multiple endocrine | 1.7 |
| 80 | 115794 | AA424900 | Hs.112227 | membrane-associated nucleic acid binding | 1.7 |
| | 102083 | T35901 | Hs.75117 | interleukin enhancer binding factor 2, 4 | 1.7 |
| | 100188 | AW247090 | Hs.57101 | minichromosome maintenance deficient (S, | 1.7 |
| | 130688 | AB037855 | Hs.171917 | hypothetical protein FLJ11085 | 1.7 |
| | 110493 | AI247707 | Hs.36915 | ESTs | 1.7 |

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|--------|------------------|--|
| 129969 | genbank_N57818 | |
| 117031 | genbank_H88353 | |
| 101447 | entrez_M21305 | |
| 124540 | genbank_N63232 | |
| 124554 | genbank_N65961 | |
| 117348 | genbank_N24157 | |
| 117357 | genbank_N24829 | |
| 124677 | genbank_R01073 | |
| 124694 | genbank_R08108 | |
| 103138 | entrez_X65965 | |
| 103305 | entrez_X82279 | |
| 103392 | entrez_X94563 | |
| 103403 | entrez_X95406 | |
| 119229 | genbank_T03229 | |
| 119302 | genbank_T25725 | |
| 126825 | 430458_1 | AA100230 AA100274 |
| 105225 | genbank_AA211777 | |
| 121292 | genbank_AA401807 | |
| 112853 | genbank_T02843 | T02843 |
| 121387 | genbank_AA405854 | |
| 114601 | genbank_AA075566 | |
| 100221 | entrez_D28383 | D28383 |
| 123197 | genbank_AA489250 | AA489250 |
| 114740 | 379876_1 | N70103 N70020 AW383189 AJ207469 W00935 W00906 AA551569 AJ343637 AA135199 |
| 123331 | genbank_AA497013 | |
| 107794 | genbank_AA019255 | |
| 100554 | tigr_HT2241 | M95923 |
| 123423 | genbank_AA598484 | |
| 123474 | genbank_AA599209 | |
| 109061 | genbank_AA160896 | |

TABLE 3A: About 1346 Genes Up-regulated in Acute Lymphocytic Leukemia (ALL) Compared to Normal Adult Hematopoietic Tissues

Table 3A lists about 1346 genes up-regulated in acute lymphocytic leukemia (ALL) compared to normal adult hematopoietic tissues. These were selected from 35403 probesets on the Affymetrix/Eos Hu01 GeneChip array such that the ratio of "average" leukemia to "average" normal adult hematopoietic tissues was greater than or equal to 3.0. The "average" leukemia level was set to the 85th percentile amongst various ALL samples. The "average" normal adult hematopoietic tissue level was set to the 75th percentile amongst various non-malignant hematopoietic tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of leukemia to hematopoietic tissues

| Pkey | ExAccn | UnigenelD | Unigene Title | R1 |
|--------|-----------|-----------|--|-------|
| 129498 | AA449789 | Hs.75511 | connective tissue growth factor | 57.88 |
| 100458 | S74019 | Hs.247979 | pre-B lymphocyte gene 1 | 49.45 |
| 133774 | X54079 | Hs.76067 | heat shock 27kD protein 1 | 48.42 |
| 102564 | U59423 | Hs.79067 | MAD (mothers against decapentaplegic, Dr | 41.49 |
| 130650 | AB040951 | Hs.284208 | DKFZP434N161 protein | 35.88 |
| 132922 | AF249745 | Hs.6066 | Rho guanine nucleotide exchange factor | 35.74 |
| 112254 | AA852097 | Hs.25829 | ras-related protein | 33.28 |
| 106706 | AB037810 | Hs.18760 | KIAA1389 protein | 32.39 |
| 101050 | AU077324 | Hs.1832 | neuropeptide Y | 30.68 |
| 102455 | U48705 | Hs.75562 | discoidin domain receptor family, member | 26.81 |
| 101838 | BE243845 | Hs.75511 | connective tissue growth factor | 25.46 |
| 113374 | T79925 | Hs.269165 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 24.69 |
| 134125 | NM_014781 | Hs.50421 | KIAA0203 gene product | 24.63 |
| 106943 | AW888222 | Hs.9973 | tensin | 23.14 |
| 130069 | AJ754813 | Hs.146428 | collagen, type V, alpha 1 | 23.06 |
| 119073 | BE245360 | Hs.279477 | ESTs | 22.53 |
| 130444 | M12125 | Hs.300772 | tropomyosin 2 (beta) | 21.96 |
| 100420 | D86983 | Hs.118893 | Melanoma associated gene | 21.05 |
| 114324 | AF084481 | Hs.26077 | Wolfram syndrome 1 (wolframin) | 18.95 |
| 101400 | M15990 | Hs.194148 | v-yes-1 Yamaguchi sarcoma viral oncogene | 18.46 |
| 102759 | NM_005100 | Hs.788 | A kise (PRKA) anchor protein (gravin) | 17.88 |
| 100893 | BE245294 | Hs.180789 | S164 protein | 16.75 |
| 131689 | AB012124 | Hs.30696 | transcription factor-like 5 (basic helix | 16.60 |
| 106410 | AB037787 | Hs.26229 | neurotigin 2 | 16.51 |
| 101304 | AA001021 | Hs.6685 | thyroid hormone receptor Interactor 8 | 15.60 |
| 131524 | AB040927 | Hs.301804 | KIAA1494 protein | 15.01 |
| 107794 | AA019255 | | gb:ze56e10.s1 Soares refi N2b4HR Homo | 14.78 |
| 129213 | AJ146494 | Hs.109525 | ESTs, Weakly similar to IRX2_HUMAN IROQU | 14.76 |
| 116068 | AA328041 | Hs.194329 | hypothetical protein FLJ21174 | 14.24 |
| 134416 | X68264 | Hs.211579 | melanoma cell adhesion molecule | 14.06 |
| 134545 | AJ902899 | Hs.85155 | butyrate response factor 1 (EGF-response | 14.03 |
| 114009 | AJ248544 | Hs.103000 | KIAA0831 protein | 13.93 |
| 115110 | AK001671 | Hs.11387 | KIAA1453 protein | 13.75 |
| 130107 | AF112977 | Hs.172887 | phytanoyl-CoA hydroxylase (Refsum diseas | 13.60 |
| 133558 | X68945 | Hs.748 | fibroblast growth factor receptor 1 (fms | 13.60 |
| 100871 | T85231 | Hs.179661 | tubulin, beta 5 | 13.50 |
| 101462 | AL035668 | Hs.73853 | bone morphogenetic protein 2 | 13.48 |
| 120809 | AA346495 | | gb:EST52657 Fetal heart II Homo sapiens | 13.33 |

| | | | | | |
|----|--------|-----------|-----------|---|-------|
| 5 | 123340 | AA504264 | Hs.182937 | peptidylprolyl isomerase A (cyclophilin) | 13.25 |
| | 103460 | AI021993 | Hs.14331 | S100 calcium-binding protein A13 | 13.25 |
| | 102460 | U48959 | Hs.211582 | myosin, light polypeptide kise | 13.14 |
| | 100168 | H73444 | Hs.394 | adrenomedullin | 13.09 |
| | 115844 | AI373062 | Hs.332938 | hypothetical protein MGC5370 | 13.00 |
| | 130103 | Y13492 | Hs.149098 | smoothelin | 12.92 |
| | 102407 | AW602154 | Hs.82143 | E74-like factor 2 (els domain transcript) | 12.03 |
| | 113632 | T94907 | Hs.188572 | ESTs | 11.85 |
| 10 | 118951 | NM_000448 | Hs.73958 | recombination activating gene 1 | 11.73 |
| | 100305 | NM_004941 | Hs.171872 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypep | 11.63 |
| | 109737 | AA055415 | Hs.13233 | ESTs, Moderately similar to A47582 B-cell | 11.55 |
| | 122577 | AA829725 | Hs.334437 | hypothetical protein MGC4248 | 11.49 |
| | 115147 | AA745781 | Hs.38399 | hypothetical protein MGC2454 | 11.40 |
| 15 | 132303 | BE177330 | Hs.325093 | Homo sapiens cD: FLJ21210 fis, clone C | 11.37 |
| | 103176 | AL021154 | Hs.76884 | inhibitor of D binding 3, dominant neg | 11.17 |
| | 108358 | M81933 | Hs.1634 | cell division cycle 25A | 11.15 |
| | 104584 | AA704538 | Hs.193777 | ESTs | 11.12 |
| | 106777 | AF037261 | Hs.33787 | vinexin beta (SH3-containing adaptor mol | 11.08 |
| 20 | 121054 | AW976570 | Hs.97387 | ESTs | 10.90 |
| | 119400 | T92767 | | gb:ye27d06.s1 Stratagene lung (937210) H | 10.83 |
| | 126610 | AI911353 | Hs.191391 | ESTs | 10.83 |
| | 134555 | U34879 | Hs.85279 | hydroxysteroid (17-beta) dehydrogese 1 | 10.80 |
| | 131555 | T47364 | Hs.278613 | interferon, alpha-inducible protein 27 | 10.79 |
| 25 | 130979 | NM_012446 | Hs.169833 | single-stranded-D-binding protein | 10.70 |
| | 113783 | AL359588 | Hs.7041 | hypothetical protein DKFZp7628226 | 10.65 |
| | 123503 | AW975051 | Hs.293156 | ESTs, Weakly similar to I78885 serine/th | 10.60 |
| | 117031 | H88353 | | gb:yu21a02.s1 Morton Fetal Cochlea Homo | 10.45 |
| | 100752 | T81309 | Hs.251664 | insulin-like growth factor 2 (somatomedi | 10.44 |
| 30 | 102618 | AL037672 | Hs.81071 | extracellular matrix protein 1 | 10.36 |
| | 113089 | T40707 | Hs.270862 | ESTs | 10.33 |
| | 132089 | W22007 | Hs.39122 | hypothetical protein MGC15737 | 10.29 |
| | 101663 | NM_003528 | Hs.2178 | H2B histone family, member Q | 10.23 |
| 35 | 104876 | AI933128 | Hs.25220 | like-glycosyltransferase | 10.23 |
| | 106370 | AF039843 | Hs.18676 | sprouty (Drosophila) homolog 2 | 10.18 |
| | 129406 | AB018255 | Hs.111138 | KIAA0712 gene product | 10.18 |
| | 115354 | AA281636 | Hs.334827 | ESTs | 10.13 |
| | 123077 | AA485229 | Hs.105649 | ESTs | 10.05 |
| | 131273 | AW206008 | Hs.283378 | Homo sapiens cD: FLJ21778 fis, clone H | 9.95 |
| 40 | 126177 | AW752782 | Hs.129750 | hypothetical protein FLJ10546 | 9.83 |
| | 133699 | BE501689 | Hs.75617 | collagen, type IV, alpha 2 | 9.80 |
| | 110855 | AB007928 | Hs.28169 | KIAA0459 protein | 9.65 |
| | 111826 | R35975 | | gb:yh91b07.s1 Soares placenta Nb2HP Homo | 9.58 |
| | 126947 | Z40778 | Hs.191837 | ESTs | 9.50 |
| 45 | 116674 | AI768015 | Hs.92127 | ESTs | 9.48 |
| | 129087 | AI348027 | Hs.108557 | hypothetical protein PP1057 | 9.46 |
| | 114837 | BE244930 | Hs.166895 | ESTs | 9.45 |
| | 120009 | AI080491 | Hs.93270 | ESTs, Moderately similar to S65657 alpha | 9.45 |
| 50 | 112483 | AW969785 | Hs.285885 | Homo sapiens cD FLJ11321 fis, clone PL | 9.40 |
| | 103487 | AA743603 | Hs.172108 | nucleoporin 88kD | 9.30 |
| | 105675 | AL390083 | Hs.271277 | hypothetical protein from EUROMIMAGE 3636 | 9.28 |
| | 129158 | NM_004413 | Hs.109 | dipeptidase 1 (rel) | 9.23 |
| | 114394 | T34462 | Hs.103291 | neuritin | 9.17 |
| | 133331 | Y14487 | Hs.738 | ribosomal protein L14 | 9.11 |
| 55 | 114787 | AA156509 | Hs.231892 | ESTs, Weakly similar to S65657 alpha-1C- | 9.10 |
| | 125502 | AW977181 | Hs.194718 | zinc finger protein 265 | 9.03 |
| | 132325 | N37065 | Hs.44856 | hypothetical protein FLJ12116 | 9.01 |
| | 127968 | AA830201 | Hs.124347 | ESTs | 9.00 |
| | 114605 | AL157423 | Hs.306478 | Homo sapiens mR; cD DKFZp76100511 (f | 8.93 |
| 60 | 114875 | AA235609 | Hs.236443 | Homo sapiens mR; cD DKFZp564N1063 (f | 8.93 |
| | 129898 | AI672731 | Hs.13256 | ESTs | 8.89 |
| | 106263 | W21493 | Hs.28329 | hypothetical protein FLJ14005 | 8.89 |
| | 117130 | AA748850 | Hs.125830 | bladder cancer overexpressed protein | 8.88 |
| | 105553 | AA256756 | Hs.31178 | ESTs | 8.85 |
| 65 | 103657 | Z73677 | | gb:H.sapiens gene encoding plakophilin 1 | 8.83 |
| | 105831 | AA329449 | Hs.247302 | twisted gastrulation | 8.82 |
| | 106375 | AW872878 | Hs.289072 | hypothetical protein FLJ22175 | 8.80 |
| | 114518 | AW163267 | Hs.106469 | suppressor of var1 (S.cerevisiae) 3-like | 8.75 |
| | 123433 | AW450922 | Hs.112478 | ESTs | 8.67 |
| 70 | 134558 | NM_001773 | Hs.85289 | CD34 antigen | 8.67 |
| | 115893 | AI652127 | Hs.48419 | ESTs | 8.67 |
| | 128621 | AA032197 | Hs.102558 | Homo sapiens, clone MGC:5352, mR, comp | 8.60 |
| | 122798 | AW366286 | Hs.145696 | splicing factor (CC1.3) | 8.58 |
| | 112554 | R71489 | Hs.29196 | EST | 8.55 |
| 75 | 129969 | N57818 | | gb:yu59d07.s1 Soares fetal liver spleen | 8.53 |
| | 131558 | AA453208 | Hs.28726 | RAB9, member RAS oncogene family | 8.45 |
| | 134027 | Z97630 | Hs.226117 | H1 histone family, member 0 | 8.45 |
| | 134138 | AB023169 | Hs.7935 | KIAA0952 protein | 8.43 |
| | 120030 | AI076355 | Hs.58694 | ESTs | 8.43 |
| 80 | 101005 | NM_005239 | Hs.85146 | v-ets avian erythroblastosis virus E26 o | 8.33 |
| | 115423 | AI499516 | Hs.89303 | ESTs | 8.33 |
| | 104946 | AW242407 | Hs.73848 | carcinoembryonic antigen-related cell ad | 8.30 |
| | 131965 | W79283 | Hs.35962 | ESTs | 8.30 |
| | 126426 | AA125984 | | gb:zn27h06.r1 Stratagene neuroepithelium | 8.28 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| 5 | 108886 | AW248434 | Hs.91521 | hypothetical protein | 8.26 |
| | 107985 | T40064 | Hs.71968 | Homo sapiens mR: cD DKFZp564F053 (fr | 8.25 |
| | 114239 | AL137667 | Hs.267445 | Homo sapiens mR: cD DKFZp434B231 (fr | 8.23 |
| | 124281 | AJ333756 | Hs.111801 | arsenic resistance protein ARS2 | 8.23 |
| | 117099 | H93699 | | gbcyv16a11.s1 Soares fetal liver spleen | 8.20 |
| 10 | 119432 | AL120247 | Hs.40109 | KIAA0872 protein | 8.15 |
| | 115957 | AI745379 | Hs.42911 | ESTs | 8.15 |
| | 132355 | D87942 | Hs.46328 | glucosyltransferase 2 (secretor status in | 8.13 |
| | 108339 | AW151340 | Hs.51615 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 8.10 |
| | 131694 | NM_000246 | Hs.3076 | MHC class II transactivator | 8.05 |
| 15 | 104897 | N33937 | Hs.10336 | ESTs | 8.03 |
| | 120266 | AI807264 | Hs.205442 | ESTs, Weakly similar to T34036 hypotheti | 8.03 |
| | 130404 | AI672727 | Hs.76753 | endoglin (Osler-Rendu-Weber syndrome 1) | 8.00 |
| | 115729 | AA417812 | Hs.38775 | ESTs | 8.00 |
| | 127216 | AI798703 | Hs.143702 | ESTs, Weakly similar to S70029 probable | 7.95 |
| 20 | 131693 | AW963776 | Hs.110796 | SAR1 protein | 7.93 |
| | 113107 | AI821027 | Hs.8429 | ESTs | 7.90 |
| | 122282 | BE246331 | Hs.98401 | Homo sapiens mR full length insert cDN | 7.90 |
| | 111040 | AI435502 | Hs.14931 | ESTs | 7.90 |
| | 127987 | AI022103 | Hs.124511 | ESTs | 7.90 |
| 25 | 125317 | Z99348 | Hs.112461 | ESTs, Weakly similar to I38022 hypotheti | 7.88 |
| | 105242 | AI564857 | Hs.27888 | ESTs, Weakly similar to serine/threonine | 7.75 |
| | 100421 | D86985 | Hs.79276 | KIAA0232 gene product | 7.71 |
| | 114359 | NM_016929 | Hs.283021 | chloride intracellular channel 5 | 7.70 |
| | 119772 | AJ250839 | Hs.58241 | gene for serine/threonine protein kinase | 7.70 |
| 30 | 124040 | U23752 | Hs.32964 | SRY (sex determining region Y)-box 11 | 7.65 |
| | 134361 | BE549343 | Hs.82208 | acyl-Coenzyme A dehydrogenase, very long | 7.57 |
| | 105476 | AL117352 | Hs.120828 | Human D sequence from clone RP5-876B10 | 7.55 |
| | 113289 | T66900 | Hs.188446 | ESTs | 7.50 |
| | 122707 | NM_002039 | Hs.239706 | GRB2-associated binding protein 1 | 7.50 |
| 35 | 130055 | AJ568248 | Hs.146355 | v-abl Abelson murine leukemia viral onco | 7.49 |
| | 108766 | AF145713 | Hs.61490 | schwannomin-interacting protein 1 | 7.45 |
| | 107957 | Z36842 | Hs.57548 | ESTs | 7.45 |
| | 123116 | AW190412 | Hs.183738 | FERM, RhoGEF (ARHGEF) and pleckstrin dom | 7.38 |
| | 123190 | AA489212 | Hs.105228 | EST | 7.38 |
| 40 | 129574 | AA026815 | Hs.11463 | UMP-CMP kinase | 7.38 |
| | 115274 | C01566 | Hs.86671 | ESTs | 7.35 |
| | 102571 | U60115 | Hs.239069 | four and a half LIM domains 1 | 7.34 |
| | 116845 | AA649530 | | gbms44f05.s1 NCL CGAP_Alv1 Homo sapiens | 7.33 |
| | 134851 | AB011124 | Hs.90232 | KIAA0552 gene product | 7.33 |
| 45 | 101780 | M82882 | Hs.154365 | E74-like factor 1 (ets domain transcript | 7.28 |
| | 125042 | T78906 | Hs.269432 | ESTs, Moderately similar to ALU1_HUMAN A | 7.28 |
| | 118472 | AL157545 | Hs.42179 | bromodomain and PHD finger containing, 3 | 7.25 |
| | 108700 | AA121518 | Hs.193540 | ESTs, Moderately similar to 2109260A B c | 7.23 |
| | 109411 | R98881 | Hs.109655 | sex comb on midleg (Drosophila)-like 1 | 7.20 |
| 50 | 127692 | AI021912 | Hs.187983 | ESTs | 7.18 |
| | 128501 | AL133572 | Hs.199009 | protein containing CXXC domain 2 | 7.18 |
| | 107727 | AA149707 | Hs.173091 | ubiquitin-like 3 | 7.14 |
| | 118089 | AI762507 | Hs.47878 | ESTs | 7.12 |
| | 106025 | AV653785 | Hs.173334 | ELL-RELATED R POLYMERASE II, ELONGATIO | 7.10 |
| 55 | 122111 | AW593206 | Hs.98785 | Ksp37 protein | 7.08 |
| | 119674 | V60379 | Hs.57773 | ESTs | 7.05 |
| | 126607 | V87425 | Hs.114688 | ESTs | 7.05 |
| | 121545 | AA412442 | Hs.98132 | ESTs | 7.05 |
| | 113287 | T66847 | Hs.194040 | ESTs, Weakly similar to I38022 hypotheti | 7.03 |
| 60 | 126672 | AA255592 | Hs.203631 | ESTs, Weakly similar to alternatively sp | 7.00 |
| | 132087 | H14486 | Hs.3903 | Cdc42 effector protein 4; binder of Rho | 6.97 |
| | 118697 | N22706 | Hs.43234 | ESTs | 6.97 |
| | 100295 | M74782 | Hs.172689 | interleukin 3 receptor, alpha (low affin | 6.95 |
| | 101188 | L20320 | Hs.184298 | cyclin-dependent kinase 7 (homolog of Xe | 6.95 |
| 65 | 121481 | AA411931 | | gbzu03g05.s1 Soares_testis_NHT Homo sap | 6.95 |
| | 113003 | AW292315 | Hs.7215 | ESTs | 6.93 |
| | 101851 | BE260964 | Hs.82045 | midkine (neurite growth-promoting factor | 6.91 |
| | 113529 | AI190741 | Hs.177415 | Finkel-Biskis-Reilly murine sarcoma viru | 6.90 |
| | 132887 | AA195831 | Hs.273385 | guanine nucleotide binding protein (G pr | 6.90 |
| 70 | 113560 | T91015 | Hs.268626 | ESTs | 6.85 |
| | 123440 | AI733692 | Hs.112488 | ESTs | 6.83 |
| | 130390 | AA490770 | Hs.182382 | ESTs | 6.83 |
| | 133889 | U48959 | Hs.211582 | myosin, light polypeptide kinase | 6.83 |
| | 113573 | R89379 | Hs.15990 | ESTs | 6.80 |
| 75 | 112453 | R63899 | Hs.28455 | ESTs | 6.78 |
| | 125221 | AA236115 | Hs.120785 | ESTs | 6.78 |
| | 134081 | AL034349 | Hs.79005 | protein tyrosine phosphatase, receptor t | 6.77 |
| | 127610 | AA960867 | Hs.150271 | ESTs, Highly similar to unmed protein | 6.75 |
| | 105486 | AW449258 | Hs.6187 | ESTs | 6.75 |
| 80 | 107796 | AA058848 | Hs.60797 | ESTs | 6.71 |
| | 132754 | AI752244 | Hs.75309 | eukaryotic translation elongation factor | 6.71 |
| | 105806 | AF206019 | Hs.110347 | REV1 (yeast homolog)-like | 6.70 |
| | 110837 | H03109 | Hs.108920 | HT018 protein | 6.65 |
| | 117698 | N62293 | Hs.45107 | ESTs | 6.65 |
| | 128994 | AF205849 | Hs.107740 | Kruppel-like factor 2 (lung) | 6.65 |
| | 129131 | AB026436 | Hs.177534 | dual specificity phosphatase 10 | 6.65 |
| | 108528 | AA650558 | Hs.325202 | ESTs, Highly similar to GBAS_HUMAN GUANI | 6.62 |

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|----|--------|-----------|-----------|--|------|
| | 131009 | AF169802 | Hs.22142 | cytochrome b5 reductase b5R.2 | 6.61 |
| | 129389 | NM_012445 | Hs.288126 | spondin 2, extracellular matrix protein | 6.60 |
| | 125278 | AI218439 | Hs.129998 | enhancer of polycomb 1 | 6.59 |
| 5 | 124667 | W24320 | Hs.102941 | Homo sapiens cD: FLJ21531 fis, clone C | 6.59 |
| | 105640 | AA001021 | Hs.6685 | thyroid hormone receptor interactor 8 | 6.58 |
| | 106474 | BE383668 | Hs.42484 | hypothetical protein FLJ10618 | 6.58 |
| | 105808 | AI133161 | Hs.286131 | CGI-101 protein | 6.53 |
| | 120087 | AF186780 | Hs.79219 | RaiGDS-like gene; KIAA0959 protein | 6.52 |
| 10 | 100514 | AU076887 | Hs.28491 | spermidine/spermine N1-acetyltransferase | 6.50 |
| | 108378 | AI368460 | Hs.74815 | platelet-derived growth factor receptor, | 6.50 |
| | 133350 | AI499220 | Hs.71573 | hypothetical protein FLJ10074 | 6.50 |
| | 115673 | AA406341 | Hs.269908 | Homo sapiens cD FLJ11991 fis, clone HE | 6.48 |
| | 133410 | Y07847 | Hs.73088 | RAS-related on chromosome 22 | 6.48 |
| 15 | 131281 | AA251716 | Hs.25227 | ESTs | 6.46 |
| | 105510 | Z42047 | Hs.283978 | Homo sapiens PRO2751 mR, complete cds | 6.45 |
| | 128766 | AW160432 | Hs.296460 | craniofacial development protein 1 | 6.45 |
| | 114530 | AA601038 | Hs.191797 | ESTs, Weakly similar to S65657 alpha-1C- | 6.43 |
| | 120120 | BE547267 | Hs.59791 | hypothetical protein MGC13183 | 6.40 |
| 20 | 120593 | AA748355 | Hs.193522 | ESTs | 6.40 |
| | 125832 | AA628600 | Hs.117587 | ESTs | 6.38 |
| | 129637 | NM_004606 | Hs.1179 | TATA box binding protein (TBP)-associate | 6.38 |
| | 115302 | AL109719 | Hs.47578 | ESTs | 6.33 |
| | 126137 | AA312594 | Hs.99115 | hypothetical protein FLJ20689 | 6.30 |
| 25 | 114465 | BE621056 | Hs.131731 | hypothetical protein FLJ11099 | 6.29 |
| | 125562 | AI494372 | Hs.98968 | hypothetical protein FLJ23058 | 6.29 |
| | 127380 | AF070554 | Hs.15535 | Homo sapiens clone 24582 mR sequence | 6.26 |
| | 106956 | R06428 | Hs.226351 | ESTs | 6.25 |
| | 105962 | AW880358 | Hs.339808 | hypothetical protein FLJ10120 | 6.25 |
| 30 | 109416 | BE268388 | Hs.86945 | ESTs, Weakly similar to A46010 X-linked | 6.23 |
| | 111116 | AK002039 | Hs.26243 | Homo sapiens cD FLJ11177 fis, clone PL | 6.23 |
| | 127282 | AA347158 | Hs.185780 | ESTs | 6.23 |
| | 113074 | AK001335 | Hs.31137 | protein tyrosine phosphatase, receptor I | 6.21 |
| | 101664 | AA436989 | Hs.121017 | H2A histone family, member A | 6.20 |
| 35 | 103317 | X83441 | Hs.166091 | ligase IV, D, ATP-dependent | 6.20 |
| | 133894 | AW021235 | Hs.180433 | rTS beta protein | 6.19 |
| | 109260 | AW978515 | Hs.131915 | KIAA0863 protein | 6.18 |
| | 112772 | AI992283 | Hs.35437 | ESTs, Moderately similar to I38026 MLN 6 | 6.18 |
| | 132050 | AI267615 | Hs.38022 | ESTs | 6.18 |
| 40 | 113009 | T23699 | Hs.7246 | ESTs | 6.17 |
| | 118835 | AA535246 | Hs.50852 | ESTs | 6.16 |
| | 125626 | AI038854 | Hs.180789 | S164 protein | 6.15 |
| | 117086 | AA581602 | Hs.41840 | ESTs | 6.14 |
| | 101960 | AL036287 | Hs.194662 | calponin 3, acidic | 6.13 |
| 45 | 104488 | N56191 | Hs.106511 | protocadherin 17 | 6.13 |
| | 127695 | AA714731 | Hs.291457 | ESTs, Weakly similar to heterogeneous ri | 6.13 |
| | 127894 | AL121053 | Hs.5534 | Homo sapiens cD FLJ12961 fis, clone NT | 6.13 |
| | 113595 | T92056 | Hs.290240 | ESTs, Moderately similar to ALU2_HUMAN A | 6.10 |
| | 120784 | AW752101 | Hs.16580 | hypothetical protein FLJ11026 | 6.10 |
| 50 | 115004 | AA329340 | Hs.4867 | mannosyl (alpha-1,3)-glycoprotein beta- | 6.08 |
| | 129740 | BE165866 | Hs.83623 | nuclear receptor subfamily 1, group I, m | 6.05 |
| | 117483 | N72185 | Hs.44189 | ESTs | 6.04 |
| | 103815 | BE245294 | Hs.180789 | S164 protein | 6.03 |
| | 122040 | AA847758 | Hs.111030 | ESTs | 6.03 |
| 55 | 109538 | AW977747 | Hs.119120 | E3 ubiquitin ligase SMURF1 | 6.02 |
| | 112727 | T91029 | Hs.15069 | ESTs | 6.01 |
| | 120273 | AA176688 | Hs.269284 | ESTs | 6.00 |
| | 122127 | AW207175 | Hs.106771 | ESTs | 6.00 |
| | 126046 | AA804957 | Hs.119840 | ESTs | 5.99 |
| 60 | 119774 | AB032977 | Hs.6298 | KIAA1151 protein | 5.98 |
| | 106265 | AA412176 | Hs.236463 | Homo sapiens mR; cD DKFZp586i0521 (f | 5.98 |
| | 111987 | NM_015310 | Hs.6763 | KIAA0942 protein | 5.98 |
| | 123619 | AA602964 | | gb:nc097c02.s1 NCL_CGAP_Pr2 Homo sapiens | 5.96 |
| | 128122 | AI267491 | Hs.160593 | ESTs | 5.95 |
| 65 | 128473 | T78277 | Hs.100293 | O-linked N-acetylglucosamine (Glc) tr | 5.95 |
| | 102283 | AW161552 | Hs.83381 | guanine nucleotide binding protein 11 | 5.94 |
| | 122468 | AA448172 | Hs.137687 | ESTs, Highly similar to K6B1_HUMAN RIBOS | 5.93 |
| | 101801 | M86407 | Hs.1216 | actinin, alpha 3 | 5.93 |
| | 107059 | BE614410 | Hs.23044 | RAD51 (S. cerevisiae) homolog (E coli Re | 5.92 |
| 70 | 108908 | AA136569 | Hs.10848 | KIAA0187 gene product | 5.90 |
| | 121470 | AA558958 | Hs.324751 | ESTs | 5.90 |
| | 131938 | AF176085 | Hs.34956 | neural polypyrimidine tract binding prot | 5.89 |
| | 109613 | H47315 | Hs.27519 | ESTs | 5.89 |
| | 109384 | AA219172 | Hs.86849 | ESTs | 5.88 |
| 75 | 118559 | N68456 | Hs.49519 | ESTs | 5.88 |
| | 102010 | U02687 | Hs.385 | fms-related tyrosine kinase 3 | 5.85 |
| | 105921 | AA421973 | Hs.169119 | ESTs, Weakly similar to T25731 hypotheti | 5.85 |
| | 124298 | H91679 | | gb:yy04a07.s1 Soares fetal liver spleen | 5.84 |
| 80 | 120827 | AA382525 | Hs.132967 | Human EST clone 122887 mariner transposo | 5.82 |
| | 103331 | AI825463 | Hs.147996 | protein kinase, X-linked | 5.80 |
| | 135052 | AL136653 | Hs.93675 | decidual protein induced by progesterone | 5.78 |
| | 115219 | AA262776 | Hs.269314 | Homo sapiens cD FLJ14123 fis, clone MA | 5.78 |
| | 121899 | R55341 | Hs.50421 | KIAA0203 gene product | 5.78 |
| | 135217 | AA453880 | Hs.9658 | hypothetical protein FLJ11790 | 5.77 |

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|----|--------|-----------|-----------|--|------|
| | 123973 | C14805 | | gb:C14805 Clontech human aorta polyA+ mR | 5.77 |
| | 112605 | R79374 | Hs.29852 | ESTs | 5.76 |
| | 110151 | H18835 | Hs.31608 | hypothetical protein FLJ20041 | 5.75 |
| 5 | 129889 | AA810932 | Hs.131899 | ESTs, Weakly similar to T00370 hypotheti | 5.75 |
| | 102638 | U67319 | Hs.9216 | ESTs, Weakly similar to T00370 hypotheti | 5.73 |
| | 121501 | AA470687 | Hs.104772 | ESTs | 5.73 |
| | 124921 | R93082 | Hs.332635 | ESTs | 5.70 |
| | 109850 | AI150548 | Hs.23155 | ESTs | 5.70 |
| 10 | 120594 | AW136478 | Hs.5094 | ring finger protein 10 | 5.70 |
| | 126433 | AA325606 | | gb:EST28707 Cerebellum II Homo sapiens c | 5.70 |
| | 100455 | AW888941 | Hs.75789 | N-myc downstream regulated | 5.69 |
| | 106565 | NM_014892 | Hs.227602 | KIAA1116 protein | 5.68 |
| | 120912 | AA376690 | Hs.187650 | ESTs | 5.68 |
| 15 | 127209 | AA305023 | Hs.81964 | SEC24 (S. cerevisiae) related gene famil | 5.68 |
| | 107606 | AF207989 | Hs.330425 | Homo sapiens, Similar to G protein-coupl | 5.67 |
| | 106597 | AI091277 | Hs.302634 | frizzled (Drosophila) homolog 8 | 5.66 |
| | 102126 | AW950870 | Hs.78961 | protein phosphatase 1, regulatory (inhib | 5.65 |
| | 100064 | | | AFX control - TrpX-3 | 5.63 |
| 20 | 108758 | AA127395 | Hs.222414 | ESTs | 5.63 |
| | 101392 | NM_002507 | Hs.1827 | nerve growth factor receptor (TNFR super | 5.61 |
| | 102211 | BE314524 | Hs.78776 | putative transmembrane protein | 5.60 |
| | 107427 | W26975 | Hs.46736 | hypothetical protein FLJ23476 | 5.60 |
| | 135175 | M91463 | Hs.95958 | solute carrier family 2 (facilitated glu | 5.60 |
| 25 | 111764 | AA420368 | Hs.290259 | ESTs, Weakly similar to I38022 hypotheti | 5.58 |
| | 119405 | T93865 | Hs.91085 | ESTs | 5.58 |
| | 126464 | AI990046 | Hs.54780 | transcription termination factor, R po | 5.58 |
| | 133865 | AB011155 | Hs.170290 | discs, large (Drosophila) homolog 5 | 5.58 |
| | 123255 | AA830335 | Hs.105273 | ESTs | 5.57 |
| | 122861 | AA335721 | Hs.119394 | ESTs | 5.56 |
| 30 | 112046 | AA383343 | Hs.22116 | CDC14 (cell division cycle 14, S. cerevi | 5.55 |
| | 132906 | BE613337 | Hs.234896 | geminin | 5.55 |
| | 109001 | AI056548 | Hs.72116 | hypothetical protein FLJ20992 similar to | 5.55 |
| | 115816 | BE042915 | Hs.287588 | Homo sapiens cD FLJ13675 fis, clone PL | 5.55 |
| 35 | 128401 | R01865 | Hs.268586 | ESTs | 5.53 |
| | 129296 | AI051967 | Hs.110122 | ESTs | 5.53 |
| | 120314 | T10013 | Hs.221040 | HBS1 (S. cerevisiae)-like | 5.51 |
| | 132815 | AI815189 | Hs.57475 | sex comb on midleg homolog 1 | 5.50 |
| | 113983 | W87415 | Hs.55296 | HLA-B associated transcript-1 | 5.50 |
| 40 | 105002 | AA224244 | Hs.182704 | ESTs, Moderately similar to altitivel | 5.49 |
| | 132025 | AA011117 | Hs.3745 | milk fat globule-EGF factor 8 protein | 5.49 |
| | 110732 | AW070838 | Hs.174174 | KIAA601 protein | 5.48 |
| | 112891 | T03927 | Hs.293147 | ESTs, Moderately similar to A46010 X-fin | 5.48 |
| | 126758 | AI559444 | Hs.293960 | ESTs | 5.48 |
| 45 | 129426 | AF077953 | Hs.111323 | Protein inhibitor of activated STAT X | 5.47 |
| | 103217 | NM_001841 | Hs.73037 | carbinoid receptor 2 (macrophage) | 5.46 |
| | 132261 | U80743 | Hs.306094 | trinucleotide repeat containing 12 | 5.45 |
| | 105586 | AA865118 | Hs.191538 | ESTs | 5.43 |
| | 109454 | AA232255 | Hs.295232 | ESTs, Moderately similar to A46010 X-fin | 5.43 |
| 50 | 113063 | W15573 | Hs.5027 | ESTs, Weakly similar to A47582 B-cell gr | 5.43 |
| | 134092 | AA218558 | Hs.7905 | sorting nexin 9 | 5.41 |
| | 119316 | AI114630 | Hs.208334 | Homo sapiens cD: FLJ21874 fis, clone H | 5.38 |
| | 108019 | AI017773 | Hs.249159 | adrenergic, alpha-2A-, receptor | 5.38 |
| | 109421 | AW604652 | Hs.332442 | ESTs | 5.38 |
| 55 | 111929 | AF027208 | Hs.112360 | prominin (mouse)-like 1 | 5.38 |
| | 119718 | W69216 | Hs.92848 | ESTs | 5.38 |
| | 106154 | BE540255 | Hs.6994 | Homo sapiens cD: FLJ22044 fis, clone H | 5.35 |
| | 108544 | W39433 | Hs.23971 | hypothetical protein DKFZp547N043 | 5.35 |
| | 119580 | AL079310 | Hs.92260 | high-mobility group protein 2-like 1 | 5.35 |
| 60 | 126777 | AL157491 | Hs.145211 | Homo sapiens mR: cD DKFZp434K1111 (f | 5.35 |
| | 112944 | H18063 | Hs.13254 | ESTs | 5.34 |
| | 103149 | NM_006201 | Hs.171834 | PCTAIRE protein kinase 1 | 5.34 |
| | 132437 | AA152105 | Hs.4859 | cyclin L ania-6a | 5.33 |
| | 103860 | AW976877 | Hs.38057 | ESTs | 5.33 |
| 65 | 104865 | T79340 | Hs.22575 | B-cell CLL/lymphoma 6, member B (zinc fi | 5.33 |
| | 129914 | NM_012421 | Hs.13321 | rearranged L-myc fusion sequence | 5.33 |
| | 130309 | AF067804 | Hs.15423 | hypothetical protein HDCCMC04P | 5.31 |
| | 116312 | BE379794 | Hs.65403 | hypothetical protein | 5.30 |
| | 124191 | T96509 | Hs.248549 | ESTs, Moderately similar to S65657 alpha | 5.28 |
| 70 | 125583 | AA195667 | Hs.86022 | ESTs | 5.28 |
| | 130591 | N59646 | Hs.169745 | crumbs (Drosophila) homolog 1 | 5.28 |
| | 116355 | AA789133 | Hs.88650 | ESTs | 5.26 |
| | 115553 | AJ275986 | Hs.71414 | transcription factor (SMIF gene) | 5.26 |
| | 122802 | AI687303 | Hs.285529 | G protein-coupled receptor 49 | 5.25 |
| 75 | 128495 | NM_005904 | Hs.100602 | MAD (mothers against decapentaplegic, Dr | 5.24 |
| | 117667 | U59305 | Hs.44708 | Ser-Thr protein kinase related to the my | 5.23 |
| | 127890 | AA294934 | Hs.293902 | ESTs, Weakly similar to ISHUS5 protein d | 5.22 |
| | 134843 | AA428520 | Hs.90061 | progesterone binding protein | 5.21 |
| | 120968 | AA528283 | Hs.292737 | ESTs | 5.21 |
| 80 | 102076 | BE299197 | Hs.179665 | cyclin-dependent kinase inhibitor 1A (p2 | 5.20 |
| | 100934 | J03019 | Hs.99913 | adrenergic, beta-1-, receptor | 5.20 |
| | 112667 | BE538516 | Hs.15423 | hypothetical protein HDCCMC04P | 5.20 |
| | 119304 | AW249266 | Hs.98493 | X-ray repair complementing defective rep | 5.20 |
| | 131868 | AW408296 | Hs.33532 | zinc finger protein 151 (pH2-67) | 5.20 |

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|----|--------|-----------|-----------|--|------|
| 5 | 105914 | AW245680 | Hs.9701 | growth arrest and D-damage-inducible, | 5.18 |
| | 102258 | NM_001546 | Hs.34853 | inhibitor of D binding 4, dominant neg | 5.18 |
| | 103850 | AA187101 | Hs.213194 | hypothetical protein MGC10895 | 5.18 |
| | 112516 | T83909 | | gb:yd67f10.1 Soares fetal liver spleen | 5.18 |
| | 133640 | AW246428 | Hs.75355 | ubiquitin-conjugating enzyme E2N (homolo | 5.18 |
| 10 | 135180 | D90070 | Hs.96 | phorbol-12-myristate-13-acetate-induced | 5.18 |
| | 135309 | AI564123 | Hs.42500 | ADP-ribosylation factor-like 5 | 5.18 |
| | 134801 | S76825 | Hs.89695 | insulin receptor | 5.17 |
| | 133362 | AK001519 | Hs.7194 | CGI-74 protein | 5.17 |
| | 135206 | AB024703 | Hs.96334 | ring finger protein 11 | 5.15 |
| 15 | 111480 | R06453 | Hs.19706 | ESTs | 5.15 |
| | 118466 | N66741 | | gb:yz33g08.s1 Morton Fetal Cochlea Homo | 5.15 |
| | 125757 | AI274906 | Hs.166835 | ESTs, Highly similar to 1814460A p53-ass | 5.15 |
| | 127140 | AI273507 | Hs.303966 | ESTs | 5.15 |
| | 109223 | AW000714 | Hs.65818 | ESTs | 5.14 |
| 20 | 103656 | Z73497 | Hs.247802 | Human D sequence from clone U240C2 on | 5.14 |
| | 133388 | AW245631 | Hs.182447 | heterogeneous nuclear ribonucleoprotein | 5.12 |
| | 100511 | M76676 | Hs.116840 | ESTs | 5.10 |
| | 101941 | S77583 | | gb:HERVK10/HUMMTV reverse transcriptase | 5.10 |
| | 109937 | AI084066 | Hs.20072 | myosin regulatory light chain interactin | 5.10 |
| 25 | 122996 | AI436216 | Hs.191715 | ESTs, Weakly similar to ZN91_HUMAN ZINC | 5.10 |
| | 128242 | AA992626 | Hs.269755 | ESTs, Moderately similar to ALU5_HUMAN A | 5.10 |
| | 112374 | NM_016323 | Hs.26663 | cyclin-E binding protein 1 | 5.10 |
| | 124506 | BE273688 | Hs.182447 | heterogeneous nuclear ribonucleoprotein | 5.10 |
| | 104216 | AB002313 | Hs.3989 | plexin B2 | 5.09 |
| 30 | 135051 | AI272141 | Hs.83484 | SRY (sex determining region Y)-box 4 | 5.08 |
| | 131629 | Z45794 | Hs.238809 | ESTs | 5.08 |
| | 111722 | R23924 | Hs.23596 | EST | 5.07 |
| | 107034 | AF257770 | Hs.20930 | poly(rC)-binding protein 4 | 5.06 |
| | 110243 | H26683 | | gb:yl14g03.s1 Soares breast 2NbHBst Homo | 5.05 |
| 35 | 125837 | AW968123 | Hs.333513 | small inducible cytokine subfamily E, me | 5.05 |
| | 130300 | X58288 | Hs.154151 | protein tyrosine phosphatase, receptor t | 5.05 |
| | 103957 | AL120051 | Hs.144700 | ephrin-B1 | 5.04 |
| | 112678 | AI418466 | Hs.33665 | ESTs | 5.03 |
| | 124963 | F06600 | Hs.101375 | Homo sapiens mR; cD DKFZp434H205 (tr | 5.03 |
| 40 | 131379 | AK001123 | Hs.26176 | hypothetical protein FLJ10261 | 5.03 |
| | 109451 | N32264 | Hs.44330 | ESTs | 5.02 |
| | 101396 | BE267931 | Hs.78996 | proliferating cell nuclear antigen | 5.02 |
| | 131038 | W87778 | Hs.169388 | hypothetical protein DKFZp761H2024 | 5.01 |
| | 101208 | L25081 | Hs.179735 | ras homolog gene family, member C | 5.01 |
| 45 | 104973 | NM_015310 | Hs.6763 | KIAA0942 protein | 4.99 |
| | 103141 | X68113 | Hs.75584 | polymyositis/scleroderma autoantigen 2 { | 4.98 |
| | 111260 | AB033035 | Hs.51965 | KIAA1209 protein | 4.98 |
| | 128142 | T67162 | Hs.135127 | ESTs, Weakly similar to unmed protein | 4.98 |
| | 113857 | AW243158 | Hs.5297 | DKFZP564A2416 protein | 4.96 |
| 50 | 105292 | AF128542 | Hs.166846 | polymerase (D directed), epsilon | 4.95 |
| | 114341 | AF270491 | Hs.28249 | hepatocellular carcinoma-associated anti | 4.95 |
| | 100615 | W32474 | Hs.301746 | RAP2A, member of RAS oncogene family | 4.95 |
| | 103208 | AW411340 | Hs.31314 | retinoblastoma-binding protein 7 | 4.95 |
| | 121121 | AA399371 | Hs.189095 | similar to SALL1 (sal (Drosophila)-like | 4.95 |
| 55 | 125321 | T86652 | Hs.178294 | ESTs | 4.95 |
| | 101145 | L13210 | Hs.79339 | lectin, galactoside-binding, soluble, 3 | 4.95 |
| | 100551 | M73980 | Hs.129053 | Homo sapiens NOTCH 1 (N1) mR, complete | 4.93 |
| | 126182 | AA721331 | Hs.293771 | ESTs | 4.93 |
| | 127925 | AA805151 | Hs.3628 | mitogen-activated protein kinase kinase | 4.93 |
| 60 | 133969 | AA569112 | Hs.78 | GA-binding protein transcription factor, | 4.93 |
| | 120873 | AA358015 | | gb:EST66864 Fetal lung III Homo sapiens | 4.92 |
| | 125219 | AI804331 | Hs.99423 | ATP-dependent R helicase | 4.91 |
| | 102790 | BE245277 | Hs.154195 | E4F transcription factor 1 | 4.90 |
| | 129486 | NM_005754 | Hs.220689 | Ras-GTPase-activating protein SH3-domain | 4.89 |
| 65 | 130381 | L47345 | Hs.155202 | transcription elongation factor B (SIII) | 4.88 |
| | 132389 | AA310393 | Hs.190044 | ESTs | 4.88 |
| | 100260 | D38491 | Hs.322478 | KIAA0117 protein | 4.88 |
| | 109585 | N59650 | Hs.27252 | ESTs | 4.88 |
| | 111603 | R11529 | Hs.20634 | EST | 4.88 |
| 70 | 120514 | AA258335 | | gb:zr59b02.s1 Soares_NhHMPu_S1 Homo sapi | 4.88 |
| | 130314 | NM_014674 | Hs.154332 | KIAA0212 gene product | 4.86 |
| | 108958 | AF142482 | Hs.203846 | TEA domain family member 3 | 4.86 |
| | 126503 | W86510 | Hs.185736 | ESTs | 4.85 |
| | 100406 | AI962060 | Hs.118397 | AE-binding protein 1 | 4.85 |
| 75 | 116238 | AV660717 | Hs.47144 | DKFZP586N0819 protein | 4.84 |
| | 105288 | N99673 | Hs.3585 | ESTs, Weakly similar to AF126743 1 DJ | 4.83 |
| | 118753 | AA346206 | Hs.50471 | ESTs, Weakly similar to T14267 Xln prote | 4.82 |
| | 113070 | AB032977 | Hs.6298 | KIAA1151 protein | 4.81 |
| | 107908 | AF087999 | Hs.42826 | ESTs | 4.80 |
| 80 | 119678 | AI658666 | Hs.6106 | R binding motif protein 4 | 4.80 |
| | 100415 | D86970 | Hs.75822 | TGFB1-induced anti-apoptotic factor 1 | 4.79 |
| | 126360 | F12374 | | gb:HS398101 normalized infant brain cDN | 4.78 |
| | 133101 | AK000299 | Hs.180952 | dyctin 4 (p62) | 4.78 |
| | 103507 | AJ000512 | Hs.296323 | serum/glucocorticoid regulated kinase | 4.78 |
| | 107666 | AA010611 | Hs.60418 | EST | 4.78 |
| | 108030 | AI378523 | Hs.62011 | ESTs | 4.78 |
| | 131479 | D86181 | Hs.273 | galactosylceramidase (Krabbe disease) | 4.78 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| 5 | 133140 | AF180581 | Hs.6582 | Rho guanine exchange factor (GEF) 12 | 4.78 |
| | 134654 | AK001741 | Hs.8739 | hypothetical protein FLJ10879 | 4.78 |
| | 106288 | AB037742 | Hs.24336 | KIAA1321 protein | 4.76 |
| | 101524 | NM_000448 | Hs.73958 | recombination activating gene 1 | 4.75 |
| | 113095 | AA828380 | Hs.126733 | ESTs | 4.75 |
| 10 | 114924 | AI338053 | Hs.87329 | HSPC072 protein | 4.75 |
| | 127543 | AK000787 | Hs.157392 | Homo sapiens cD FLJ20780 fis, clone CO | 4.75 |
| | 115866 | AW062629 | Hs.52081 | KIAA0867 protein | 4.75 |
| | 101382 | AU076772 | Hs.1279 | complement component 1, r subcomponent | 4.74 |
| | 126509 | R47400 | Hs.23850 | ESTs | 4.74 |
| 15 | 127930 | AA809572 | Hs.123304 | ESTs | 4.73 |
| | 127824 | AI911516 | Hs.127811 | ESTs | 4.73 |
| | 110049 | H12449 | Hs.31159 | EST, Weakly similar to ALUB_HUMAN !!! A | 4.73 |
| | 127115 | H77859 | Hs.65450 | reticulin 4 | 4.73 |
| | 104727 | N81203 | Hs.20047 | zinc finger protein, subfamily 2A (FYVE | 4.72 |
| 20 | 127532 | AJ003429 | | gb:AJ003429 Selected chromosome 21 cD | 4.71 |
| | 127304 | AI741577 | Hs.99962 | proteoglycan 2, bone marrow (tural kil | 4.70 |
| | 105409 | AW505076 | Hs.301855 | DiGeorge syndrome critical region gene 8 | 4.70 |
| | 114969 | AW162998 | Hs.24684 | KIAA1376 protein | 4.70 |
| | 115125 | AA193588 | Hs.85888 | ESTs | 4.70 |
| 25 | 118348 | AW408586 | Hs.91052 | ESTs, Moderately similar to ALU5_HUMAN A | 4.70 |
| | 123130 | AA487200 | | gb:ab19f02.s1 Stratagene lung (937210) H | 4.70 |
| | 130881 | AA809875 | Hs.25933 | ESTs | 4.70 |
| | 132074 | AA478486 | Hs.3852 | KIAA0368 protein | 4.70 |
| | 106897 | AF039023 | Hs.167496 | RAN binding protein 6 | 4.69 |
| 30 | 131121 | AA120865 | Hs.23136 | ESTs | 4.69 |
| | 116046 | BE395293 | Hs.94491 | hypothetical protein FLJ20297 | 4.68 |
| | 112868 | AW388359 | Hs.10667 | ESTs | 4.68 |
| | 116877 | AA708958 | Hs.168732 | ESTs | 4.68 |
| | 131241 | BE501914 | Hs.24654 | Homo sapiens cD FLJ11640 fis, clone HE | 4.68 |
| 35 | 132027 | AF151020 | Hs.181444 | hypothetical protein | 4.68 |
| | 133323 | BE336654 | Hs.70937 | H3 histone family, member A | 4.68 |
| | 114269 | AA175769 | Hs.23450 | mitochondrial ribosomal protein S25 | 4.67 |
| | 122713 | AI089443 | Hs.99436 | ESTs | 4.67 |
| | 133571 | BE515037 | Hs.177556 | melanoma antigen, family D, 1 | 4.66 |
| 40 | 134453 | AI272141 | Hs.83484 | SRY (sex determining region Y)-box 4 | 4.66 |
| | 115510 | BE299339 | Hs.72249 | three-PDZ containing protein similar to | 4.66 |
| | 115322 | L08895 | Hs.78995 | MADS box transcription enhancer factor 2 | 4.66 |
| | 129315 | NM_014563 | Hs.174038 | spondyloepiphyseal dysplasia, late | 4.65 |
| | 104674 | AI935962 | Hs.26289 | ESTs | 4.65 |
| 45 | 106276 | AA625947 | Hs.25750 | ESTs | 4.65 |
| | 108216 | AA524743 | Hs.44883 | ESTs | 4.65 |
| | 120376 | AA227469 | | gb:zr18a07.s1 Stratagene NT2 neuro pr | 4.65 |
| | 121743 | AA397636 | | gb:z179e09.r1 Soares_testis_NHT Homo sap | 4.65 |
| | 128011 | AI347067 | Hs.124636 | ESTs | 4.65 |
| 50 | 123454 | AA868510 | Hs.112496 | ESTs | 4.64 |
| | 103409 | NM_004454 | Hs.43697 | ets variant gene 5 (ets-related molecule | 4.64 |
| | 120484 | AA253170 | Hs.96473 | EST | 4.63 |
| | 127046 | AA321948 | Hs.293968 | ESTs | 4.63 |
| | 133184 | AA001021 | Hs.6685 | thyroid hormone receptor interactor 8 | 4.63 |
| 55 | 123184 | BE247767 | Hs.18166 | KIAA0870 protein | 4.62 |
| | 106627 | AK000706 | Hs.15125 | hypothetical protein FLJ20699 | 4.61 |
| | 115475 | AB033085 | Hs.40193 | hypothetical protein KIAA1259 | 4.61 |
| | 119468 | AI911535 | Hs.6657 | hypothetical protein bK1048E9.5 | 4.59 |
| | 133662 | BE409053 | Hs.299629 | peroxisomal long-chain acyl-coA thioeste | 4.58 |
| 60 | 113941 | AA531016 | Hs.22399 | hypothetical protein FLJ14824 | 4.58 |
| | 131590 | R46277 | Hs.250638 | Homo sapiens mR full length insert cDN | 4.58 |
| | 128795 | AA531287 | Hs.105805 | ESTs | 4.58 |
| | 116480 | C14088 | Hs.169476 | glyceraldehyde-3-phosphate dehydrogese | 4.58 |
| | 111713 | C75253 | Hs.220950 | ESTs | 4.58 |
| 65 | 113721 | AF143885 | Hs.18190 | EST | 4.57 |
| | 111657 | R07364 | Hs.268667 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 4.56 |
| | 102009 | BE245149 | Hs.82643 | protein tyrosine kinase 9 | 4.55 |
| | 135242 | AI583187 | Hs.9700 | cyclin E1 | 4.55 |
| | 127580 | BE548749 | Hs.148016 | ESTs | 4.55 |
| 70 | 109785 | AB011131 | Hs.12376 | piccolo (presynaptic cytomatrix protein) | 4.53 |
| | 109700 | F09609 | | gb:HSC33H092 normalized infant brain cDN | 4.53 |
| | 124882 | AI698652 | Hs.101539 | ESTs | 4.53 |
| | 131765 | AW381270 | Hs.194110 | hypothetical protein PRO2730 | 4.53 |
| | 115684 | NM_006577 | Hs.284284 | ESTs, Highly similar to beta-1,3-N-acety | 4.52 |
| 75 | 102034 | AI903474 | Hs.230 | fibromodulin | 4.52 |
| | 109776 | R43665 | Hs.12257 | ESTs | 4.50 |
| | 111650 | R16722 | Hs.124246 | ESTs | 4.50 |
| | 132993 | AB023154 | Hs.62264 | KIAA0937 protein | 4.49 |
| | 129017 | AA115333 | Hs.107968 | ESTs | 4.49 |
| 80 | 132902 | AI936442 | Hs.59838 | hypothetical protein FLJ10808 | 4.48 |
| | 114814 | AB006622 | Hs.182536 | KIAA0284 protein | 4.48 |
| | 120839 | AA348913 | | gb:EST55442 Infant adrenal gland II Homo | 4.48 |
| | 101434 | AV650066 | Hs.1430 | coagulation factor XI (plasma thrombopla | 4.48 |
| | 102018 | U03398 | Hs.1524 | tumor necrosis factor (ligand) superfam | 4.48 |
| | 104619 | AA001635 | Hs.287414 | transcriptional intermediary factor 1 ga | 4.48 |
| | 106716 | AA931198 | Hs.238928 | HT002 protein; hypertension-related calc | 4.48 |
| | 126020 | H79863 | Hs.114243 | ESTs | 4.48 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| 5 | 119899 | AI057404 | Hs.58698 | ESTs | 4.47 |
| | 115582 | AW245047 | Hs.136164 | cutaneous T-cell lymphoma-associated tum | 4.46 |
| | 125695 | W22529 | Hs.30942 | ephrin-B2 | 4.46 |
| | 105715 | BE621800 | Hs.29444 | putative small membrane protein NID67 | 4.45 |
| | 117169 | R87866 | Hs.95120 | ESTs, Weakly similar to HZHJ hemoglobin | 4.45 |
| 10 | 102757 | AW955454 | Hs.30942 | ephrin-B2 | 4.45 |
| | 120637 | AA811804 | | gb:rob39a05.s1 NCL_CGAP_GCB1 Homo sapiens | 4.45 |
| | 131579 | N62922 | Hs.29088 | ESTs | 4.45 |
| | 135287 | U82670 | Hs.9786 | zinc finger protein 275 | 4.45 |
| | 112540 | R69751 | | gb:yl40a10.s1 Soares placenta Nb2HP Homo | 4.45 |
| 15 | 125724 | AL360190 | Hs.295978 | Homo sapiens mR full length insert cDN | 4.44 |
| | 115498 | AA291070 | | gb:zs46a08.s1 NCL_CGAP_GCB1 Homo sapiens | 4.43 |
| | 102263 | U29171 | Hs.75952 | casein kise 1, delta | 4.43 |
| | 124312 | H94647 | Hs.102329 | ESTs | 4.43 |
| | 112366 | AF035318 | Hs.12533 | Homo sapiens clone 23705 mR sequence | 4.43 |
| 20 | 115955 | AF263513 | Hs.44198 | intracellular membrane-associated calciu | 4.43 |
| | 103562 | NM_002702 | Hs.2815 | POU domain, class 6, transcription facto | 4.42 |
| | 100169 | AL037228 | Hs.82043 | D123 gene product | 4.40 |
| | 108928 | AA143802 | Hs.71781 | ESTs | 4.40 |
| | 125908 | AF265555 | Hs.250646 | baculoviral IAP repeat-containing 6 | 4.40 |
| 25 | 126996 | BE161065 | Hs.167531 | methylcrotonoyl-Coenzyme A carboxylase 2 | 4.40 |
| | 129512 | T88845 | Hs.112200 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 4.40 |
| | 134570 | U66615 | Hs.172280 | SW/SNF related, matrix associated, acti | 4.40 |
| | 135073 | W55956 | Hs.94030 | Homo sapiens mR; cD DKFZp586E1624 (f | 4.40 |
| | 105011 | BE091926 | Hs.16244 | mitotic spindle coiled-coil related prot | 4.40 |
| 30 | 128793 | AB011125 | Hs.105749 | KIAA0553 protein | 4.40 |
| | 107292 | BE166479 | Hs.4789 | Homo sapiens serologically defined breas | 4.38 |
| | 126144 | H84455 | Hs.40639 | ESTs | 4.38 |
| | 130783 | X07282 | Hs.171495 | relinoic acid receptor, beta | 4.38 |
| | 135192 | U83993 | Hs.321709 | purinergic receptor P2X, ligand-gated io | 4.38 |
| 35 | 100284 | D43767 | Hs.66742 | small inducible cytokine subfamily A (Cy | 4.37 |
| | 117269 | N21621 | Hs.91142 | KH-type splicing regulatory protein (FUS | 4.36 |
| | 104261 | AW248364 | Hs.5409 | R polymerase 1 subunit | 4.35 |
| | 108609 | BE409857 | Hs.69499 | hypothetical protein | 4.35 |
| | 126319 | D81689 | | gb:HUM184E05B Human fetal brain (TFujiwa | 4.35 |
| 40 | 127445 | AA906286 | Hs.193942 | ESTs | 4.35 |
| | 130772 | BE270640 | Hs.19192 | cyclin-dependent kise 2 | 4.35 |
| | 134625 | AA977638 | Hs.184389 | ESTs | 4.35 |
| | 135397 | L14922 | Hs.166563 | replication factor C (activator 1) 1 (14 | 4.35 |
| | 128070 | AA886944 | Hs.303908 | ESTs | 4.35 |
| 45 | 135045 | AI494054 | Hs.93589 | hypothetical protein DKFZp56481162 | 4.33 |
| | 101881 | NM_004957 | Hs.754 | foliypolyglutamate synthase | 4.33 |
| | 129838 | AB007863 | Hs.185140 | KIAA0403 protein | 4.33 |
| | 130974 | NM_003528 | Hs.2178 | H2B histone family, member Q | 4.33 |
| | 107763 | AA018220 | Hs.106730 | chromosome 22 open reading frame 3 | 4.32 |
| 50 | 129818 | T71092 | Hs.172572 | hypothetical protein FLJ20093 | 4.31 |
| | 129407 | AL137597 | Hs.11114 | hypothetical protein dJ1181N3.1 | 4.30 |
| | 110846 | BE277343 | Hs.297875 | endoplasmic reticulum chaperone SIL1, ho | 4.30 |
| | 111433 | R01452 | Hs.40193 | hypothetical protein KIAA1259 | 4.30 |
| | 114860 | AL157545 | Hs.42179 | bromodomain and PHD finger containing, 3 | 4.30 |
| 55 | 115853 | AW978561 | Hs.191548 | ESTs | 4.30 |
| | 116165 | AI184751 | Hs.75874 | pregnancy-associated plasma protein A | 4.30 |
| | 126911 | AA428049 | Hs.1501 | syndecan 2 (heparan sulfate proteoglycan | 4.30 |
| | 131230 | NM_005865 | Hs.274407 | protease, serine, 16 (thymus) | 4.30 |
| | 100349 | D64110 | Hs.77311 | BTG family, member 3 | 4.29 |
| 60 | 100175 | BE258769 | Hs.32500 | acetyl-Coenzyme A acyltransferase 2 (mit | 4.29 |
| | 105335 | AW291165 | Hs.25447 | ESTs | 4.29 |
| | 122507 | BE567620 | Hs.99210 | ESTs | 4.28 |
| | 105397 | AA814807 | Hs.7395 | hypothetical protein FLJ23182 | 4.28 |
| | 133674 | AW851121 | Hs.75497 | Homo sapiens cD: FLJ22139 fis, clone H | 4.28 |
| 65 | 102826 | NM_007274 | Hs.8679 | cytosolic acyl coenzyme A thioester hydr | 4.28 |
| | 103272 | NM_006680 | Hs.2838 | malic enzyme 3, DP(+)-dependent, mitoc | 4.28 |
| | 111887 | R38635 | Hs.12328 | KIAA1005 protein | 4.28 |
| | 120336 | N85785 | Hs.181165 | eukaryotic translation elongation factor | 4.28 |
| | 133736 | D49958 | Hs.75819 | glycoprotein M6A | 4.28 |
| 70 | 130356 | AF127577 | Hs.155017 | nuclear receptor interacting protein 1 | 4.27 |
| | 119830 | AW054922 | Hs.53478 | Homo sapiens cD FLJ12366 fis, clone MA | 4.27 |
| | 108758 | AB014564 | Hs.22616 | KIAA0664 protein | 4.25 |
| | 109709 | F09749 | Hs.187405 | ESTs | 4.25 |
| | 110463 | H52931 | Hs.165067 | ESTs | 4.25 |
| 75 | 124472 | N52517 | Hs.102670 | EST | 4.25 |
| | 109770 | R40322 | Hs.248420 | ESTs, Moderately similar to A47582 B-col | 4.24 |
| | 131487 | F13036 | Hs.27373 | Homo sapiens mR; cD DKFZp564O1763 (f | 4.23 |
| | 107216 | D51069 | Hs.211579 | melanoma cell adhesion molecule | 4.23 |
| | 123562 | AA177088 | Hs.190065 | ESTs | 4.23 |
| 80 | 125986 | W02410 | Hs.205555 | ESTs | 4.23 |
| | 126221 | N20514 | Hs.172965 | ESTs | 4.23 |
| | 127092 | T26985 | | gb:NIBT065H01R Infant brain, LLNL array | 4.23 |
| | 132349 | AW975654 | Hs.181286 | serine protease inhibitor, Kazal type 1 | 4.23 |
| | 118946 | N92834 | | gb:zb67R03.s1 Soares_fetal_jung_NbHL19W | 4.22 |
| | 101531 | AI199711 | Hs.576 | fucoosidase, alpha-L- 1, tissue | 4.21 |
| | 105322 | T87179 | Hs.16346 | ESTs, Weakly similar to S57447 HPBRIL-7 | 4.21 |
| | 104219 | AB002323 | Hs.7720 | dynein, cytoplasmic, heavy polypeptide 1 | 4.20 |

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|----|--------|-----------|-----------|--|------|
| 5 | 102825 | BE262386 | Hs.7137 | clones 23667 and 23775 zinc finger prote | 4.20 |
| | 103571 | AI675749 | Hs.211608 | nucleoporin 153kD | 4.20 |
| | 106942 | AA995351 | Hs.31314 | retinoblastoma-binding protein 7 | 4.20 |
| | 112685 | R87650 | Hs.33439 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 4.20 |
| | 123107 | AA225048 | Hs.104207 | ESTs | 4.20 |
| | 132659 | Z75190 | Hs.54481 | low density lipoprotein receptor-related | 4.20 |
| | 130084 | AI929377 | Hs.173724 | creatine kinase, brain | 4.19 |
| | 114553 | BE219860 | Hs.22505 | hypothetical protein FLJ10159 | 4.18 |
| 10 | 129528 | U38945 | Hs.1174 | cyclin-dependent kinase inhibitor 2A (me | 4.18 |
| | 102266 | U29725 | Hs.3080 | mitogen-activated protein kinase 7 | 4.18 |
| | 110637 | AI241470 | Hs.268982 | ESTs | 4.18 |
| | 127520 | T51239 | | gb:yb20d12.s1 Stratagene fetal spleen (9 | 4.18 |
| | 130322 | NM_014247 | Hs.154545 | PDZ domain containing guanine nucleotide | 4.17 |
| | 104768 | D82319 | Hs.11056 | RALBP1 protein | 4.17 |
| 15 | 123360 | AA532718 | Hs.178604 | ESTs | 4.17 |
| | 133110 | AA608177 | Hs.65228 | ESTs | 4.16 |
| | 130923 | H96115 | Hs.21293 | UDP-N-acetylglucosamine pyrophosphorylas | 4.16 |
| | 109878 | BE620775 | Hs.4866 | Homo sapiens cD FLJ14387 fis, clone HE | 4.16 |
| 20 | 119265 | BE539706 | Hs.285363 | ESTs | 4.16 |
| | 124214 | H58608 | Hs.151323 | ESTs | 4.15 |
| | 106193 | AA057478 | Hs.23272 | ESTs | 4.15 |
| | 105169 | BE245294 | Hs.180789 | S164 protein | 4.15 |
| | 123204 | AA610002 | Hs.44296 | hypothetical protein FLJ22324 | 4.15 |
| 25 | 131600 | NM_004377 | Hs.29331 | camitine palmitoyltransferase I, muscle | 4.14 |
| | 131365 | M93415 | Hs.26014 | activin A receptor, type II | 4.14 |
| | 121993 | AW297880 | Hs.98661 | ESTs | 4.14 |
| | 110779 | AI391472 | Hs.12561 | ESTs, Highly similar to C212_HUMAN 28.3 | 4.13 |
| | 126383 | AB032977 | Hs.6298 | KIAA1151 protein | 4.13 |
| 30 | 104446 | AF084555 | Hs.7351 | cyclic AMP phosphoprotein, 19 kD | 4.13 |
| | 131475 | AA992841 | Hs.27263 | KIAA1458 protein | 4.13 |
| | 128933 | NM_002050 | Hs.334695 | GATA-binding protein 2 | 4.12 |
| | 113141 | AI493276 | Hs.9187 | ESTs | 4.11 |
| | 134833 | L20965 | Hs.89901 | phosphodiesterase 4A, cAMP-specific (dun | 4.11 |
| 35 | 106461 | AI630759 | Hs.17481 | Homo sapiens clone 24606 mR sequence | 4.10 |
| | 128056 | AI990131 | Hs.276973 | potassium large conductance calcium-acti | 4.10 |
| | 114757 | AW970579 | Hs.291031 | ESTs | 4.10 |
| | 134653 | AI765883 | Hs.87385 | ESTs | 4.09 |
| | 100472 | D90084 | Hs.1023 | pyruvate dehydrogenase (lipoamide) alpha | 4.08 |
| 40 | 103102 | X61177 | Hs.68876 | interleukin 5 receptor, alpha | 4.08 |
| | 106779 | BE276013 | Hs.172364 | Homo sapiens mR for FLJ00086 protein, | 4.08 |
| | 133615 | M62843 | Hs.75236 | ELAV (embryonic lethal, abnormal vision, | 4.08 |
| | 130178 | U20982 | Hs.1516 | insulin-like growth factor-binding prote | 4.07 |
| | 124659 | AI680737 | Hs.289068 | Homo sapiens cD FLJ11918 fis, clone HE | 4.07 |
| 45 | 127861 | AW295020 | Hs.198529 | ESTs | 4.07 |
| | 112129 | AB037715 | Hs.183639 | hypothetical protein FLJ10210 | 4.07 |
| | 100918 | AK001335 | Hs.31137 | protein tyrosine phosphatase; receptor I | 4.06 |
| | 124677 | R01073 | | gb:ye84c03.s1 Soares fetal liver spleen | 4.05 |
| | 102722 | F13271 | Hs.79981 | Human clone 23560 mR sequence | 4.05 |
| 50 | 111117 | AB037721 | Hs.173871 | KIAA1300 protein | 4.05 |
| | 122506 | AA449120 | Hs.99209 | ESTs | 4.05 |
| | 126392 | AI356294 | Hs.3280 | caspase 6, apoptosis-related cysteine pr | 4.05 |
| | 130760 | AW379130 | Hs.18953 | phosphodiesterase 9A | 4.05 |
| | 104220 | AB002324 | Hs.301094 | KIAA0326 protein | 4.05 |
| 55 | 112774 | R95770 | Hs.35455 | ESTs | 4.04 |
| | 111128 | AW505364 | Hs.19074 | LATS (large tumor suppressor, Drosophila | 4.04 |
| | 113146 | BE151985 | Hs.5722 | hypothetical protein FLJ23316 | 4.04 |
| | 124940 | AF068846 | Hs.103804 | heterogeneous nuclear ribonucleoprotein | 4.03 |
| | 105498 | H68279 | Hs.24937 | transformer-2 alpha (htra-2 alpha) | 4.03 |
| 60 | 112631 | R82040 | | gb:yj06b06.s1 Soares placenta Nb2HP Homo | 4.03 |
| | 118244 | N62516 | Hs.48556 | ESTs | 4.03 |
| | 118720 | N73515 | | gb:za49d07.s1 Soares fetal liver spleen | 4.03 |
| | 129232 | R98881 | Hs.109655 | sex comb on midleg (Drosophila)-like 1 | 4.03 |
| | 134192 | H01345 | Hs.24139 | Homo sapiens cD: FLJ23137 fis, clone L | 4.03 |
| 65 | 131893 | BE336886 | Hs.3416 | adipose differentiation-related protein | 4.02 |
| | 116793 | T77781 | | gb:yd20a11.s1 Soares fetal liver spleen | 4.02 |
| | 125674 | AL036166 | Hs.323378 | coated vesicle membrane protein | 4.01 |
| | 116640 | X89984 | Hs.211563 | B-cell CLL/lymphoma 7A | 4.01 |
| | 105057 | AA134233 | Hs.336942 | Homo sapiens cD: FLJ21488 fis, clone C | 4.00 |
| 70 | 105158 | AW976357 | Hs.234545 | hypothetical protein NUF2R | 4.00 |
| | 116245 | AB033107 | Hs.42796 | KIAA1281 protein | 4.00 |
| | 119946 | AA932283 | Hs.58925 | ESTs | 4.00 |
| | 121975 | AA740679 | Hs.98631 | ESTs | 4.00 |
| | 132037 | AA352702 | Hs.332541 | Homo sapiens, Similar to RIKEN cD 2700 | 4.00 |
| 75 | 133669 | NM_006925 | Hs.166975 | splicing factor, arginine/serine-rich 5 | 4.00 |
| | 109468 | NM_015310 | Hs.6763 | KIAA0942 protein | 3.99 |
| | 106829 | AW959893 | Hs.27099 | hypothetical protein FLJ23293 similar to | 3.99 |
| | 134682 | AW882645 | Hs.88044 | sprouty (Drosophila) homolog 1 (antagoni | 3.98 |
| | 105966 | AA142984 | Hs.5344 | adaptor-related protein complex 1, gamma | 3.98 |
| 80 | 100448 | AF234887 | Hs.57652 | cadherin, EGF LAG seven-pass G-type rece | 3.98 |
| | 102589 | AU076728 | Hs.8867 | cysteine-rich, angiogenic inducer, 61 | 3.98 |
| | 104146 | AW880614 | Hs.146381 | R binding motif protein, X chromosome | 3.98 |
| | 111465 | AI968256 | Hs.15470 | putative ring zinc finger protein NY-REN | 3.98 |
| | 126499 | AK001779 | Hs.110445 | CGF-97 protein | 3.98 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| 5 | 134388 | AW405434 | Hs.82575 | small nuclear ribonucleoprotein polypept | 3.98 |
| | 105554 | BE616694 | Hs.288042 | hypothetical protein FLJ14299 | 3.97 |
| | 115206 | AW183695 | Hs.186572 | ESTs | 3.96 |
| | 103853 | AF272390 | Hs.111782 | myosin 5C | 3.96 |
| | 110542 | H58373 | Hs.332938 | hypothetical protein MGC5370 | 3.96 |
| | 106797 | AI768801 | Hs.169943 | Homo sapiens cD FLJ13569 fis, clone PL | 3.96 |
| | 130589 | AL110226 | Hs.16441 | DKFZP434H204 protein | 3.95 |
| | 122788 | AI828638 | Hs.99514 | hypothetical protein FLJ20574 | 3.95 |
| 10 | 104518 | H20816 | Hs.112423 | Homo sapiens mR; cD DKFZp5661420 (f | 3.95 |
| | 130640 | NM_004753 | Hs.17144 | short-chain dehydrogenase/reductase 1 | 3.95 |
| | 110847 | N30169 | Hs.279807 | ESTs, Weakly similar to 2004399A chromos | 3.95 |
| | 116156 | AA461045 | Hs.50701 | ESTs | 3.95 |
| | 122096 | AA431162 | Hs.98590 | ESTs | 3.95 |
| 15 | 122160 | AI769281 | Hs.97439 | ESTs | 3.95 |
| | 123930 | AA740878 | Hs.112982 | ESTs | 3.95 |
| | 126280 | Z19417 | | gb:HSB26B122 STRATAGENE Human skeletal m | 3.95 |
| | 126547 | U47732 | Hs.84072 | transmembrane 4 superfamily member 3 | 3.95 |
| | 134757 | AA913267 | Hs.211576 | IL2-inducible T-cell kine | 3.95 |
| 20 | 117296 | AL133427 | Hs.42506 | Homo sapiens mR full length insert cDN | 3.95 |
| | 112261 | AL050297 | Hs.300861 | ESTs, Highly similar to T08701 hypotheti | 3.95 |
| | 112268 | W39609 | Hs.22003 | solute carrier family 6 (neurotransmitte | 3.94 |
| | 131844 | AI419294 | Hs.324342 | ESTs | 3.94 |
| | 101607 | X60111 | Hs.1244 | CD9 antigen (p24) | 3.94 |
| 25 | 121613 | AA416879 | Hs.193195 | ESTs, Weakly similar to 2109260A B cell | 3.94 |
| | 115815 | AW905328 | Hs.180842 | ribosomal protein L13 | 3.93 |
| | 125684 | AW589427 | Hs.158849 | Homo sapiens cD: FLJ21663 fis, clone C | 3.93 |
| | 126783 | AA083531 | | gb:zn09d10.s1 Stratagene hNT neuron (937 | 3.93 |
| | 129201 | H18359 | Hs.109390 | ESTs | 3.93 |
| 30 | 128954 | AA346839 | Hs.209100 | DKFZP434C171 protein | 3.92 |
| | 122939 | AA477141 | | gb:zu37g06.s1 Soares ovary tumor NbHOT H | 3.92 |
| | 130348 | AB032957 | Hs.210850 | KIAA1131 protein | 3.92 |
| | 125847 | AW161885 | Hs.249034 | ESTs | 3.91 |
| | 120452 | AL022328 | Hs.104335 | hypothetical protein IMAGE3510317 | 3.91 |
| 35 | 123143 | AA487595 | | gb:aa95e02.s1 Stratagene fetal reti 93 | 3.91 |
| | 105729 | H46612 | Hs.293815 | Homo sapiens HSPC285 mR, partial cds | 3.91 |
| | 106605 | AW772298 | Hs.21103 | Homo sapiens mR; cD DKFZp564B076 (fr | 3.90 |
| | 126714 | AF114491 | Hs.137354 | egf-like module containing, mucin-like, | 3.90 |
| 40 | 121611 | M31669 | Hs.1735 | inhibin, beta B (activin AB beta polypep | 3.90 |
| | 120468 | AW967675 | Hs.96487 | ESTs, Highly similar to S08228 ribosomal | 3.90 |
| | 101356 | AW878229 | Hs.80642 | sigl transducer and activator of trans | 3.89 |
| | 133668 | L77964 | Hs.271980 | mitogen-activated protein kine 6 | 3.89 |
| | 109114 | BE622787 | Hs.84045 | hypothetical protein FLJ20288 | 3.88 |
| 45 | 115134 | AW968073 | Hs.194331 | ESTs, Highly similar to A55713 inositol | 3.88 |
| | 107850 | AA022910 | Hs.295446 | ESTs, Moderately similar to B10024C cyto | 3.88 |
| | 130907 | AA322866 | Hs.21107 | neurofilin | 3.88 |
| | 101679 | AA176374 | Hs.243886 | nuclear autoantigenic sperm protein (his | 3.88 |
| | 104267 | AF043244 | Hs.278439 | nucleolar protein 3 (apoptosis repressor | 3.88 |
| | 112232 | BE253927 | Hs.24983 | hypothetical protein from EUROMAGE 2021 | 3.88 |
| 50 | 113248 | T63857 | | gb:yc16e01.s1 Stratagene lung (937210) H | 3.88 |
| | 114044 | BE327427 | Hs.79953 | ESTs | 3.88 |
| | 115414 | AA662240 | Hs.283099 | AF15q14 protein | 3.88 |
| | 129598 | N30436 | Hs.11556 | Homo sapiens cD FLJ12566 fis, clone NT | 3.88 |
| 55 | 102134 | AL036967 | Hs.2324 | prolamine 2 | 3.87 |
| | 105310 | R98185 | Hs.17240 | ESTs | 3.87 |
| | 116470 | AI272141 | Hs.83484 | SRY (sex determining region Y)-box 4 | 3.86 |
| | 110947 | AW298410 | Hs.21475 | ESTs | 3.85 |
| | 115839 | BE300266 | Hs.28935 | transducin-like enhancer of split 1, hom | 3.85 |
| 60 | 103534 | AW970672 | Hs.9247 | protein kine, AMP-activated, alpha 1 c | 3.85 |
| | 105209 | AB023197 | Hs.227743 | KIAA0980 protein | 3.85 |
| | 108749 | AA127017 | Hs.71052 | ESTs | 3.85 |
| | 110565 | AI884970 | Hs.4983 | ESTs | 3.85 |
| | 110799 | AI089660 | Hs.323401 | dpy-30-like protein | 3.85 |
| 65 | 117068 | H91257 | Hs.41391 | EST | 3.85 |
| | 130956 | NM_001135 | Hs.2159 | aggrecan 1 (chondroitin sulfate proteogl | 3.85 |
| | 102273 | BE391815 | Hs.75981 | ubiquitin specific protease 14 (IR-gua | 3.85 |
| | 112960 | AL110209 | Hs.6770 | LCAT-like lysophospholipase | 3.84 |
| | 114414 | AW152166 | Hs.182113 | ESTs | 3.84 |
| | 109665 | AA249439 | Hs.27027 | hypothetical protein DKFZp762H1311 | 3.84 |
| 70 | 106208 | AK001674 | Hs.22630 | cofactor required for Sp1 transcrip | 3.84 |
| | 122311 | NM_014913 | Hs.131915 | KIAA0853 protein | 3.84 |
| | 124271 | AW293223 | Hs.8928 | hypothetical protein FLJ20291 | 3.83 |
| | 106650 | AL049951 | Hs.22370 | Homo sapiens mR; cD DKFZp56400122 (f | 3.83 |
| | 112167 | N99591 | Hs.25587 | ESTs, Weakly similar to T00329 hypotheti | 3.83 |
| 75 | 122354 | AL157579 | Hs.153610 | KIAA0751 gene product | 3.83 |
| | 111462 | R05296 | | gb:ye91e08.s1 Soares fetal liver spleen | 3.81 |
| | 128109 | AW269421 | Hs.128093 | ESTs | 3.81 |
| | 127003 | AW816515 | Hs.173540 | ATPase, Class V, type 10D | 3.81 |
| | 109210 | AA669722 | Hs.272137 | ESTs | 3.81 |
| 80 | 132543 | BE568452 | Hs.5101 | protein regulator of cytokinesis 1 | 3.80 |
| | 106827 | AA457456 | Hs.11408 | hypothetical protein FLJ20435 | 3.80 |
| | 124232 | H63391 | Hs.339677 | ESTs, Weakly similar to I380222 hypotheti | 3.80 |
| | 126039 | AL137523 | Hs.181102 | p30 DBC protein | 3.80 |
| | 128022 | AW195569 | Hs.125906 | ESTs | 3.80 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 132005 | AA149707 | Hs.173091 | ubiquitin-like 3 | 3.79 |
| | 131392 | AA235153 | Hs.26320 | TRABID protein | 3.79 |
| | 131775 | AB014548 | Hs.31921 | KIAA0648 protein | 3.79 |
| 5 | 126257 | N99638 | | gb:za39g11.1 Soares fetal liver spleen | 3.79 |
| | 121950 | AA429515 | | gb:zw75c05.s1 Soares_testis_NHT Homo sap | 3.79 |
| | 116067 | AA454827 | Hs.293637 | ESTs | 3.78 |
| | 104658 | AA360954 | Hs.27268 | Homo sapiens cD: FLJ21933 fis, clone H | 3.78 |
| | 104493 | AW960427 | Hs.79059 | transforming growth factor, beta recepto | 3.77 |
| 10 | 100163 | W44671 | Hs.124 | gene predicted from cD with a complete | 3.77 |
| | 116223 | AF045458 | Hs.47061 | unc-51 (C. elegans)-like kise 1 | 3.77 |
| | 120586 | AL031778 | Hs.797 | nuclear transcription factor Y, alpha | 3.76 |
| | 128764 | AW024282 | Hs.104938 | hypothetical protein MGC15905 | 3.75 |
| | 111574 | AI024145 | Hs.188526 | ESTs | 3.75 |
| | 117396 | W20128 | Hs.296039 | ESTs | 3.75 |
| 15 | 119052 | R10889 | | gb:zf38d02.s1 Soares fetal liver spleen | 3.75 |
| | 121806 | AA424313 | Hs.98402 | ESTs | 3.75 |
| | 122410 | AA446854 | Hs.271004 | ESTs, Weakly similar to I38022 hypothei | 3.75 |
| | 126638 | AA649257 | Hs.188602 | ESTs | 3.75 |
| | 127879 | AA768098 | Hs.189079 | ESTs | 3.75 |
| 20 | 121095 | AA320134 | Hs.196029 | Homo sapiens mR for KIAA1657 protein, | 3.75 |
| | 103430 | BE564090 | Hs.20716 | translocase of inner mitochondrial membr | 3.74 |
| | 101230 | AW504300 | Hs.295605 | mannosidase, alpha, class 2A, member 2 | 3.74 |
| | 100200 | H94688 | Hs.173737 | ras-related C3 botulinum toxin substrate | 3.73 |
| | 106913 | AI219346 | Hs.86178 | M-phase phosphoprotein 9 | 3.73 |
| 25 | 110975 | H17012 | Hs.14633 | ESTs | 3.73 |
| | 117314 | N32498 | Hs.42829 | ESTs | 3.73 |
| | 118737 | AA199686 | | gb:zq75g09.r1 Stratagene hNT neuron (937 | 3.73 |
| | 124169 | BE079334 | Hs.271630 | ESTs | 3.73 |
| | 124580 | N68420 | Hs.107992 | ESTs | 3.73 |
| 30 | 125747 | NM_002884 | Hs.865 | RAP1A, member of RAS oncogene family | 3.73 |
| | 124879 | R73588 | Hs.101533 | ESTs | 3.72 |
| | 128527 | AA504583 | Hs.101047 | transcription factor 3 (E2A immunoglobul | 3.72 |
| | 103544 | M13305 | Hs.247787 | opsin 1 (cone pigments), long-wave-sensi | 3.72 |
| | 106044 | N90344 | Hs.149436 | kinesin family member 5B | 3.71 |
| 35 | 127867 | C18530 | | gb:C18530 Human placenta cD (TFujwara | 3.71 |
| | 133828 | T28472 | Hs.7655 | U2 small nuclear ribonucleoprotein auxl | 3.71 |
| | 107387 | D86983 | Hs.118893 | Melanoma associated gene | 3.71 |
| | 104160 | AA455706 | Hs.44581 | heat shock protein hsp70-related protein | 3.71 |
| 40 | 106098 | BE278344 | Hs.7970 | DKFZP434B027 protein | 3.70 |
| | 133691 | M85289 | Hs.211573 | heparan sulfate proteoglycan 2 (perlecan | 3.70 |
| | 120717 | AA904681 | Hs.154434 | ESTs, Weakly similar to unknown [H.sapie | 3.70 |
| | 119263 | T15977 | | gb:I82328 Infant brain, Benlo Soares Hom | 3.70 |
| | 102305 | AL043202 | Hs.90073 | chromosome segregation 1 (yeast homolog) | 3.70 |
| 45 | 106566 | BE298210 | | gb:601118016F1 NIH_MGC_17 Homo sapiens c | 3.70 |
| | 110708 | N33878 | Hs.306117 | KIAA0306 protein | 3.70 |
| | 114357 | R41677 | Hs.6107 | Homo sapiens cD FLJ14839 fis, clone OV | 3.70 |
| | 115285 | AW972872 | Hs.293736 | ESTs | 3.70 |
| | 123034 | AL359571 | Hs.44054 | ninein (GSK3B interacting protein) | 3.70 |
| 50 | 126396 | T06298 | Hs.153326 | EST | 3.70 |
| | 132597 | Y11192 | Hs.5299 | aldehyde dehydrogenase 5 family, member | 3.70 |
| | 105823 | AI559444 | Hs.293960 | ESTs | 3.70 |
| | 102644 | T59816 | Hs.173311 | C18B11 homolog (44.9kD) | 3.70 |
| | 133513 | AF136407 | Hs.7446 | chromosome 6 open reading frame 5 | 3.70 |
| 55 | 116450 | AI654450 | Hs.47274 | Homo sapiens mR; cD DKFZp564B176 (fr | 3.69 |
| | 104596 | AF067804 | Hs.15423 | hypothetical protein HDCMC04P | 3.69 |
| | 133579 | X75346 | Hs.75074 | mitogen-activated protein kise-activat | 3.68 |
| | 124556 | N29317 | Hs.236463 | Homo sapiens mR; cD DKFZp586I0521 (f | 3.68 |
| | 120534 | AI635113 | Hs.270366 | ESTs, Weakly similar to I78885 serine/th | 3.68 |
| | 103156 | BE259039 | Hs.129953 | Ewing sarcoma breakpoint region 1 | 3.68 |
| 60 | 134992 | AA464444 | Hs.5831 | tissue inhibitor of metalloprotease 1 | 3.68 |
| | 106730 | BE467313 | Hs.260707 | ESTs | 3.68 |
| | 120880 | AA360240 | Hs.97019 | EST | 3.68 |
| | 123731 | AA609839 | | gb:ae62f01.s1 Stratagene lung carcinoma | 3.68 |
| 65 | 126973 | W46653 | Hs.251928 | nuclear pore complex interacting protein | 3.67 |
| | 103646 | AW248439 | Hs.2340 | junction plakoglobin | 3.67 |
| | 116333 | AF155827 | Hs.203963 | hypothetical protein FLJ10339 | 3.67 |
| | 120922 | AA481003 | Hs.97128 | ESTs | 3.67 |
| | 127407 | AW089514 | Hs.279681 | heterogeneous nuclear ribonucleoprotein | 3.67 |
| 70 | 106578 | AA836381 | Hs.315111 | nuclear receptor co-repressor/HDAC3 comp | 3.67 |
| | 123000 | AI584156 | Hs.105640 | Homo sapiens, clone IMAGE:4139775, mR, | 3.67 |
| | 101464 | AA852431 | Hs.51299 | DH dehydrogenase (ubiquinone) flavopro | 3.67 |
| | 101397 | M26380 | Hs.180878 | lipoprotein lipase | 3.67 |
| | 131135 | NM_016569 | Hs.267182 | TBX3-iso protein | 3.66 |
| 75 | 106112 | AL117518 | Hs.3686 | KIAA0978 protein | 3.66 |
| | 123974 | NM_015678 | Hs.3821 | neurobeachin | 3.66 |
| | 127742 | AW293496 | Hs.180138 | ESTs | 3.66 |
| | 112908 | BE281000 | Hs.3530 | TLS-associated serine-arginine protein 2 | 3.66 |
| | 131802 | AL137406 | Hs.296356 | Homo sapiens mR; cD DKFZp434M162 (fr | 3.65 |
| 80 | 135162 | AI187925 | Hs.95667 | F-box protein 30 | 3.65 |
| | 124984 | BE313210 | Hs.223241 | eukaryotic translation elongation factor | 3.65 |
| | 118844 | AL035364 | Hs.50891 | hypothetical protein | 3.65 |
| | 125429 | AI023654 | Hs.114191 | ESTs | 3.65 |
| | 125596 | R25698 | | gb:yg44h11.2 Soares infant brain 1N1B H | 3.65 |

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|----|--------|-----------|-----------|--|
| | 125792 | AA496205 | Hs.193700 | Homo sapiens mR; cD DKFZp586i0324 (f |
| | 126965 | AI470523 | Hs.139336 | ATP-binding cassette, sub-family C (CFTR |
| | 130776 | AF167706 | Hs.19280 | cysteine-rich motor neuron 1 |
| 5 | 131949 | AK000010 | Hs.258798 | hypothetical protein FLJ120003 |
| | 116612 | C14904 | Hs.45184 | Homo sapiens cD FLJ12284 tis, clone MA |
| | 123749 | AA609949 | Hs.112790 | EST |
| | 134203 | AA161219 | Hs.799 | diphtheria toxin receptor (heparin-bindi |
| | 133605 | AL038165 | Hs.75187 | translocase of outer mitochondrial membr |
| 10 | 109235 | AI381800 | Hs.300684 | calitonin gene-related peptide-receptor |
| | 125447 | AI582222 | Hs.128686 | ESTs |
| | 122942 | AI277829 | Hs.111862 | KIAA0590 gene product |
| | 122748 | AA458822 | Hs.193815 | ESTs |
| | 103840 | AW975861 | Hs.47367 | KJAA0788 protein |
| 15 | 105333 | AA234831 | Hs.246112 | KJAA0788 protein |
| | 108807 | AI652236 | Hs.49376 | hypothetical protein FLJ20644 |
| | 114699 | AA127386 | | gb:zn50409.r1 Stratagene lung carcinoma |
| | 126040 | Z28444 | Hs.24119 | Homo sapiens mR; cD DKFZp586G2222 (f |
| | 131028 | AI879165 | Hs.2227 | CCAAT/enhancer binding protein (C/EBP), |
| 20 | 131710 | NM_015368 | Hs.30985 | pannexin 1 |
| | 100164 | AW372032 | Hs.173714 | MORF-related gene X |
| | 120837 | BE149656 | Hs.306621 | Homo sapiens cD FLJ11963 tis, clone HE |
| | 131089 | Z42645 | Hs.22870 | Homo sapiens mR full length insert cDN |
| | 126428 | AA412436 | Hs.301985 | ESTs |
| 25 | 129148 | AW501216 | Hs.108945 | KIAA0515 protein |
| | 102337 | AI814663 | Hs.170133 | forkhead box O1A (rhabdomyosarcoma) |
| | 104520 | AI702384 | Hs.76925 | hypothetical protein FLJ14981 |
| | 112954 | AA928953 | Hs.6655 | Homo sapiens EST from clone 208499, full |
| | 125197 | AF086270 | Hs.278554 | heterochromatin-like protein 1 |
| 30 | 128124 | AI125748 | Hs.130194 | ESTs |
| | 129553 | AW015763 | Hs.113065 | ESTs |
| | 123998 | AA203429 | Hs.79474 | tyrosine 3-mono-oxygenase/tryptophan 5-mo |
| | 128835 | AK001731 | Hs.106390 | Homo sapiens mR; cD DKFZp586H0924 (f |
| | 129226 | BE222494 | Hs.180919 | inhibitor of D binding 2, dominant neg |
| 35 | 135131 | AI582743 | Hs.94953 | Homo sapiens, Similar to complement comp |
| | 128955 | AA775076 | Hs.185807 | Homo sapiens, Similar to PRO0478 protein |
| | 100225 | D28539 | Hs.167185 | glutamate receptor, metabotropic 5 |
| | 101572 | AA437199 | Hs.656 | cell division cycle 25C |
| | 102277 | U31099 | Hs.158326 | prostaglandin D2 receptor (DP) |
| 40 | 103667 | Z80788 | Hs.247815 | H4 histone family, member L |
| | 112373 | AW963357 | Hs.7847 | ESTs |
| | 119284 | AL041224 | Hs.65379 | ESTs |
| | 125422 | AA903229 | Hs.153717 | ESTs |
| | 126381 | M76665 | Hs.275215 | ESTs |
| 45 | 129168 | AI132988 | Hs.109052 | hydroxysteroid (11-beta) dehydrogense 1 |
| | 123133 | AA487264 | Hs.154974 | chromosome 14 open reading frame 2 |
| | 128789 | AW368576 | Hs.139851 | Homo sapiens mR; cD DKFZp667N064 (fr |
| | 104172 | AA476418 | | caveolin 2 |
| | 134263 | AW973443 | Hs.8086 | gb:zn02a12.s1 Soares_total_fetus_Nb2HF8_ |
| 50 | 101759 | M80244 | Hs.184601 | R (guanine-7-) methyltransferase |
| | 104942 | NM_016348 | Hs.10235 | scavenger carrier family 7 (cationic amino |
| | 123443 | BE244537 | Hs.167382 | chromosome 5 open reading frame 4 |
| | 110707 | AI239832 | Hs.15617 | triethyl peptide receptor A/guanylate |
| | 105787 | AI492261 | Hs.32450 | ESTs, Weakly similar to ALU4_HUMAN ALU S |
| 55 | 112940 | AK001757 | Hs.281348 | ESTs |
| | 115301 | T11832 | Hs.127797 | hypothetical protein FLJ10895 |
| | 125978 | N65843 | Hs.35608 | Homo sapiens cD FLJ11381 tis, clone HE |
| | 128002 | AI985897 | Hs.125293 | ESTs |
| | 119847 | H81136 | Hs.334604 | ESTs |
| 60 | 134595 | NM_002401 | Hs.29282 | Homo sapiens mR for KIAA1870 protein, |
| | 121309 | AA293834 | Hs.97312 | mitogen-activated protein kase kase |
| | 122679 | AA811286 | Hs.192837 | ESTs |
| | 106061 | AA565356 | Hs.13250 | ESTs, Weakly similar to ALU5_HUMAN ALU S |
| | 127207 | AA377165 | Hs.44833 | ESTs |
| 65 | 129563 | AF119664 | Hs.27299 | ESTs |
| | 105951 | R48700 | Hs.20733 | transcriptional regulator protein |
| | 115643 | AA404276 | Hs.123253 | Homo sapiens cD FLJ22356 tis, clone H |
| | 130473 | U11690 | Hs.1572 | hypothetical protein FLJ22009 |
| | 104246 | AF016032 | Hs.201377 | faciogenital dysplasia (Aarskog-Scott sy |
| 70 | 120562 | BE244580 | Hs.302267 | lysosomal |
| | 101211 | AA355357 | Hs.263429 | hypothetical protein FLJ10330 |
| | 100774 | J05581 | Hs.89603 | SMC (mouse) homolog, X chromosome |
| | 108407 | AA075519 | | gb:zm87h09.s1 Stratagene ovarian cancer |
| | 113538 | AJ554947 | Hs.15167 | ESTs, Weakly similar to S37482 finger pr |
| 75 | 113876 | AI799751 | Hs.5635 | ESTs |
| | 110731 | NM_014899 | Hs.188006 | KIAA0878 protein |
| | 125845 | AK001440 | Hs.131840 | hypothetical protein FLJ10578 |
| | 112945 | AW138458 | Hs.20787 | Homo sapiens cD FLJ21686 tis, clone C |
| | 131686 | NM_012296 | Hs.30687 | GRB2-associated binding protein 2 |
| | 125413 | AI887951 | Hs.74566 | dihydropyrimidine-like 3 |
| 80 | 129360 | AJ000534 | Hs.110708 | sarcoglycan, epsilon |
| | 128819 | R38007 | Hs.77578 | ubiquitin specific protease 9, X chromos |
| | 101973 | U41514 | Hs.80120 | UDP-N-acetyl-alpha-D-galactosamine:polyp |
| | 103616 | NM_002647 | Hs.32971 | phosphoinositide 3-kinase, class 2 |

| | |
|---|------|
| Homo sapiens mR; cD DKFZp586G0324 (f | 3.65 |
| ATP-binding cassette, sub-family C (CFTR | 3.65 |
| cysteine-rich motor neuron 1 | 3.65 |
| hypothetical protein FLJ120003 | 3.65 |
| Homo sapiens cD FLJ112284 fis, clone MA | 3.65 |
| EST | 3.65 |
| diphtheria toxin receptor (heparin-bindi | 3.64 |
| translocase of outer mitochondrial membr | 3.64 |
| calcitonin gene-related peptide receptor | 3.64 |
| ESTs | 3.63 |
| KIAA0590 gene product | 3.63 |
| ESTs | 3.63 |
| KIAA1785 protein | 3.63 |
| KIAA0788 protein | 3.63 |
| hypothetical protein FLJ20644 | 3.63 |
| gb:zn90009.r1 Stratagene lung carcinoma | 3.63 |
| Homo sapiens mR; cD DKFZp586G2222 (f | 3.63 |
| CCAAT/enhancer binding protein (C/EBP), | 3.63 |
| pannexin 1 | 3.63 |
| MORF-related gene X | 3.62 |
| Homo sapiens cD FLJ11953 fis, clone HE | 3.62 |
| Homo sapiens mR full length insert cDN | 3.62 |
| ESTs | 3.62 |
| KIAA0515 protein | 3.61 |
| forkhead box O1A (rhabdomyosarcoma) | 3.61 |
| hypothetical protein FLJ14981 | 3.60 |
| Homo sapiens EST from clone 208499, full | 3.60 |
| heterochromatin-like protein 1 | 3.60 |
| ESTs | 3.60 |
| ESTs | 3.60 |
| tyrosine 3-mono-oxygenase/tryptophan 5-mo | 3.60 |
| Homo sapiens mR; cD DKFZp586H0924 (f | 3.59 |
| inhibitor of D binding 2, dominant neg | 3.59 |
| Homo sapiens, Similar to proo4478 comp | 3.59 |
| Homo sapiens, Similar to PR00478 protein | 3.58 |
| glutamate receptor, metabotropic 5 | 3.58 |
| cell division cycle 25C | 3.58 |
| prostaglandin D2 receptor (DP) | 3.58 |
| H4 histone family, member L | 3.58 |
| ESTs | 3.58 |
| ESTs | 3.58 |
| ESTs | 3.58 |
| hydroxysteroid (11-beta) dehydrogenase 1 | 3.58 |
| chromosome 14 open reading frame 2 | 3.58 |
| Homo sapiens mR; cD DKFZp667N064 (fr | 3.57 |
| caveolin 2 | 3.57 |
| gb:zx02a12.s1 Soares_total_fetus_Nb2HF8_ | 3.57 |
| R (guanine-7-) methyltransferase | 3.57 |
| solute carrier family 7 (cationic amino | 3.57 |
| chromosome 5 open reading frame 4 | 3.56 |
| triuretic peptide receptor Arguanylate | 3.56 |
| ESTs, Weakly similar to ALU4_HUMAN ALU S | 3.55 |
| ESTs | 3.55 |
| hypothetical protein FLJ10895 | 3.55 |
| Homo sapiens cD FLJ111381 fis, clone HE | 3.55 |
| ESTs | 3.55 |
| ESTs | 3.55 |
| Homo sapiens mR for KIAA1870 protein, | 3.55 |
| mitogen-activated protein kase kase | 3.55 |
| ESTs | 3.55 |
| ESTs, Weakly similar to ALU5_HUMAN ALU S | 3.54 |
| ESTs | 3.54 |
| ESTs | 3.54 |
| transcriptional regulator protein | 3.54 |
| Homo sapiens cD: FLJ22356 fis, clone H | 3.53 |
| hypothetical protein FLJ22009 | 3.53 |
| faciogenital dysplasia (Aarskog-Scott sy | 3.53 |
| lysosomal | 3.53 |
| hypothetical protein FLJ10330 | 3.53 |
| SMC (mouse) homolog, X chromosome | 3.53 |
| mucin 1, transmembrane | 3.53 |
| gb:zm87h09.s1 Stratagene ovarian cancer | 3.53 |
| ESTs, Weakly similar to S37482 finger pr | 3.53 |
| ESTs | 3.53 |
| KIAA0878 protein | 3.52 |
| hypothetical protein FLJ10578 | 3.51 |
| Homo sapiens cD: FLJ21686 fis, clone C | 3.51 |
| GRB2-associated binding protein 2 | 3.51 |
| dihydropyrimidase-like 3 | 3.51 |
| sarcoglycan, epsilon | 3.50 |
| ubiquitin specific protease 9, X chromos | 3.50 |
| UDP-N-acetyl-alpha-D-galactosamine:polyp | 3.50 |
| phosphoinositide-3-kinase, class 3 | 3.50 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 105535 | AI459519 | Hs.297681 | serine (or cysteine) protease inhibitor | 3.50 |
| | 118767 | AI038653 | Hs.50500 | ESTs | 3.50 |
| | 126634 | AW361109 | Hs.43627 | SRY (sex determining region Y)-box 22 | 3.50 |
| 5 | 130851 | R65282 | Hs.20247 | ESTs, Weakly similar to S65657 alpha-1C- | 3.50 |
| | 134353 | AL138201 | Hs.82120 | nuclear receptor subfamily 4, group A, m | 3.50 |
| | 111394 | AA412227 | Hs.16131 | hypothetical protein FLJ12876 | 3.50 |
| | 102696 | BE540274 | Hs.239 | forkhead box M1 | 3.49 |
| | 113037 | R17268 | Hs.259873 | axol transport of synaptic vesicles | 3.49 |
| 10 | 111028 | H59346 | Hs.30151 | ESTs, Weakly similar to I38022 hypotheti | 3.49 |
| | 131688 | AI935413 | Hs.30692 | p21 (CDKN1A)-activated kinase 2 | 3.49 |
| | 115613 | AW135951 | Hs.173946 | hypothetical protein FLJ10486 | 3.48 |
| | 116975 | H81076 | Hs.269001 | ESTs | 3.48 |
| | 100210 | D25361 | Hs.3104 | KIAA0042 gene product | 3.48 |
| | 110147 | H18700 | Hs.268799 | ESTs | 3.48 |
| 15 | 115600 | AA081395 | Hs.42173 | Homo sapiens cD FLJ10366 fis, clone NT | 3.48 |
| | 119088 | R39261 | Hs.90790 | Homo sapiens cD: FLJ22930 fis, clone K | 3.48 |
| | 120347 | AA211068 | Hs.120247 | nuclear fragile X mental retardation pro | 3.48 |
| | 122702 | AI220089 | Hs.99439 | ESTs | 3.48 |
| 20 | 125552 | H09701 | Hs.278366 | ESTs, Weakly similar to I38022 hypotheti | 3.48 |
| | 126461 | AI381659 | Hs.267086 | ESTs | 3.48 |
| | 128572 | AA933022 | Hs.256583 | interleukin enhancer binding factor 3, 9 | 3.48 |
| | 118397 | BE139479 | Hs.161492 | ESTs | 3.47 |
| | 127999 | AW978827 | Hs.69851 | nucleolar protein family A, member 1 (H/ | 3.47 |
| 25 | 132066 | AI929392 | Hs.181195 | DJ (Hsp40) homolog, subfamily B, membe | 3.47 |
| | 105693 | BE250951 | Hs.181368 | U5 snRNP-specific protein (220 kD), orth | 3.47 |
| | 128874 | H06245 | Hs.106801 | ESTs, Weakly similar to PC4259 laminin | 3.46 |
| | 119984 | AA230228 | Hs.59197 | ESTs | 3.46 |
| | 104000 | AI146527 | Hs.80475 | polymerase (R) II (D directed) polyp | 3.46 |
| 30 | 101488 | BE547216 | Hs.181128 | ELK1, member of ETS oncogene family | 3.46 |
| | 101045 | J05614 | | gb:Human proliferating cell nuclear anti | 3.46 |
| | 120149 | AA227609 | Hs.94834 | ESTs | 3.46 |
| | 107025 | AA825523 | Hs.21255 | ESTs, Weakly similar to I38022 hypotheti | 3.45 |
| | 101716 | AF050658 | Hs.2563 | tachykinin, precursor 1 (substance K, su | 3.45 |
| 35 | 102899 | AI815559 | Hs.75730 | sigl recognition particle receptor (rd | 3.45 |
| | 123075 | AW293133 | Hs.101340 | ESTs, Weakly similar to A42442 integrin | 3.45 |
| | 124695 | AA594979 | Hs.239307 | tyrosyl-HR synthetase | 3.45 |
| | 127669 | N28989 | Hs.22891 | solute carrier family 7 (cationic amino | 3.45 |
| | 129793 | AW207000 | Hs.126857 | Homo sapiens cD FLJ12936 fis, clone NT | 3.44 |
| 40 | 120095 | AA693774 | Hs.59601 | ESTs | 3.44 |
| | 110915 | BE092285 | Hs.29724 | hypothetical protein FLJ13187 | 3.43 |
| | 130542 | U64675 | Hs.179825 | RAN binding protein 2-like 1 | 3.43 |
| | 100488 | BE273749 | Hs.752 | FK506-binding protein 1A (12kD) | 3.43 |
| | 115027 | AA743331 | Hs.272572 | hemoglobin, alpha 2 | 3.43 |
| 45 | 119298 | NM_001241 | Hs.155478 | cyclin T2 | 3.43 |
| | 126486 | AI065133 | Hs.152316 | hypothetical protein PRO0971 | 3.43 |
| | 130021 | M24470 | Hs.1435 | guanosine monophosphate reductase | 3.43 |
| | 127166 | AW954605 | Hs.263395 | sema domain, transmembrane domain (TM), | 3.42 |
| 50 | 114988 | AA251089 | | gb:zs04f05.s1 NCI_CGAP_GCB1 Homo sapiens | 3.42 |
| | 133817 | AW578716 | Hs.7644 | H1 histone family, member 2 | 3.41 |
| | 133562 | M60721 | Hs.74870 | H2.0 (Drosophila)-like homeo box 1 | 3.41 |
| | 105610 | AA280072 | Hs.99872 | fatal Alzheimer antigen | 3.41 |
| | 129007 | AK001521 | Hs.107882 | hypothetical protein FLJ10659 | 3.41 |
| 55 | 100662 | AI368680 | Hs.816 | SRY (sex determining region Y)-box 2 | 3.41 |
| | 120159 | R60781 | Hs.92927 | putative 47 kDa protein | 3.41 |
| | 134966 | AW402389 | Hs.920 | modulator recognition factor 1 | 3.41 |
| | 100369 | D79988 | Hs.115778 | KIAA0166 gene product | 3.41 |
| | 104260 | AF008192 | Hs.194283 | putative GR6 protein | 3.40 |
| | 100134 | AA305746 | Hs.49 | macrophage scavenger receptor 1 | 3.40 |
| 60 | 116015 | AA338648 | Hs.50334 | testes development-related NYD-SP22 | 3.40 |
| | 119251 | T15753 | Hs.65250 | EST | 3.40 |
| | 127176 | BE387162 | Hs.280858 | ESTs, Highly similar to A35661 D excis | 3.40 |
| | 123422 | AA598484 | | gb:ae38f04.s1 Gessler Wilms tumor Homo s | 3.39 |
| | 123094 | AA761073 | Hs.146847 | TRAF family member-associated NFKB activ | 3.39 |
| 65 | 105289 | AB020638 | Hs.103000 | KIAA0831 protein | 3.39 |
| | 111219 | N68836 | Hs.19247 | ESTs, Moderately similar to ALUC_HUMAN I | 3.38 |
| | 127963 | AI299013 | Hs.87779 | Homo sapiens cD: FLJ23087 fis, clone L | 3.38 |
| | 109412 | BE543313 | Hs.209473 | hypothetical protein FLJ10520 | 3.38 |
| | 118794 | AW517051 | Hs.118210 | ESTs | 3.38 |
| 70 | 112040 | R43286 | | gb:yg17e11.s1 Soares infant brain 1N1B H | 3.38 |
| | 111180 | AI798851 | Hs.283108 | hemoglobin, gamma G | 3.38 |
| | 117329 | AA524065 | Hs.93670 | Homo sapiens cD: FLJ22664 fis, clone H | 3.38 |
| | 104371 | AI288696 | Hs.194081 | ESTs, Weakly similar to I38022 hypotheti | 3.38 |
| | 109265 | AA195285 | Hs.85982 | ESTs | 3.38 |
| 75 | 109557 | AW452405 | Hs.6427 | ESTs | 3.38 |
| | 120753 | AA312551 | Hs.230157 | ESTs | 3.38 |
| | 120970 | AA398118 | Hs.97579 | ESTs, Weakly similar to A46010 X-linked | 3.38 |
| | 127094 | F13215 | Hs.287849 | ESTs, Weakly similar to T22074 hypotheti | 3.38 |
| | 127746 | AI239495 | Hs.120189 | ESTs | 3.38 |
| 80 | 123553 | AI494291 | Hs.111977 | ESTs | 3.37 |
| | 130652 | M31669 | Hs.1735 | inhibin, beta B (activin AB beta polypep | 3.37 |
| | 135101 | U82275 | Hs.94498 | leukocyte immunoglobulin-like receptor, | 3.37 |
| | 121799 | AI885670 | Hs.124027 | SELENOPHOSPHATE SYNTHETASE ; Human selen | 3.37 |
| | 112278 | Z41698 | Hs.26039 | Homo sapiens cD FLJ13937 fis, clone Y7 | 3.36 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| 5 | 113401 | AA610175 | Hs.179647 | Homo sapiens cD FLJ12195 fis, clone MA | 3.36 |
| | 109292 | AW975746 | Hs.188662 | KIAA1702 protein | 3.36 |
| | 135026 | N92165 | Hs.93231 | ESTs | 3.36 |
| | 118210 | N49233 | Hs.46914 | ESTs, Weakly similar to A46010 X-linked | 3.35 |
| | 123476 | AA384564 | Hs.108829 | ESTs | 3.35 |
| | 111076 | N59129 | Hs.20851 | ESTs | 3.35 |
| | 111520 | A1985369 | Hs.301134 | ESTs | 3.35 |
| | 133383 | BE313555 | Hs.7252 | KIAA1224 protein | 3.35 |
| 10 | 103731 | AA070545 | | gb:zm70c03.r1 Stratagene neuroepithelium | 3.35 |
| | 110828 | AK002114 | Hs.23495 | hypothetical protein FLJ11252 | 3.35 |
| | 112520 | R68654 | Hs.30814 | ESTs | 3.35 |
| | 115725 | AW899053 | Hs.76917 | F-box only protein 8 | 3.35 |
| | 125867 | H13331 | Hs.123721 | ESTs | 3.35 |
| 15 | 127719 | A1242163 | Hs.22670 | chromodomain helicase D binding protei | 3.35 |
| | 129863 | BE379765 | Hs.129872 | sperm associated antigen 9 | 3.35 |
| | 130816 | M61877 | Hs.1985 | spectrin, alpha, erythrocytic 1 (ellipto | 3.35 |
| | 130888 | AL044315 | Hs.173094 | Homo sapiens mR for KIAA1750 protein, | 3.35 |
| | 133377 | AJ131245 | Hs.7239 | SEC24 (S. cerevisiae) related gene famil | 3.35 |
| 20 | 118986 | AF148713 | Hs.125830 | bladder cancer overexpressed protein | 3.35 |
| | 101723 | U34304 | | gb:Human nonmuscle myosin heavy chain II | 3.34 |
| | 134693 | N70361 | Hs.8854 | Human transcription unit PVT gene, exons | 3.34 |
| | 102856 | M26150 | Hs.248177 | H3 histone family, member L | 3.34 |
| 25 | 105593 | AA279341 | Hs.174151 | aldehyde oxidase 1 | 3.34 |
| | 134748 | L34059 | Hs.89484 | cadherin 4, type 1, R-cadherin (retu) | 3.34 |
| | 109149 | AA831179 | Hs.40065 | hypothetical protein MGC4825 | 3.33 |
| | 115026 | AA251972 | Hs.188718 | ESTs | 3.33 |
| | 103546 | Z14244 | Hs.75752 | cytochrome c oxidase subunit VIIb | 3.33 |
| | 111189 | N67603 | Hs.272130 | ESTs, Weakly similar to S65824 reverse t | 3.33 |
| 30 | 127076 | A1422951 | Hs.146162 | ESTs | 3.33 |
| | 124949 | A1903210 | Hs.336780 | tubulin, beta polypeptide | 3.33 |
| | 111012 | A1077389 | Hs.269818 | ESTs, Weakly similar to Z195_HUMAN ZINC | 3.33 |
| | 113412 | AW628660 | Hs.44131 | KIAA0974 protein | 3.33 |
| | 116351 | AL133623 | Hs.82501 | similar to mouse Xrn1 / Dhm2 protein | 3.33 |
| 35 | 121633 | AA417011 | Hs.98175 | EST | 3.33 |
| | 124591 | N69243 | Hs.192974 | hypothetical protein FLJ12735 | 3.33 |
| | 130225 | AB021179 | Hs.15299 | HMBA-inducible | 3.33 |
| | 131945 | NM_002916 | Hs.35120 | replication factor C (activator 1) 4 (37 | 3.33 |
| | 132581 | AK000631 | Hs.52256 | hypothetical protein FLJ20624 | 3.33 |
| 40 | 105726 | NM_012068 | Hs.9754 | activating transcription factor 5 | 3.32 |
| | 101867 | M96132 | | gb:Human MHC class II HLA-DR-beta-1*0901 | 3.32 |
| | 105004 | BE616023 | Hs.25298 | KIAA1813 protein | 3.32 |
| | 100288 | AL039103 | Hs.153834 | pumilio (Drosophila) homolog 1 | 3.32 |
| 45 | 118349 | N63786 | Hs.94149 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.32 |
| | 103352 | H09366 | Hs.78853 | uracil-D glycosylase | 3.30 |
| | 107436 | W27720 | Hs.12450 | protocadherin 9 | 3.30 |
| | 109062 | AA160941 | | gb:zq40d12.s1 Stratagene hNT neuron (937 | 3.30 |
| | 110379 | A1300505 | Hs.33130 | Homo sapiens cD: FLJ23486 fis, clone L | 3.30 |
| | 111221 | AB037782 | Hs.15119 | KIAA1361 protein | 3.30 |
| 50 | 117903 | AA768283 | Hs.47111 | ESTs | 3.30 |
| | 123265 | AA491209 | | gb:aa47a08.s1 NCL_CGAP_GCB1 Homo sapiens | 3.30 |
| | 128226 | A1284940 | Hs.289082 | GM2 ganglioside activator protein | 3.30 |
| | 111945 | R40663 | Hs.124944 | ESTs | 3.30 |
| | 126214 | AW748336 | Hs.168052 | KIAA0421 protein | 3.30 |
| 55 | 121073 | H46199 | Hs.112184 | DKFZP586J0619 protein | 3.30 |
| | 102083 | T35901 | Hs.75117 | interleukin enhancer binding factor 2, 4 | 3.30 |
| | 100992 | NM_007289 | Hs.1298 | membrane metallo-endopeptidase (neutral | 3.30 |
| | 134021 | L13720 | Hs.78501 | growth arrest-specific 6 | 3.30 |
| | 126452 | R26867 | | gb:yh52e01.s1 Soares placenta Nb2HP Homo | 3.29 |
| 60 | 117195 | A1798425 | Hs.42710 | ESTs | 3.29 |
| | 127863 | AK000452 | Hs.10340 | hypothetical protein FLJ20445 | 3.29 |
| | 113677 | Z70200 | Hs.246112 | KIAA0788 protein | 3.28 |
| | 132398 | AA876616 | Hs.16979 | ESTs, Weakly similar to A43932 mucin 2 p | 3.28 |
| | 109533 | AL043979 | Hs.259729 | KIAA0596 protein | 3.28 |
| 65 | 102915 | X07820 | Hs.2258 | matrix metalloprotease 10 (stromelysin | 3.28 |
| | 104348 | H05405 | Hs.19221 | hypothetical protein DKFZp566G1424 | 3.28 |
| | 113047 | A1571940 | Hs.7549 | ESTs | 3.28 |
| | 113203 | AA743563 | Hs.10305 | ESTs | 3.28 |
| | 114503 | AL040600 | Hs.188083 | ESTs | 3.28 |
| 70 | 122100 | AA431220 | Hs.41086 | pleckstrin homology domain-containing, f | 3.28 |
| | 123073 | AA485061 | Hs.105652 | ESTs | 3.28 |
| | 130253 | A1078570 | Hs.167473 | phosphoglucosyltransferase 5 | 3.28 |
| | 130365 | W56119 | Hs.155103 | eukaryotic translation initiation factor | 3.28 |
| | 130762 | D84371 | Hs.1898 | paraoxase 1 | 3.28 |
| 75 | 132360 | AW893660 | Hs.46440 | solute carrier family 21 (organic anion | 3.28 |
| | 110763 | A1928445 | Hs.92254 | sytoplasmic-like 2 | 3.27 |
| | 103437 | AV655598 | Hs.184211 | peptidase (mitochondrial processing) bet | 3.27 |
| | 114840 | AA447591 | Hs.87359 | ESTs, Highly similar to RB18_HUMAN RAS-R | 3.27 |
| | 106888 | AA020964 | Hs.24734 | oxysterol binding protein | 3.27 |
| 80 | 129896 | BE295568 | Hs.13225 | UDP-Galactose 4-epimerase | 3.26 |
| | 113459 | T80206 | Hs.14716 | ESTs | 3.26 |
| | 134332 | D86962 | Hs.81875 | growth factor receptor-bound protein 10 | 3.26 |
| | 117048 | H89732 | Hs.230113 | EST | 3.26 |
| | 109249 | AA194730 | Hs.268189 | hypothetical protein FLJ20436 | 3.26 |

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|----|--------|-----------|-----------|--|------|
| | 134663 | W73428 | Hs.8750 | uncharacterized bone marrow protein BM04 | 3.26 |
| | 114440 | AL046511 | Hs.106525 | hypothetical protein FLJ12567 | 3.25 |
| | 102196 | BE266830 | Hs.75238 | chromatin assembly factor 1, subunit B (| 3.25 |
| | 109581 | R45584 | Hs.23025 | ESTs, Weakly similar to ALU5_HUMAN ALU S | 3.25 |
| 5 | 120814 | AW867796 | Hs.96860 | ESTs, Weakly similar to I38022 hypothe | 3.25 |
| | 122391 | AA446316 | Hs.191622 | ESTs | 3.25 |
| | 122553 | AA451884 | Hs.190121 | ESTs | 3.25 |
| | 124755 | R38087 | Hs.267690 | KIAA1228 protein | 3.25 |
| | 130943 | U20760 | Hs.272429 | calcium-sensing receptor (hypocalciuric | 3.25 |
| 10 | 115185 | BE299677 | Hs.105461 | hypothetical protein FLJ20357 | 3.25 |
| | 114297 | AA149707 | Hs.173091 | ubiquitin-like 3 | 3.25 |
| | 106657 | AW854339 | Hs.33476 | hypothetical protein FLJ11937 | 3.25 |
| | 124320 | H95749 | Hs.102342 | EST | 3.25 |
| | 124087 | H08773 | Hs.288590 | Homo sapiens cD FLJ11454 fis, clone HE | 3.24 |
| 15 | 110705 | AB007902 | Hs.32168 | KIAA0442 protein | 3.24 |
| | 106508 | AI205785 | Hs.30348 | ESTs | 3.24 |
| | 112538 | AA908813 | | gb:cg77h06.s1 NCL_CGAP_Ov8 Homo sapiens | 3.24 |
| | 100130 | NM_000304 | Hs.103724 | peripheral myelin protein 22 | 3.24 |
| | 106017 | AA477956 | Hs.26268 | ESTs | 3.24 |
| 20 | 113921 | AW976530 | Hs.28355 | hypothetical protein FLJ22402 | 3.23 |
| | 121520 | AA412163 | Hs.164785 | ESTs | 3.23 |
| | 129255 | AI961727 | Hs.109804 | H1 histone family, member X | 3.23 |
| | 125069 | H81306 | Hs.194485 | ESTs | 3.23 |
| 25 | 119863 | AA081218 | Hs.58608 | Homo sapiens cD FLJ14206 fis, clone NT | 3.23 |
| | 111273 | N70934 | | gb:za33106.s1 Soares fetal liver spleen | 3.23 |
| | 102971 | X16609 | Hs.183805 | ankyrin 1, erythrocytic | 3.23 |
| | 103937 | AA934063 | Hs.13836 | ESTs, Weakly similar to I38022 hypothe | 3.23 |
| | 121770 | NM_015902 | Hs.278428 | progesterin induced protein | 3.23 |
| 30 | 128972 | AA528140 | Hs.107515 | ESTs, Weakly similar to T00329 hypothe | 3.23 |
| | 132528 | T78736 | Hs.50758 | SMC4 (structural maintenance of chromoso | 3.23 |
| | 134835 | L04569 | Hs.89925 | calcium channel, voltage-dependent, L ty | 3.23 |
| | 103158 | BE242587 | Hs.118651 | hematopoietically expressed homeobox | 3.22 |
| | 118405 | AL117518 | Hs.3686 | KIAA0978 protein | 3.22 |
| 35 | 104631 | AA002064 | Hs.18920 | ESTs | 3.22 |
| | 114253 | BE149866 | Hs.14831 | Homo sapiens, Similar to zinc finger pro | 3.22 |
| | 134607 | AI675881 | Hs.86538 | ESTs | 3.22 |
| | 135114 | AW340493 | Hs.175043 | ancient conserved domain protein 4 | 3.22 |
| | 120191 | BE407106 | Hs.65907 | Homo sapiens, clone IMAGE:3959816, mR, | 3.22 |
| 40 | 105029 | AI122691 | Hs.13268 | ESTs | 3.21 |
| | 128550 | AA418276 | Hs.170142 | ESTs | 3.21 |
| | 119873 | AI660149 | Hs.44865 | lysosomal | 3.21 |
| | 130115 | T47294 | Hs.149923 | X-box binding protein 1 | 3.21 |
| | 133916 | AL039185 | Hs.77558 | thyroid hormone receptor interactor 7 | 3.21 |
| 45 | 120259 | AW014786 | Hs.192742 | hypothetical protein FLJ12785 | 3.21 |
| | 110721 | H97678 | Hs.31319 | ESTs | 3.21 |
| | 130062 | AL049415 | Hs.278679 | a disintegrin and metalloprotease doma | 3.21 |
| | 100265 | D38521 | Hs.112396 | KIAA0077 protein | 3.20 |
| | 100624 | AB001025 | Hs.9349 | ryanodine receptor 3 | 3.20 |
| 50 | 122275 | AA437124 | Hs.187247 | ESTs | 3.20 |
| | 127089 | AA347668 | | gb:EST54026 Fetal heart II Homo sapiens | 3.20 |
| | 134321 | BE538082 | Hs.8172 | ESTs, Moderately similar to A46010 X-fin | 3.20 |
| | 132809 | AF036144 | Hs.5734 | meningioma expressed antigen 5 (hyaluron | 3.20 |
| | 101125 | AJ250562 | Hs.82749 | transmembrane 4 superfamily member 2 | 3.20 |
| 55 | 128339 | AL121087 | Hs.296406 | KIAA0685 gene product | 3.19 |
| | 117121 | H95044 | Hs.321386 | EST | 3.19 |
| | 124760 | AW408586 | Hs.91052 | ESTs, Moderately similar to ALU5_HUMAN A | 3.19 |
| | 132232 | AI522273 | Hs.42640 | ESTs | 3.19 |
| | 125919 | W26713 | Hs.256972 | ESTs | 3.19 |
| 60 | 123324 | AB018352 | Hs.105399 | KIAA0809 protein | 3.19 |
| | 100157 | D14661 | Hs.119 | Wilms' tumour 1-associating protein | 3.19 |
| | 101447 | M21305 | | gb:Human alpha satellite and satellite 3 | 3.19 |
| | 124345 | NM_014487 | Hs.120766 | nucleolar cysteine-rich protein | 3.18 |
| | 122583 | NM_012447 | Hs.20132 | stromal antigen 3 | 3.18 |
| 65 | 128961 | AL133014 | Hs.107387 | CGI-20 protein | 3.18 |
| | 111321 | AI569766 | Hs.13205 | ESTs | 3.18 |
| | 134977 | AL044963 | Hs.306121 | leukocyte receptor cluster (LRC) encoded | 3.18 |
| | 131535 | N22120 | Hs.75277 | hypothetical protein FLJ13910 | 3.18 |
| | 109950 | H08200 | Hs.268770 | ESTs, Weakly similar to 2004399A chromos | 3.18 |
| 70 | 129875 | AA181018 | Hs.13056 | hypothetical protein FLJ13920 | 3.18 |
| | 101654 | M60298 | Hs.733 | erythrocyte membrane protein band 4.2 | 3.18 |
| | 104732 | AL079294 | Hs.29952 | Homo sapiens mR full length insert cDN | 3.18 |
| | 106857 | AB037744 | Hs.34892 | KIAA1323 protein | 3.18 |
| | 108301 | AA069728 | Hs.184582 | ribosomal protein L24 | 3.18 |
| 75 | 118042 | AI432389 | Hs.161465 | ESTs | 3.18 |
| | 120900 | AA830712 | Hs.291931 | ESTs | 3.18 |
| | 129312 | T97579 | Hs.110334 | ESTs, Weakly similar to I78885 serine/th | 3.18 |
| | 116291 | AW410377 | Hs.41502 | hypothetical protein FLJ21276 | 3.17 |
| | 110672 | AW612890 | Hs.191178 | ESTs | 3.17 |
| 80 | 115665 | BE072425 | Hs.44579 | hypothetical protein FLJ20199 | 3.17 |
| | 127581 | AK000680 | Hs.266175 | phosphoprotein associated with GEMs | 3.17 |
| | 129584 | AV656017 | Hs.184325 | CGI-76 protein | 3.16 |
| | 108830 | AA131743 | Hs.193352 | ESTs | 3.16 |
| | 124443 | AI857519 | Hs.302031 | zinc finger protein, subfamily 1A, 4 (Eo | 3.16 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| 5 | 106290 | AW961393 | Hs.16364 | hypothetical protein FLJ10955 | 3.16 |
| | 122787 | AI209093 | Hs.99512 | ESTs | 3.16 |
| | 133112 | T15465 | Hs.182231 | thyrotropin-releasing hormone | 3.16 |
| | 116435 | AA186761 | Hs.334812 | hypothetical protein DKFZp586K0717 | 3.16 |
| | 109121 | BE389387 | Hs.49767 | DH dehydrogenase (ubiquinone) Fe-S pro | 3.16 |
| | 126721 | AW579621 | Hs.125359 | Thy-1 cell surface antigen | 3.15 |
| | 102526 | AA203429 | Hs.79474 | tyrosine 3-monooxygenase/tryptophan 5-mo | 3.15 |
| | 100512 | D13317 | Hs.78915 | GA-binding protein transcription factor, | 3.15 |
| 10 | 105299 | AF098951 | Hs.194720 | ATP-binding cassette, sub-family G (WHIT | 3.15 |
| | 117842 | AI984505 | Hs.161121 | ESTs | 3.15 |
| | 123049 | BE047680 | Hs.211869 | dickkopf (Xenopus laevis) homolog 2 | 3.15 |
| | 128639 | AW582962 | Hs.102897 | CGI-47 protein | 3.15 |
| | 130343 | AB040914 | Hs.278628 | KIAA1481 protein | 3.15 |
| 15 | 115705 | AB004849 | Hs.50748 | chromosome 21 open reading frame 18 | 3.15 |
| | 120673 | AW968634 | Hs.105093 | ESTs | 3.15 |
| | 132116 | AW960474 | Hs.40289 | ESTs | 3.15 |
| | 116217 | AU076474 | Hs.123178 | translocase of inner mitochondrial membr | 3.15 |
| | 104926 | BE298808 | Hs.33363 | DKFZP434N093 protein | 3.14 |
| 20 | 105297 | NM_015905 | Hs.183858 | transcriptio intermediary factor 1 | 3.14 |
| | 125343 | AJ475495 | Hs.304101 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 3.14 |
| | 115618 | H11695 | Hs.322901 | disrupter of silencing 10 | 3.14 |
| | 124893 | AA830185 | Hs.269680 | ESTs | 3.13 |
| | 105461 | BE53071 | Hs.69388 | hypothetical protein FLJ20505 | 3.13 |
| 25 | 126165 | A1741816 | Hs.125897 | ESTs | 3.13 |
| | 105212 | AA205334 | Hs.324278 | Homo sapiens mR; cD DKFZp566M063 (fr | 3.13 |
| | 101628 | M57506 | Hs.72918 | small inducible cytokine A1 (I-309, homo | 3.13 |
| | 107951 | AJ300077 | Hs.61690 | ESTs | 3.13 |
| | 109166 | AA219691 | Hs.73625 | RAB6 interacting, kinesin-like (rabkines | 3.13 |
| 30 | 117299 | N75768 | | gb:yyw30b07.r1 Morton Felal Cochlea Homo | 3.13 |
| | 119694 | AA041350 | Hs.57847 | ESTs, Moderately similar to ICE4_HUMAN C | 3.13 |
| | 124840 | R56146 | Hs.164515 | EST, Weakly similar to AF090930 1 PRO047 | 3.13 |
| | 127433 | AW979155 | Hs.298275 | amino acid transporter 2 | 3.13 |
| | 128337 | AH123529 | Hs.166592 | ESTs | 3.13 |
| 35 | 134053 | AW626686 | Hs.78851 | KIAA0217 protein | 3.13 |
| | 134475 | NM_014733 | Hs.83790 | KIAA0305 gene product | 3.13 |
| | 128761 | BE300341 | Hs.104925 | ectodermal-neural cortex (with BTB-like | 3.12 |
| | 124971 | T23800 | Hs.151001 | hypothetical protein FLJ14728 | 3.12 |
| | 128314 | T87479 | Hs.291797 | ESTs | 3.12 |
| 40 | 134695 | AB036829 | Hs.178347 | SKIP for skeletal muscle and kidney enri | 3.12 |
| | 131333 | BE244603 | Hs.25726 | transposon-derived Buster1 transposase-I | 3.12 |
| | 119781 | AJ278016 | Hs.55565 | ankyrin repeat domain 3 | 3.12 |
| | 131824 | U28838 | Hs.32935 | TATA box binding protein (TBP)-associate | 3.11 |
| | 124595 | AW194851 | Hs.111801 | arsenite resistance protein ARS2 | 3.11 |
| 45 | 116115 | AL042355 | Hs.70202 | WD repeat domain 10 | 3.11 |
| | 129415 | AI907084 | Hs.111243 | MADS box transcription enhancer factor 2 | 3.11 |
| | 111552 | T97939 | Hs.191185 | ESTs | 3.10 |
| | 134861 | NM_000937 | Hs.171880 | polymerase (R) II (D directed) polyp | 3.10 |
| | 104971 | BE311926 | Hs.15830 | hypothetical protein FLJ12691 | 3.10 |
| 50 | 126536 | AA156151 | | gb:zo48c06.r1 Stralagene endothelial cei | 3.10 |
| | 128246 | AI990512 | Hs.214818 | DMRT-like family C2 | 3.10 |
| | 106412 | AA453734 | Hs.10198 | ESTs | 3.10 |
| | 107902 | AA026627 | Hs.61358 | ESTs | 3.10 |
| | 112495 | AI346487 | Hs.28739 | ESTs | 3.09 |
| 55 | 131870 | NM_014874 | Hs.3363 | KIAA0214 gene product | 3.09 |
| | 105301 | AW352357 | Hs.7457 | MAGE1 protein | 3.09 |
| | 123670 | AI189844 | Hs.112708 | ESTs, Moderately similar to ZN91_HUMAN Z | 3.09 |
| | 116474 | AW160774 | Hs.159154 | tubulin, beta, 4 | 3.09 |
| | 112064 | AL049390 | Hs.22689 | Homo sapiens mR; cD DKFZp586O1318 (f | 3.09 |
| 60 | 130525 | AA361850 | Hs.322149 | Human clone 137308 mR, partial cds | 3.08 |
| | 120398 | AL133649 | Hs.110953 | retinoic acid induced 1 | 3.08 |
| | 102735 | AF111106 | Hs.3382 | protein phosphatase 4, regulatory subuni | 3.08 |
| | 124748 | R34617 | | gb:yh85h12.s1 Soares placenta Nb2HP Homo | 3.08 |
| | 120755 | AA312934 | Hs.190745 | Homo sapiens cD; FLJ21326 fs, clone C | 3.08 |
| 65 | 118895 | BE304917 | Hs.31097 | hypothetical protein FLJ21478 | 3.08 |
| | 107463 | AW952022 | Hs.315164 | hypothetical protein similar to actin re | 3.08 |
| | 114290 | R51383 | Hs.25793 | ESTs | 3.08 |
| | 119005 | AL038511 | Hs.125316 | ESTs, Weakly similar to S33990 finger pr | 3.08 |
| | 125676 | BE612918 | Hs.151973 | hypothetical protein FLJ23511 | 3.08 |
| 70 | 127766 | AA723659 | Hs.290607 | EST | 3.08 |
| | 132693 | BE244200 | Hs.55075 | KIAA0410 gene product | 3.07 |
| | 106812 | BE251590 | Hs.239370 | DKFZP7271051 protein | 3.07 |
| | 125654 | X96753 | Hs.9004 | chondroitin sulfate proteoglycan 4 (mela | 3.07 |
| | 111836 | R58394 | Hs.25119 | ESTs, Weakly similar to YEX0_YEAST HYPOT | 3.06 |
| 75 | 101682 | AF043045 | Hs.81008 | filamin B, beta (actin-binding protein-2 | 3.06 |
| | 110004 | H10413 | Hs.268774 | ESTs | 3.06 |
| | 117591 | N64777 | Hs.44656 | ESTs | 3.06 |
| | 110737 | AA335609 | Hs.7589 | ESTs, Weakly similar to A46010 X-linked | 3.06 |
| | 134337 | NM_004922 | Hs.81964 | SEC24 (S. cerevisiae) related gene famil | 3.06 |
| 80 | 132450 | AA100912 | Hs.48827 | hypothetical protein FLJ12085 | 3.06 |
| | 125556 | AB033054 | Hs.334806 | KIAA1238 protein | 3.06 |
| | 101811 | NM_002556 | Hs.24734 | oxysterol binding protein | 3.06 |
| | 131530 | AA574309 | Hs.283402 | TCR eta | 3.06 |
| | 105049 | AB032945 | Hs.172506 | myosin VB | 3.06 |

| | | | | | |
|----|-------------|---------------------------------------|---|--|------|
| 5 | 126614 | AA701941 | Hs.187555 | ESTs | 3.05 |
| | 130960 | AF035621 | Hs.21611 | kinesin family member 3C | 3.05 |
| | 105503 | AW963624 | Hs.31707 | ESTs, Weakly similar to YEW4_YEAST HYPOT | 3.05 |
| | 107361 | U72513 | Hs.159486 | Human RPL13-2 pseudogene mR, complete | 3.05 |
| | 107575 | D81886 | Hs.59908 | ESTs | 3.05 |
| | 116999 | H84644 | Hs.40707 | EST | 3.05 |
| | 119554 | W38188 | | (NONE) | 3.05 |
| 10 | 120934 | AA226199 | | gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens | 3.05 |
| | 125805 | A1160594 | Hs.166656 | ESTs, Highly similar to S49460 glutamate | 3.05 |
| | 127263 | AA331156 | | gb:EST35034 Embryo, 6 week, subtracted (| 3.05 |
| | 128025 | T64877 | Hs.108479 | ESTs | 3.05 |
| | 131090 | A1143139 | Hs.2288 | visinin-like 1 | 3.05 |
| | 112197 | NM_003655 | Hs.5637 | ESTs | 3.05 |
| 15 | 133492 | L40397 | Hs.74137 | transmembrane trafficking protein | 3.04 |
| | 118485 | AA508515 | Hs.291049 | ESTs | 3.04 |
| | 113893 | AJ373741 | Hs.59384 | hypothetical protein MGC3047 | 3.04 |
| | 116911 | AW205577 | Hs.308435 | ESTs, Moderately similar to KIAA0745 pro | 3.04 |
| | 132833 | U78525 | Hs.57783 | eukaryotic translation initiation factor | 3.04 |
| 20 | 124724 | H20816 | Hs.112423 | Homo sapiens mR; cD DKFZp586I1420 (f | 3.04 |
| | 105894 | AJ904740 | Hs.25691 | receptor (calcatonin) activity modifying | 3.04 |
| | 129991 | R28386 | Hs.179925 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 3.04 |
| | 128714 | T85231 | Hs.179661 | tubulin, beta 5 | 3.04 |
| | 134550 | U76376 | Hs.87247 | harakini, BCL2-interacting protein (cont | 3.04 |
| 25 | 106851 | AI458623 | | gb:lk04g09.x1 NCI_CGAP_Lu24 Homo sapiens | 3.04 |
| | 133445 | AC005262 | Hs.73797 | guanine nucleotide binding protein (G pr | 3.04 |
| | 102581 | AJ077228 | Hs.77256 | enhancer of zeste (Drosophila) homolog 2 | 3.04 |
| | 127542 | AA703684 | Hs.245474 | ESTs, Moderately similar to ALU5_HUMAN A | 3.03 |
| | 113043 | AI628789 | Hs.7483 | ESTs | 3.03 |
| 30 | 134710 | AI433797 | Hs.8889 | serine hydroxymethyltransferase 1 (solub | 3.03 |
| | 119245 | AI815733 | Hs.114360 | transforming growth factor beta-stimulat | 3.03 |
| | 106391 | AW959538 | Hs.321214 | hypothetical protein DKFZp564D0478 | 3.03 |
| | 114607 | AF041260 | Hs.129057 | breast carcinoma amplified sequence 1 | 3.03 |
| | 116083 | AA455706 | Hs.44581 | heat shock protein hsp70-related protein | 3.03 |
| 35 | 132079 | AJ701457 | Hs.38694 | ESTs | 3.03 |
| | 103825 | AI571835 | Hs.55468 | ESTs | 3.03 |
| | 106438 | AI141031 | Hs.21342 | ESTs | 3.03 |
| | 124359 | N22508 | Hs.139315 | Homo sapiens cD: FLJ21479 tis, clone C | 3.03 |
| | 126384 | AW090198 | Hs.4779 | KIAA1150 protein | 3.03 |
| 40 | 127995 | AA970953 | Hs.128709 | ESTs | 3.03 |
| | 127981 | AA837029 | Hs.157463 | ESTs | 3.02 |
| | 124417 | N34059 | | gb:yy28h09.s1 Soares fetal liver spleen | 3.02 |
| | 124357 | N22401 | | gb:yyw37g07.s1 Morton Fetal Cochlea Homo | 3.02 |
| | 105437 | AF151076 | Hs.25199 | hypothetical protein | 3.02 |
| 45 | 101158 | AW327723 | Hs.76122 | splicing factor, arginine/serine-rich 4 | 3.02 |
| | 113897 | R91601 | Hs.4947 | hypothetical protein FLJ22584 | 3.02 |
| | 100159 | AA285268 | Hs.23488 | KIAA0107 gene product | 3.02 |
| | 106487 | AJ697340 | Hs.135265 | Homo sapiens clone FLB8436 PRO2277 mR, | 3.02 |
| | 124977 | F04819 | Hs.190452 | KIAA0365 gene product | 3.02 |
| 50 | 131631 | AA022569 | Hs.29802 | slit (Drosophila) homolog 2 | 3.01 |
| | 102259 | AL041219 | Hs.82222 | sema domain, immunoglobulin domain (lg), | 3.01 |
| | 104399 | AL022316 | Hs.301947 | kraken-like | 3.01 |
| | 116536 | BE218027 | Hs.89969 | ESTs | 3.00 |
| | 125889 | AA351978 | Hs.4943 | hepatocellular carcinoma associated prot | 3.00 |
| 55 | 102233 | AW163045 | Hs.79334 | nuclear factor, Interleukin 3 regulated | 3.00 |
| | 102628 | U90322 | Hs.27812 | G protein-coupled receptor 23 | 3.00 |
| | 112812 | H55977 | Hs.35810 | ESTs | 3.00 |
| | 114654 | AA101840 | Hs.103679 | ESTs | 3.00 |
| | 118555 | N68372 | | gb:zza58c10.s1 Soares_fetal_lung_NbHL19W | 3.00 |
| 60 | 120005 | W90105 | Hs.94942 | EST | 3.00 |
| | 123596 | AA421130 | Hs.112640 | EST | 3.00 |
| | 126134 | AL133033 | Hs.4084 | KIAA1025 protein | 3.00 |
| | 126194 | H98755 | Hs.302975 | ESTs, Weakly similar to Z195_HUMAN ZINC | 3.00 |
| | 129778 | AK001676 | Hs.12457 | hypothetical protein FLJ10814 | 3.00 |
| 65 | Table 3B: | | | | |
| | Pkey: | Unique Eos probeset identifier number | | | |
| | CAT number: | Gene cluster number | | | |
| | Accession: | Genbank accession numbers | | | |
| 70 | Pkey | CAT number | Accession | | |
| | 123619 | 371681_1 | AA602984 AA609200 | | |
| | 124417 | 1642364_1 | N34059 N46979 | | |
| | 117299 | 1632586_1 | N75768 N22543 | | |
| 75 | 116845 | 393481_1 | AA649530 AA659316 H64973 | | |
| | 124748 | 1715080_1 | R34617 | | |
| | 125596 | 1708455_1 | R25698 R56582 R56018 | | |
| | 126257 | 182217_1 | N99638 AW973750 AA328271 H90994 AA558020 AA234435 N59599 R94815 | | |
| | 126280 | 1572221_1 | Z19417 H20866 | | |
| 80 | 126319 | 1528523_1 | D81689 D81802 | | |
| | 104172 | 273499_1 | AA476418 AA393338 AA398747 AA476518 | | |
| | 126426 | 110687_1 | AA125984 AA127189 AA065075 AA070377 AA100017 AA079891 AA113255 AA075168 AA082764 AA083380 N64829 AA084752 | | |
| | | | AA076512 AA085119 AA085208 AA085045 | | |
| | 126433 | 127143_1 | AA325606 AA099517 N89423 | | |

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| | 127092 | 177998_1 | T26985 Z44165 |
| | 127099 | 244301_1 | AA347668 AW956810 Z44271 F07065 F07064 R13506 |
| | 126535 | 149206_1 | AA156151 Z25109 C05177 |
| 5 | 103731 | 112052_1 | AA070545 AA131490 AA131373 |
| | 127263 | 232161_1 | AA331156 AA331157 AA331155 |
| | 126783 | 113388_1 | AA083531 AA126047 AA074915 AA148649 |
| | 118946 | 1683457_1 | N92834 W25061 |
| | 127520 | 656170_1 | T51239 |
| 10 | 127532 | 353907_1 | AJ003429 AJ003367 AA564825 |
| | 112516 | 1744223_1 | T83909 R68586 |
| | 112538 | 504579_1 | AA908813 R70255 |
| | 112540 | 1605263_1 | R69751 R70467 H69771 H80879 H80878 |
| | 113248 | 328626_1 | T63857 AW971220 AA493469 T63699 |
| 15 | 112631 | 1746257_1 | R82040 R70934 |
| | 128360 | 1540098_1 | F12374 T74059 |
| | 120514 | 25532_3 | AA258335 AA258499 |
| | 127867 | 1511945_1 | C18530 T63953 |
| | 120637 | 200885_1 | AA811804 AA809404 AA286907 AW977624 |
| 20 | 121481 | 123001_1 | AA411931 AA411930 |
| | 120934 | 177521_1 | AA226198 AA226513 AA383773 |
| | 106566 | 120358_1 | BE298210 AI672315 AW086489 BE298417 AA455921 AA902537 BE327124 R14963 AA085210 AW274273 AI333584 AI369742 |
| | | | AI039658 AI885095 AI476470 AI287650 AI885299 AI985381 AW592624 AW340136 AI266556 AA456390 AI310815 AA484951 |
| 25 | 121743 | 274582_1 | AA397636 AA421144 |
| | 114699 | 135322_1 | AA127386 R15644 AA127404 |
| | 106851 | 322947_1 | AI458623 AA639708 AA485409 R22065 AA485570 |
| | 123731 | genbank_AA609839 | AA609839 |
| | 123973 | 506369_1 | C14805 |
| | 116793 | 74964_1 | T77781 AW014157 D12422 AI918246 AA452599 AA628404 N35886 AA464593 AW301738 T77780 AI042309 AI095302 H60603 |
| 30 | 109700 | genbank_F09609 | AW510576 H37814 W61360 AI373286 AI702287 AA152465 AW169067 AW169012 AW340355 AI289311 |
| | 118466 | genbank_N86741 | F09609 |
| | 111273 | genbank_N70934 | N66741 |
| | 118555 | genbank_N68372 | N70934 |
| 35 | 111462 | genbank_R05296 | N68372 |
| | 118720 | genbank_N73515 | R05296 |
| | 118737 | 382979_1 | N73515 |
| | 111826 | genbank_R35975 | AA199686 N73861 |
| 40 | 120376 | genbank_AA227469 | R35975 |
| | 120809 | genbank_AA346495 | AA227469 |
| | 120839 | genbank_AA348913 | AA346495 |
| | 120873 | genbank_AA358015 | AA348913 |
| | 115498 | genbank_AA291070 | AA358015 |
| | 101045 | entrez_J05614 | AA291070 |
| 45 | 129969 | genbank_N57818 | J05614 |
| | 108407 | genbank_AA075519 | N57818 |
| | 122939 | genbank_AA477141 | AA075519 |
| | 117031 | genbank_H88353 | AA477141 |
| | 124298 | genbank_H91679 | H88353 |
| 50 | 117099 | 321871_1 | H91679 |
| | 101447 | entrez_M21305 | H93699 H97976 H80036 |
| | 124357 | genbank_N22401 | M21305 |
| | 101723 | 2603_1 | N22401 |
| 55 | | | U34304 AA355800 M69181 AA375523 AA093590 AA365595 S67247 AI371761 AW351920 AW181991 H28934 W79172 AA653543 |
| | | | AA122005 W95572 AF086505 C02448 W57668 T11988 W95465 AA425179 F05724 F12205 F06285 R16384 T66222 F08515 |
| | | | F07288 AA150346 H83264 T86770 N36366 AA337253 H12001 H82899 H69395 H69380 N29054 N30920 T97385 T96819 |
| | | | AA463807 AL079860 T11987 AA305048 AA149133 T82813 AA029555 AA035109 AA449123 AA340297 AA724155 W05196 |
| | | | AI859528 AA149134 C16426 C16097 C16587 C16138 C16107 AW021754 C16500 N30019 R55718 R60552 N84522 AI143322 |
| | | | AW519024 AA490700 N20675 AW296747 C16068 D58331 C16518 AI141214 N67221 C16423 C16537 C16094 C16152 H28935 |
| | | | T66152 C16382 AW022425 AA602899 AA694603 H22255 W74368 C16356 AI129361 AI917986 AI582253 AI923898 AI038907 |
| 60 | | | AW191970 AI678861 C16429 C16345 AI277790 R42325 AI640420 AI004136 AI277797 C16100 F09836 T71212 AA152316 |
| | | | AW090781 AI055902 T16084 AW022915 C16556 AW473979 T96820 AA476595 N75446 F02570 H69286 T89992 AA907493 |
| | | | T34275 AA156107 H11758 AI650288 H82900 AI474575 N66718 F04914 AA505470 AA993349 F01973 AI123277 F04729 C16236 |
| | | | AA879148 AA029574 AA887046 R08127 D57339 AA490477 AI669818 AI190995 AA035507 AL119272 AL135029 AA258725 |
| | | | AL079521 N40299 AI630191 N86148 AA341165 T28492 N83749 AI382123 AI065033 AI950411 AI935653 AI275551 AW027482 |
| 65 | | | AW197337 AI158323 AI336930 AI094099 AI351490 AA258563 AI634763 AI492374 AA983970 AI123565 T72559 F09890 |
| | | | AA669531 AI445824 T07180 AW084799 AA306254 R60606 W28367 R55928 W27995 AL044845 AA501890 N84045 T97274 |
| | | | N87532 AL135219 AA116056 T06000 AA116057 T07181 R08126 |
| | | | R01073 |
| 70 | 124677 | genbank_R01073 | H26683 |
| | 110243 | genbank_H26683 | M96132 |
| | 101867 | entrez_M96132 | S77583 |
| | 101941 | entrez_S77583 | R10889 R10888 |
| | 119052 | 149538_1 | R25867 R27438 |
| | 126452 | 209811_1 | T15977 |
| | 119263 | genbank_T15977 | R43286 |
| 75 | 112040 | genbank_R43286 | Z73677 |
| | 103657 | entrez_Z73677 | T92767 |
| | 119400 | genbank_T92767 | W38188 |
| | 119554 | NOT_FOUND_entrez_W38188 | AA487200 |
| | 123130 | genbank_AA487200 | AA487595 |
| 80 | 123143 | genbank_AA487595 | AA429515 |
| | 121950 | genbank_AA429515 | AA491209 |
| | 123265 | genbank_AA491209 | AA251089 |
| | 114988 | genbank_AA251089 | AA019255 |
| | 107794 | genbank_AA019255 | |

123422 genbank_AA598484 AA598484
109062 genbank_AA160941 AA160941

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TABLE 4A: ABOUT 1164 GENES UPREGULATED IN GLIOBLASTOMA

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of brain tumor to body atlas
R2: Ratio of brain tumor to normal brain

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| Pkey | ExAccn | UnigeneID | Unigene Title | R1 | R2 |
|--------|-----------|-----------|---|-------|------|
| 412719 | AW016610 | Hs.129911 | ESTs | 117.8 | 3.3 |
| 428321 | AI699994 | Hs.301347 | ESTs | 108.9 | 3.9 |
| 455601 | AI368680 | Hs.816 | SRY (sex determining region Y)-box 2 | 107.5 | 9.9 |
| 431917 | D16181 | Hs.2868 | peripheral myelin protein 2 | 99.0 | 11.8 |
| 415817 | U88967 | Hs.78867 | protein tyrosine phosphatase, receptor-I | 72.0 | 11.3 |
| 449494 | AW237014 | Hs.286650 | aquaporin 4 | 60.0 | 2.2 |
| 439285 | AL133916 | Hs.298998 | ESTs | 58.2 | 2.2 |
| 447072 | D61594 | Hs.17279 | tyrosylprotein sulfotransferase 1 | 54.2 | 7.1 |
| 456759 | BE259150 | Hs.127792 | delta (Drosophila)-like 3 | 53.5 | 2.5 |
| 427343 | AI880044 | Hs.176977 | protein kinase C binding protein 2 | 49.6 | 2.2 |
| 425088 | AA663372 | Hs.169395 | Homo sapiens cDNA FLJ12015 fis, clone HE | 49.5 | 3.1 |
| 412959 | D87458 | Hs.75090 | KIAA0282 protein | 46.3 | 3.0 |
| 447004 | AW296968 | Hs.157539 | ESTs | 43.7 | 3.2 |
| 436878 | BE465204 | Hs.47448 | ESTs | 39.8 | 10.8 |
| 433551 | AI985544 | Hs.289048 | ESTs | 39.7 | 4.3 |
| 425842 | AI587490 | Hs.159623 | NK-2 (Drosophila) homolog B | 39.3 | 26.2 |
| 407034 | U84540 | | gb:Human dystrobrevin isoform DTN-3 (DTN | 39.1 | 39.1 |
| 431725 | X65724 | Hs.2839 | Normie disease (pseudoglioma) | 38.4 | 3.7 |
| 453392 | U23752 | Hs.32964 | SRY (sex determining region Y)-box 11 | 37.5 | 22.1 |
| 447197 | R36075 | | gb:yh88b01.s1 Soares placenta Nb2HP Homo | 37.5 | 13.9 |
| 439415 | F05538 | Hs.12825 | ESTs | 35.4 | 3.1 |
| 409395 | U46745 | Hs.54435 | dystrobrevin, alpha | 34.3 | 3.0 |
| 449539 | W80363 | Hs.58446 | ESTs | 33.6 | 33.6 |
| 408562 | AI436323 | Hs.31141 | Homo sapiens mRNA for KIAA1568 protein, | 32.8 | 5.9 |
| 431019 | NM_005249 | Hs.2714 | forkhead box G1B | 32.4 | 17.0 |
| 427540 | R12014 | Hs.20976 | ESTs | 32.1 | 2.0 |
| 425057 | AA826434 | Hs.96944 | ESTs | 31.0 | 2.3 |
| 431941 | AK000106 | Hs.272227 | Homo sapiens cDNA FLJ20059 fis, clone CO | 30.8 | 30.8 |
| 416829 | AB013805 | Hs.80220 | calenlin (cadherin-associated protein), d | 30.4 | 2.2 |
| 420807 | AA280627 | Hs.57846 | ESTs | 30.4 | 30.4 |
| 444190 | AI878918 | Hs.10526 | cysteine and glycine-rich protein 2 | 30.4 | 30.4 |
| 429466 | M85835 | Hs.12827 | ESTs | 30.2 | 7.2 |
| 444471 | AB020684 | Hs.11217 | KIAA0877 protein | 29.5 | 29.5 |
| 451678 | AA374181 | Hs.26799 | DKFZP564D0764 protein | 28.8 | 3.0 |
| 439979 | AW600291 | Hs.6823 | hypothetical protein FLJ10430 | 27.7 | 3.2 |
| 433800 | AI034361 | Hs.135150 | lung type-I cell membrane-associated gly | 27.1 | 27.1 |
| 440435 | AL042201 | Hs.21273 | ESTs | 26.9 | 26.9 |
| 411078 | AI222020 | Hs.182364 | ESTs, Weakly similar to 25 kDa trypsin i | 26.0 | 26.0 |
| 407808 | AA663559 | Hs.289109 | dimethylarginine dimethylaminohydrolase | 25.8 | 2.2 |
| 416155 | AI807264 | Hs.205442 | ESTs, Weakly similar to AF117610 1 inner | 25.5 | 25.5 |
| 421659 | NM_014459 | Hs.106511 | protocadherin 17 | 25.0 | 3.3 |
| 430132 | AA204686 | Hs.234149 | hypothetical protein FLJ20647 | 24.7 | 24.7 |
| 433332 | AI367347 | Hs.127809 | ESTs | 24.6 | 24.6 |
| 452744 | AI267652 | Hs.30504 | Homo sapiens mRNA; cDNA DKFZp434E082 (tr | 23.8 | 23.8 |
| 419271 | N34901 | Hs.238532 | ESTs | 23.6 | 5.5 |
| 447397 | BE247676 | Hs.18442 | E-1 enzyme | 23.1 | 3.2 |
| 439039 | AI656707 | Hs.48713 | ESTs | 23.0 | 7.2 |
| 414175 | AI308876 | Hs.103849 | ESTs | 22.2 | 2.0 |
| 451099 | R52795 | Hs.25954 | interleukin 13 receptor, alpha 2 | 22.0 | 7.6 |
| 410102 | AW248508 | Hs.279727 | Homo sapiens cDNA FLJ14035 fis, clone HE | 21.6 | 2.3 |
| 415910 | U20350 | Hs.78913 | chemokine (C-X3-C) receptor 1 | 21.2 | 3.0 |
| 451468 | AW503398 | Hs.210047 | ESTs | 21.0 | 4.7 |
| 454117 | BE410100 | Hs.40368 | adaptor-related protein complex 1, sigma | 20.8 | 20.8 |
| 443850 | AW014723 | Hs.134719 | ESTs | 20.4 | 38.5 |
| 418738 | AW388633 | Hs.6682 | ESTs | 20.2 | 2.2 |
| 449433 | AI672096 | Hs.9012 | ESTs | 19.9 | 16.6 |
| 435706 | W31254 | Hs.7045 | GL004 protein | 19.7 | 19.7 |
| 407192 | AA609200 | | gb:af12e02.s1 Soares_testis_NHT Homo sap | 19.7 | 19.7 |
| 416892 | L24498 | Hs.80409 | growth arrest and DNA-damage-inducible, | 19.6 | 19.6 |
| 442562 | BE379584 | Hs.34789 | ESTs | 19.4 | 19.4 |
| 439451 | AF086270 | Hs.278554 | heterochromatin-like protein 1 | 19.1 | 17.4 |
| 426320 | W47595 | Hs.169300 | transforming growth factor, beta 2 | 18.7 | 5.4 |
| 412986 | X81120 | Hs.75110 | cannabinoid receptor 1 (brain) | 18.6 | 18.6 |
| 452106 | AI141031 | Hs.21342 | ESTs | 18.6 | 10.3 |
| 431173 | AW971198 | Hs.294068 | ESTs | 18.6 | 18.6 |
| 422583 | AA410506 | Hs.118578 | H.sapiens mRNA for ribosomal protein L18 | 18.5 | 18.5 |
| 419088 | AI538323 | Hs.77496 | small nuclear ribonucleoprotein polypept | 18.5 | 18.5 |
| 443547 | AW271273 | Hs.23767 | Homo sapiens cDNA FLJ12666 fis, clone NT | 18.5 | 5.1 |
| 451592 | AI805416 | Hs.213897 | ESTs | 18.4 | 18.4 |
| 450313 | AI038989 | Hs.24809 | hypothetical protein FLJ10826 | 18.3 | 18.3 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|------|
| | 422544 | AB018259 | Hs.118140 | KIAA0716 gene product | | |
| | 408096 | BE250162 | Hs.83765 | dihydrofolate reductase | 18.2 | 4.7 |
| | 418027 | AB037807 | Hs.83293 | hypothetical protein | 18.0 | 18.0 |
| 5 | 414117 | V88559 | Hs.1787 | proteolipid protein (Pelizaeus-Merzbache | 18.0 | 8.2 |
| | 429418 | AI381028 | Hs.99283 | ESTs | 18.0 | 18.0 |
| | 432527 | AW975028 | Hs.102754 | ESTs | 17.8 | 17.8 |
| | 447809 | AW207605 | Hs.164230 | ESTs, Highly similar to phosphodiesteras | 17.7 | 4.2 |
| | 419704 | AA429104 | Hs.45057 | ESTs | 17.5 | 4.3 |
| 10 | 436476 | AA326108 | Hs.53631 | ESTs, Weakly similar to enhancer-of-spl | 17.4 | 4.6 |
| | 445133 | AW157646 | Hs.153506 | ESTs, Weakly similar to AF150755 1 micro | 17.4 | 2.1 |
| | 446659 | AI335361 | Hs.226376 | ESTs | 17.3 | 18.8 |
| | 409049 | AI423132 | Hs.146343 | ESTs | 17.2 | 2.8 |
| | 443672 | AA323362 | Hs.9667 | bulboretaine (gamma), 2-oxoglutarate di | 17.2 | 3.8 |
| | 407748 | AL079409 | Hs.38176 | KIAA0606 protein; SCN Circadian Oscillat | 17.2 | 11.0 |
| 15 | 438527 | AI969251 | Hs.143237 | ESTs | 17.0 | 6.3 |
| | 417791 | AW965339 | Hs.111471 | ESTs | 16.9 | 16.9 |
| | 417355 | D13168 | Hs.82002 | endothelin receptor type B | 16.8 | 10.5 |
| | 427897 | NM_017413 | Hs.181060 | apelin; peptide ligand for APJ receptor | 16.4 | 16.4 |
| 20 | 419721 | NM_001650 | Hs.288650 | aquaporin 4 | 16.3 | 4.2 |
| | 427701 | AA411101 | Hs.221750 | ESTs | 16.2 | 4.4 |
| | 432435 | BE218886 | Hs.282070 | ESTs | 16.1 | 3.9 |
| | 426809 | BE313114 | Hs.29706 | ESTs | 16.1 | 5.7 |
| | 407881 | AW072003 | Hs.40968 | heparan sulfate (glucosamine) 3-O-sulfot | 16.0 | 10.0 |
| 25 | 400859 | | | | 15.9 | 15.9 |
| | 409731 | AA125985 | Hs.56145 | thymosin, beta, identified in neuroblast | 15.7 | 15.7 |
| | 420092 | AA814043 | Hs.88045 | ESTs | 15.6 | 15.6 |
| | 449605 | AW138581 | Hs.198416 | ESTs | 15.6 | 5.4 |
| | 422365 | AF035537 | Hs.115521 | REV3 (yeast homolog)-like, catalytic sub | 15.5 | 3.0 |
| 30 | 449611 | AI970394 | Hs.197075 | ESTs | 15.3 | 4.6 |
| | 414922 | D00723 | Hs.77631 | glycine cleavage system protein H (amino | 15.2 | 15.2 |
| | 405238 | | | | 15.2 | 5.6 |
| | 429007 | D80642 | | gb:HUM092E098 Human fetal brain (TFujiwa | 15.1 | 2.8 |
| 35 | 409638 | AW450420 | Hs.21335 | ESTs | 15.0 | 3.5 |
| | 445888 | AF070564 | Hs.13415 | Homo sapiens clone 24571 mRNA sequence | 14.9 | 7.1 |
| | 416737 | AF154335 | Hs.79691 | LJM domain protein | 14.8 | 5.7 |
| | 429163 | AA884766 | | gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s | 14.7 | 4.2 |
| | 436870 | AW204219 | Hs.43679 | ESTs | 14.6 | 3.0 |
| | 443181 | AI039201 | Hs.54548 | ESTs | 14.6 | 2.6 |
| 40 | 436281 | AW411194 | Hs.120051 | ESTs | 14.6 | 3.5 |
| | 449448 | D60730 | Hs.57471 | ESTs | 14.5 | 8.5 |
| | 422564 | AI148006 | Hs.222120 | ESTs | 14.4 | 4.8 |
| | 448243 | AW369771 | Hs.77496 | small nuclear ribonucleoprotein polypept | 14.4 | 14.4 |
| | 428748 | AW593206 | Hs.98785 | ESTs | 14.3 | 2.4 |
| 45 | 452576 | AB023177 | Hs.29900 | KIAA0960 protein | 14.2 | 14.2 |
| | 452461 | N78223 | Hs.108106 | transcription factor | 14.1 | 8.1 |
| | 449670 | F07693 | Hs.23869 | Homo sapiens mRNA; cDNA DKFp434K2172 (f | 14.1 | 12.8 |
| | 436637 | AI783629 | Hs.26766 | ESTs | 14.1 | 14.1 |
| | 429597 | NM_003816 | Hs.2442 | a disintegrin and metalloproteinase doma | 14.0 | 2.3 |
| 50 | 419078 | M93119 | Hs.89584 | insulinoma-associated 1 | 13.9 | 13.9 |
| | 410889 | X91662 | Hs.66744 | twist (Drosophila) homolog (acrocephalos | 13.9 | 2.9 |
| | 452355 | N54926 | Hs.29202 | G protein-coupled receptor 34 | 13.9 | 4.1 |
| | 421452 | AI925946 | Hs.104530 | fetal hypothetical protein | 13.9 | 13.9 |
| | 430290 | AI734110 | Hs.136355 | ESTs | 13.9 | 13.9 |
| 55 | 430387 | AW372884 | Hs.240770 | nuclear cap binding protein subunit 2, 2 | 13.8 | 13.8 |
| | 415875 | AA894876 | Hs.5687 | protein phosphatase 1B (formerly 2C), ma | 13.6 | 13.6 |
| | 416795 | AI497778 | Hs.168053 | ESTs, Highly similar to AF227948 1 HBV p | 13.5 | 13.5 |
| | 422025 | BE348774 | Hs.122554 | ESTs | 13.5 | 13.5 |
| | 400992 | | | | 13.3 | 13.3 |
| 60 | 413174 | AA723564 | Hs.191343 | ESTs | 13.3 | 5.5 |
| | 425187 | AW014486 | Hs.22509 | ESTs | 13.2 | 2.5 |
| | 456965 | AW131888 | Hs.172792 | ESTs, Weakly similar to hypothetical pro | 13.1 | 8.2 |
| | 419852 | AW503756 | Hs.286184 | hypothetical protein dJ55102.5 | 13.1 | 2.7 |
| | 409327 | L41162 | Hs.53563 | collagen, type IX, alpha 3 | 13.0 | 2.4 |
| 65 | 439519 | AA837118 | Hs.118366 | ESTs | 12.9 | 4.0 |
| | 436299 | AK000767 | Hs.5111 | hypothetical protein FLJ20729 | 12.9 | 7.6 |
| | 446657 | AI335191 | Hs.260702 | ESTs, Moderately similar to ALU7_HUMAN A | 12.7 | 3.1 |
| | 423073 | BE252922 | Hs.123119 | MAD (mothers against decapentaplegic, Dr | 12.6 | 12.6 |
| | 424278 | AK000723 | Hs.144517 | hypothetical protein FLJ20716 | 12.6 | 12.6 |
| 70 | 451996 | AW514021 | Hs.245510 | ESTs | 12.6 | 12.6 |
| | 400860 | | | | 12.6 | 7.0 |
| | 439579 | AF086400 | | gb:Homo sapiens full length insert cDNA | 12.5 | 23.1 |
| | 408312 | AF263613 | Hs.44198 | intracellular membrane-associated calciu | 12.4 | 12.4 |
| | 419948 | AB041035 | Hs.93847 | NADPH oxidase 4 | 12.4 | 12.4 |
| 75 | 427304 | AA761526 | Hs.163853 | ESTs | 12.4 | 2.4 |
| | 419498 | AL036591 | Hs.20887 | hypothetical protein FLJ10392 | 12.3 | 12.3 |
| | 428137 | AA421792 | Hs.170999 | ESTs | 12.2 | 12.2 |
| | 432683 | AW995441 | Hs.10475 | ESTs | 12.2 | 12.2 |
| | 408622 | AA056060 | Hs.202577 | Homo sapiens cDNA FLJ12166 fis, clone MA | 12.2 | 2.0 |
| 80 | 453884 | AA355925 | Hs.36232 | KIAA0186 gene product | 12.1 | 12.1 |
| | 441440 | AI807981 | Hs.30495 | ESTs | 12.0 | 5.2 |
| | 414217 | AI309298 | Hs.279898 | Homo sapiens cDNA: FLJ23165 fis, clone L | 12.0 | 3.6 |
| | 410227 | AB009284 | Hs.61152 | exosmoses (multiple)-like 2 | 12.0 | 62.7 |
| | 439444 | AI277652 | Hs.54578 | ESTs | 11.9 | 2.9 |
| | | | | | 11.9 | 16.5 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|------|
| 5 | 433309 | AA807060 | Hs.126558 | ESTs | 11.7 | 9.0 |
| | 439170 | AA332355 | Hs.165539 | ESTs | 11.6 | 9.7 |
| | 417160 | N76497 | Hs.1787 | proteolipid protein (Pelizaeus-Merzbache | 11.5 | 7.2 |
| | 424668 | D83702 | Hs.151573 | cryptochrome 1 (photolyase-like) | 11.5 | 5.8 |
| | 410811 | AW954134 | Hs.20924 | KIAA1628 protein | 11.5 | 28.2 |
| | 437124 | AA554458 | Hs.204200 | ESTs | 11.5 | 11.5 |
| | 418858 | AW961605 | Hs.21145 | Homo sapiens cDNA: FLJ22489 fis, clone H | 11.3 | 11.3 |
| | 423600 | AI633559 | Hs.29076 | Homo sapiens cDNA: FLJ21841 fis, clone H | 11.3 | 2.8 |
| 10 | 429393 | AA383024 | Hs.201603 | ESTs, Highly similar to hypothetical pro | 11.3 | 11.3 |
| | 431103 | M57399 | Hs.44 | pleiotrophin (heparin binding growth fac | 11.3 | 3.4 |
| | 452092 | BE245374 | Hs.27842 | hypothetical protein FLJ11210 | 11.3 | 11.7 |
| | 431701 | AW935490 | Hs.14658 | ESTs | 11.3 | 2.6 |
| | 429399 | AA452244 | Hs.16727 | ESTs | 11.2 | 2.2 |
| 15 | 408988 | AL119844 | Hs.49476 | Homo sapiens clone TUA8 Cri-du-chat regi | 11.2 | 27.8 |
| | 442671 | AI005668 | Hs.134779 | EST | 11.1 | 11.1 |
| | 402524 | | | | 11.1 | 11.1 |
| | 415558 | AA885143 | Hs.125719 | ESTs | 11.1 | 11.1 |
| | 422390 | AW450893 | Hs.121830 | ESTs, Weakly similar to KIAA0924 protein | 11.0 | 8.8 |
| 20 | 418475 | AI858732 | Hs.30443 | sentrin/SUMO-specific protease | 11.0 | 6.1 |
| | 458809 | AW972512 | Hs.20985 | sin3-associated polypeptide, 30kD | 11.0 | 5.6 |
| | 410297 | AA148710 | Hs.159441 | ESTs | 11.0 | 3.3 |
| | 444017 | U04840 | Hs.214 | neuro-oncological ventral antigen 1 | 11.0 | 11.0 |
| | 437814 | AI088192 | Hs.135474 | ESTs, Weakly similar to DDX9_HUMAN ATP-D | 10.9 | 3.3 |
| 25 | 427194 | AA399018 | Hs.250835 | ESTs | 10.8 | 8.0 |
| | 432060 | AW971364 | | gb:EST383453 MAGE resequences, MAGL Homo | 10.8 | 10.0 |
| | 453861 | AI026838 | Hs.30120 | ESTs | 10.8 | 10.8 |
| | 408829 | NM_006042 | Hs.48384 | heparan sulfate (glucosamine) 3-O-sulfot | 10.6 | 3.3 |
| | 416913 | AW934714 | | gb:RC1-DT0001-031299-011-a11 DT0001 Homo | 10.6 | 3.4 |
| 30 | 418049 | AA211467 | Hs.190488 | hypothetical protein FLJ10120 | 10.6 | 10.6 |
| | 413063 | AL035737 | Hs.75184 | chitinase 3-like 1 (cartilage glycoprote | 10.6 | 27.2 |
| | 425264 | AA353953 | Hs.20369 | ESTs, Weakly similar to gonadotropin ind | 10.5 | 2.0 |
| | 434408 | AI031771 | Hs.132586 | ESTs | 10.5 | 10.5 |
| | 451697 | AW449774 | Hs.257208 | ESTs | 10.5 | 6.2 |
| 35 | 436754 | AI061288 | Hs.133437 | ESTs, Moderately similar to gonadotropin | 10.3 | 10.3 |
| | 410298 | AI693821 | Hs.182185 | ESTs | 10.3 | 2.9 |
| | 412766 | BE544475 | Hs.54347 | ESTs | 10.3 | 10.3 |
| | 450689 | AI369275 | Hs.243010 | ESTs, Moderately similar to RTC0_HUMAN G | 10.3 | 10.3 |
| | 408331 | NM_007240 | Hs.44229 | dual specificity phosphatase 12 | 10.3 | 4.5 |
| 40 | 442007 | AA301116 | Hs.142838 | Homo sapiens cDNA: FLJ23444 fis, clone H | 10.3 | 10.3 |
| | 410386 | W26187 | Hs.3327 | Homo sapiens cDNA: FLJ22219 fis, clone H | 10.2 | 2.1 |
| | 440684 | AI253123 | Hs.127356 | ESTs, Highly similar to NEST_HUMAN NESTI | 10.1 | 10.1 |
| | 420892 | AW975076 | Hs.172589 | nuclear phosphoprotein similar to S. cer | 10.0 | 10.0 |
| | 419594 | AA013051 | Hs.91417 | topoisomerase (DNA) II binding protein | 9.9 | 15.8 |
| 45 | 419972 | AL041465 | Hs.294038 | ESTs, Moderately similar to ALU2_HUMAN A | 9.7 | 23.2 |
| | 433730 | AK002135 | Hs.3542 | hypothetical protein FLJ11273 | 9.6 | 6.5 |
| | 434851 | AA806164 | Hs.116502 | ESTs | 9.5 | 6.5 |
| | 436306 | AA805939 | Hs.117927 | ESTs | 9.5 | 4.7 |
| | 453331 | AI240665 | Hs.8895 | ESTs | 9.2 | 5.8 |
| 50 | 414429 | R51494 | Hs.71818 | ESTs | 9.0 | 6.2 |
| | 424998 | U58515 | Hs.154138 | chitinase 3-like 2 | 8.9 | 18.1 |
| | 446936 | HI0207 | Hs.47314 | ESTs | 8.9 | 3.6 |
| | 410276 | AI554545 | Hs.68301 | ESTs | 8.8 | 3.8 |
| | 453857 | AL080235 | Hs.35861 | DKFZP586E1621 protein | 8.8 | 3.8 |
| 55 | 448321 | NM_005883 | Hs.20912 | adenomatous polyposis coli like | 8.8 | 2.0 |
| | 414783 | AW069569 | Hs.75839 | zinc finger protein 6 (CMPX1) | 8.7 | 3.0 |
| | 441079 | AW150697 | Hs.107418 | ESTs | 8.7 | 2.2 |
| | 437517 | AI927675 | Hs.99858 | ribosomal protein L7a | 8.6 | 4.5 |
| | 409062 | AL157488 | Hs.50150 | Homo sapiens mRNA; cDNA DKFZp564B182 (fr | 8.6 | 12.2 |
| 60 | 420630 | AL133101 | Hs.99508 | Homo sapiens mRNA; cDNA DKFZp434C0921 (f | 8.6 | 10.4 |
| | 409260 | AW242407 | Hs.18479 | ESTs | 8.5 | 11.6 |
| | 442343 | AA992480 | Hs.129874 | ESTs | 8.4 | 4.6 |
| | 416439 | AA180363 | Hs.118769 | ESTs | 8.4 | 7.2 |
| | 428054 | AI948688 | Hs.266619 | ESTs | 8.2 | 9.2 |
| 65 | 421633 | AF121860 | Hs.106260 | sorting nexin 10 | 8.2 | 2.6 |
| | 433285 | AW975944 | Hs.237396 | ESTs | 8.1 | 3.3 |
| | 433226 | AW503733 | Hs.9414 | KIAA1488 protein | 8.0 | 13.4 |
| | 424800 | AL035588 | Hs.153203 | MyoD family inhibitor | 8.0 | 2.5 |
| | 425681 | AB018297 | Hs.159183 | KIAA0754 protein | 7.9 | 4.8 |
| 70 | 445034 | AW293376 | Hs.160323 | ESTs | 7.9 | 3.7 |
| | 435020 | AW505076 | Hs.301855 | DiGeorge syndrome critical region gene 8 | 7.6 | 6.4 |
| | 446985 | AL038704 | Hs.156827 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 7.5 | 7.8 |
| | 446619 | AU076643 | Hs.313 | secreted phosphoprotein 1 (osteopontin, | 7.5 | 3.9 |
| | 418522 | AA605038 | Hs.7148 | Homo sapiens cDNA: FLJ21950 fis, clone H | 7.5 | 2.2 |
| 75 | 439864 | AI720078 | Hs.291997 | ESTs | 7.4 | 6.9 |
| | 419723 | AL120193 | Hs.92614 | Homo sapiens growth differentiation fact | 7.4 | 3.5 |
| | 447896 | AI436124 | Hs.294069 | ESTs, Weakly similar to ORF2 contains a | 7.3 | 22.1 |
| | 404210 | | | | 7.3 | 40.8 |
| | 436671 | AW137159 | Hs.146151 | ESTs | 7.2 | 11.8 |
| | 439231 | AW581935 | Hs.141480 | ESTs | 7.2 | 2.5 |
| 80 | 418030 | BE207573 | Hs.83321 | neuromedin B | 7.1 | 6.4 |
| | 459290 | NM_001546 | Hs.34853 | inhibitor of DNA binding 4, dominant neg | 7.0 | 6.7 |
| | 423869 | BE409301 | Hs.134012 | C1q-related factor | 7.0 | 4.9 |
| | 414825 | X06370 | Hs.77432 | epidermal growth factor receptor (avian | 6.9 | 6.4 |

| | | | | | | |
|----|--------|-----------|-----------|--|-----|------|
| | 420018 | U56387 | Hs.94376 | proprotein convertase subtilisin/kexin 1 | 6.9 | 8.6 |
| | 428600 | AW863261 | Hs.15036 | ESTs, Highly similar to AF161358.1 HSPC0 | 6.9 | 7.7 |
| | 438380 | T06430 | Hs.6194 | chondroitin sulfate proteoglycan BEHAB/b | 6.9 | 3.1 |
| | 402604 | | | | 6.8 | 7.0 |
| 5 | 417022 | NM_014737 | Hs.80905 | Ras association (RalGDS/AF-6) domain fam | 6.8 | 2.5 |
| | 405239 | U89281 | Hs.11958 | oxidative 3 alpha hydroxysteroid dehydro | 6.8 | 2.9 |
| | 433577 | AW007080 | Hs.8817 | ESTs | 6.6 | 2.6 |
| | 434629 | AA789081 | Hs.4029 | glioma-amplified sequence-41 | 6.6 | 13.9 |
| | 413886 | AW958264 | Hs.103832 | ESTs, Weakly similar to TRHY_HUMAN TRICH | 6.6 | 2.2 |
| 10 | 451460 | AI797550 | Hs.209652 | ESTs | 6.5 | 13.7 |
| | 442145 | AI022650 | Hs.8117 | erbB2-interacting protein ERBIN | 6.5 | 15.6 |
| | 437273 | AL137451 | Hs.120873 | ESTs, Highly similar to hypothetical pro | 6.5 | 2.4 |
| | 418365 | AW014345 | Hs.161690 | ESTs | 6.4 | 12.8 |
| | 421684 | BE281591 | Hs.106768 | hypothetical protein FLJ10511 | 6.4 | 4.3 |
| 15 | 449458 | AI805078 | Hs.208261 | ESTs | 6.4 | 2.3 |
| | 426413 | AA377823 | | gb:EST90805 Synovial sarcoma Homo sapien | 6.3 | 13.2 |
| | 426423 | NM_012446 | Hs.169833 | single-stranded-DNA-binding protein | 6.3 | 10.9 |
| | 417709 | D87434 | Hs.82426 | KIAA0247 gene product | 6.3 | 23.3 |
| | 448499 | BE613280 | Hs.250655 | prothymosin, alpha (gene sequence 28) | 6.2 | 2.9 |
| 20 | 444880 | AW118683 | Hs.154150 | ESTs | 6.2 | 19.4 |
| | 432715 | AA247152 | Hs.200483 | ESTs, Weakly similar to KIAA1074 protein | 6.2 | 12.7 |
| | 444864 | AW965446 | Hs.46637 | ESTs, Weakly similar to cDNA EST yk289g5 | 6.2 | 4.1 |
| | 407792 | AI077715 | Hs.39384 | putative secreted ligand homologous to f | 6.2 | 3.4 |
| | 431962 | AL049385 | Hs.272251 | Homo sapiens mRNA; cDNA DKFZp586M1418 (f | 6.1 | 2.6 |
| 25 | 424232 | AB015982 | Hs.143460 | protein kinase C, nu | 6.1 | 14.6 |
| | 436443 | AW138211 | Hs.128746 | ESTs | 6.1 | 2.8 |
| | 433647 | AA603367 | Hs.222294 | ESTs | 6.1 | 15.0 |
| | 449961 | AW265634 | Hs.133100 | ESTs | 6.1 | 3.4 |
| | 448704 | AW080932 | Hs.249247 | heterogeneous nuclear protein similar to | 6.1 | 6.1 |
| 30 | 408393 | AW015318 | Hs.23165 | ESTs | 6.1 | 21.6 |
| | 450593 | AW450461 | Hs.203965 | ESTs | 6.1 | 2.2 |
| | 407846 | AA426202 | Hs.40403 | Cbp/p300-interacting transactivator, wit | 6.0 | 2.4 |
| | 445817 | NM_003642 | Hs.13340 | histone acetyltransferase 1 | 6.0 | 10.9 |
| | 440650 | R44692 | Hs.6640 | ESTs | 6.0 | 2.1 |
| 35 | 417675 | AI808607 | Hs.3781 | similar to murine leucine-rich repeat pr | 6.0 | 2.4 |
| | 411083 | N41340 | Hs.68318 | hypothetical protein FLJ20344 | 6.0 | 3.6 |
| | 407910 | AA650274 | Hs.41296 | fibronectin leucine rich transmembrane p | 6.0 | 6.0 |
| | 402855 | | | | 6.0 | 2.6 |
| | 445594 | AW058463 | Hs.12940 | zinc-fingers and homeoboxes 1 | 6.0 | 11.6 |
| 40 | 418791 | AA935633 | Hs.194528 | ESTs | 5.9 | 6.7 |
| | 409262 | AK000631 | Hs.52256 | hypothetical protein FLJ20624 | 5.9 | 2.3 |
| | 435677 | AA694142 | Hs.293726 | ESTs | 5.9 | 11.8 |
| | 430334 | AI824719 | Hs.47557 | ESTs | 5.9 | 7.5 |
| | 452834 | AI638627 | Hs.105685 | ESTs | 5.9 | 2.6 |
| 45 | 427315 | AA179949 | Hs.175563 | Homo sapiens mRNA; cDNA DKFZp564N0763 (f | 5.8 | 3.1 |
| | 428250 | AW809208 | Hs.183297 | DKFZP566F2124 protein | 5.8 | 2.0 |
| | 418506 | AA084248 | Hs.85339 | G protein-coupled receptor 39 | 5.8 | 2.5 |
| | 417115 | AW952792 | Hs.1066 | small nuclear ribonucleoprotein polypept | 5.8 | 16.0 |
| | 436758 | AW977167 | Hs.155272 | ESTs | 5.8 | 3.8 |
| 50 | 446332 | AK001635 | Hs.14838 | hypothetical protein FLJ10773 | 5.7 | 5.1 |
| | 423943 | AF163570 | Hs.135756 | polymerase (DNA-directed) kappa | 5.7 | 11.1 |
| | 428180 | AI129767 | Hs.182874 | Homo sapiens cDNA: FLJ21929 fis, clone H | 5.6 | 7.1 |
| | 424343 | AW956360 | Hs.4748 | ESTs, Highly similar to JN0902 pituitary | 5.6 | 2.2 |
| | 417318 | AW953937 | Hs.12891 | ESTs | 5.6 | 25.0 |
| 55 | 423582 | BE000831 | Hs.23837 | Homo sapiens cDNA FLJ11812 fis, clone HE | 5.6 | 4.1 |
| | 427472 | AA522539 | Hs.131250 | transposon-derived Buster3 transposase-I | 5.4 | 3.5 |
| | 434701 | AA460479 | Hs.4096 | KIAA0742 protein | 5.4 | 21.2 |
| | 430147 | R60704 | Hs.234434 | hair/enhancer-of-split related with YRP | 5.3 | 2.7 |
| | 411019 | AW993097 | Hs.48617 | Homo sapiens cDNA FLJ12540 fis, clone NT | 5.3 | 4.1 |
| 60 | 424939 | AK000059 | Hs.153881 | Homo sapiens NY-REN-62 antigen mRNA, par | 5.3 | 2.4 |
| | 424028 | AF055084 | Hs.153692 | KIAA0686 protein | 5.3 | 2.7 |
| | 444534 | AW271626 | Hs.42294 | ESTs | 5.3 | 2.1 |
| | 426171 | AI128606 | Hs.301454 | ESTs | 5.2 | 3.8 |
| 65 | 431843 | AA516420 | Hs.183526 | ESTs | 5.2 | 6.2 |
| | 438204 | AI589645 | Hs.128690 | ESTs | 5.2 | 5.8 |
| | 424635 | AA420687 | Hs.115455 | Homo sapiens cDNA FLJ14259 fis, clone PL | 5.2 | 8.4 |
| | 436223 | AK001884 | Hs.23799 | ESTs | 5.2 | 2.4 |
| | 450649 | NM_001429 | Hs.297722 | Human DNA sequence from clone RP1-85F18 | 5.2 | 15.3 |
| 70 | 441689 | AI123705 | Hs.106932 | ESTs | 5.2 | 2.2 |
| | 443392 | AI055821 | Hs.293420 | ESTs | 5.1 | 3.3 |
| | 416179 | R19015 | Hs.79067 | MAD (mothers against decapentaplegic, Dr | 5.1 | 16.7 |
| | 452167 | N75238 | Hs.13075 | Homo sapiens cDNA: FLJ23013 fis, clone L | 5.1 | 18.7 |
| | 434001 | AW950905 | Hs.3697 | serine (or cysteine) proteinase inhibito | 5.0 | 2.4 |
| 75 | 458435 | AI18718 | Hs.144121 | ESTs, Weakly similar to dJ37E16.2 pLsap | 5.0 | 3.9 |
| | 433586 | T85301 | | gb:yd78d06.s1 Soares fetal liver spleen | 5.0 | 2.8 |
| | 452040 | AW973242 | Hs.293690 | ESTs | 5.0 | 4.5 |
| | 404029 | | | | 5.0 | 4.3 |
| | 421141 | AW117261 | Hs.125914 | ESTs | 5.0 | 2.1 |
| 80 | 402605 | | | | 4.9 | 4.2 |
| | 435839 | AF249744 | Hs.25951 | Rho guanine nucleotide exchange factor (| 4.9 | 2.5 |
| | 416404 | AA180138 | Hs.107924 | ESTs | 4.9 | 2.4 |
| | 435615 | Y15065 | Hs.4975 | potassium voltage-gated channel, KQT-lik | 4.9 | 7.2 |
| | 448425 | AI500359 | Hs.233401 | ESTs | 4.9 | 4.9 |

| | | | | | | |
|----|--------|-----------|-----------|--|-----|------|
| | 445773 | H73456 | Hs.13299 | Homo sapiens mRNA; cDNA DKFZp761M0111 (f | 4.9 | 2.9 |
| | 448451 | AW015994 | | gb:U1-H-B10p-abh-g-09-0-ULs1 NCJ_CGAP_S | 4.9 | 2.2 |
| | 444838 | AV651680 | Hs.208558 | ESTs | 4.8 | 6.7 |
| 5 | 452438 | BE514230 | Hs.29595 | JM4 protein | 4.8 | 2.7 |
| | 443898 | AW804296 | Hs.9950 | Sec61 gamma | 4.8 | 7.2 |
| | 452776 | AA194540 | Hs.13522 | ESTs | 4.8 | 3.4 |
| | 426108 | AA622037 | Hs.166468 | programmed cell death 5 | 4.8 | 16.7 |
| | 416774 | AI005169 | Hs.28274 | Homo sapiens cDNA: FLJ22049 fis, clone H | 4.8 | 3.2 |
| 10 | 427704 | AW971063 | Hs.292882 | ESTs | 4.8 | 23.8 |
| | 433588 | AI056872 | Hs.133366 | ESTs | 4.8 | 12.8 |
| | 410108 | AA081659 | Hs.191098 | KIAA1479 protein | 4.7 | 2.1 |
| | 433556 | W56321 | Hs.111460 | Homo sapiens cDNA: FLJ21715 fis, clone C | 4.7 | 11.2 |
| | 418962 | AA714835 | Hs.271863 | ESTs | 4.7 | 2.2 |
| | 404049 | | | | 4.7 | 3.0 |
| 15 | 436222 | AI208737 | Hs.122810 | Homo sapiens cDNA FLJ11489 fs, clone HE | 4.7 | 3.3 |
| | 425234 | AW152225 | Hs.165909 | ESTs | 4.7 | 3.1 |
| | 426490 | NM_001621 | Hs.170087 | aryl hydrocarbon receptor | 4.7 | 9.1 |
| | 426514 | BE616633 | Hs.301122 | bone morphogenetic protein 7 (osteogenic | 4.7 | 2.7 |
| 20 | 428722 | U76456 | Hs.190787 | tissue inhibitor of metalloproteinase 4 | 4.6 | 6.7 |
| | 451989 | AF169797 | Hs.27413 | adaptor protein containing pH domain, PT | 4.6 | 13.4 |
| | 412490 | AW803564 | Hs.288850 | Homo sapiens cDNA: FLJ22528 fis, clone H | 4.6 | 18.4 |
| | 422488 | AI679968 | Hs.152060 | ESTs | 4.6 | 7.7 |
| | 428862 | NM_000346 | Hs.2316 | SRY (sex-determining region Y)-box 9 (ca | 4.6 | 4.6 |
| 25 | 413724 | AA131466 | Hs.23767 | Homo sapiens cDNA FLJ12666 fis, clone NT | 4.5 | 11.9 |
| | 442495 | AI184717 | | gb:qd64b01.x1 Soares_testis_NHT Homo sap | 4.5 | 4.5 |
| | 403549 | | | | 4.5 | 11.6 |
| | 456209 | W06033 | Hs.297792 | ESTs | 4.5 | 5.1 |
| | 421181 | NM_005574 | Hs.184585 | LIM domain only 2 (rhotobolin-like 1) | 4.5 | 10.6 |
| 30 | 439566 | AF086387 | | gb:Homo sapiens full length insert cDNA | 4.4 | 2.6 |
| | 446329 | NM_013272 | Hs.14805 | solute carrier family 21 (organic anion | 4.4 | 17.2 |
| | 446488 | AB037782 | Hs.15119 | KIAA1361 protein | 4.4 | 8.4 |
| | 426110 | NM_002913 | Hs.166563 | replication factor C (activator 1) 1 (14 | 4.4 | 2.5 |
| | 427413 | BE547647 | Hs.177781 | superoxide dismutase 2, mitochondrial | 4.4 | 14.3 |
| | 424340 | AA339036 | Hs.7033 | ESTs | 4.4 | 3.9 |
| 35 | 421552 | AF026692 | Hs.105700 | secreted frizzled-related protein 4 | 4.3 | 31.1 |
| | 422033 | AW245805 | Hs.110903 | claudin 5 (transmembrane protein deleted | 4.3 | 6.1 |
| | 434476 | AW858520 | Hs.271825 | ESTs | 4.3 | 4.5 |
| | 420582 | BE047878 | Hs.99093 | Homo sapiens chromosome 19, cosmid R2837 | 4.3 | 3.6 |
| 40 | 419904 | AA974411 | Hs.18572 | ESTs | 4.3 | 17.1 |
| | 407939 | W05608 | | gb:za85e07.r1 Soares_fetal_lung_NbHL19W | 4.3 | 9.0 |
| | 425836 | AW955696 | Hs.94842 | ESTs | 4.3 | 3.2 |
| | 426304 | AA374532 | Hs.297985 | ESTs | 4.3 | 6.6 |
| | 439653 | AW021103 | Hs.6631 | hypothetical protein FLJ20373 | 4.3 | 2.3 |
| 45 | 424723 | BE409813 | Hs.152337 | protein arginine N-methyltransferase 3(h | 4.3 | 2.5 |
| | 426064 | BE387014 | Hs.166146 | Homer, neuronal immediate early gene, 3 | 4.2 | 4.1 |
| | 409509 | AL036923 | Hs.127006 | ESTs | 4.2 | 16.4 |
| | 424391 | BE550112 | Hs.112712 | ESTs | 4.2 | 3.8 |
| | 425248 | AW957442 | Hs.252766 | ESTs | 4.2 | 11.1 |
| 50 | 418259 | AA215404 | Hs.137289 | ESTs | 4.2 | 19.3 |
| | 445525 | BE149866 | Hs.14831 | ESTs | 4.2 | 3.1 |
| | 414821 | M63835 | Hs.77424 | Fc fragment of IgG, high affinity Ia, re | 4.2 | 34.8 |
| | 430935 | AW072916 | Hs.115654 | ESTs | 4.2 | 3.0 |
| | 442233 | AW967149 | Hs.28439 | ESTs, Weakly similar to ORF2 (M.musculus | 4.2 | 2.4 |
| 55 | 416959 | D28459 | Hs.80612 | ubiquitin-conjugating enzyme E2A (RAD6 h | 4.1 | 15.3 |
| | 437097 | N45312 | Hs.46506 | ESTs | 4.1 | 15.6 |
| | 428189 | AA424030 | Hs.46627 | ESTs | 4.1 | 3.6 |
| | 434963 | AW974957 | Hs.288719 | Homo sapiens cDNA FLJ12142 fis, clone MA | 4.1 | 12.2 |
| | 425500 | AB011541 | Hs.158200 | EGF-like-domain, multiple 4 | 4.1 | 2.8 |
| 60 | 435177 | AI018174 | Hs.42936 | ESTs | 4.1 | 2.1 |
| | 418357 | Z44718 | Hs.301010 | ESTs, Highly similar to AF159851 1 Rho G | 4.1 | 4.1 |
| | 419086 | NM_000216 | Hs.89591 | Kallmann syndrome 1 sequence | 4.1 | 4.1 |
| | 436557 | W15573 | Hs.5027 | ESTs | 4.0 | 2.1 |
| | 425588 | F07396 | Hs.46751 | ESTs | 4.0 | 2.2 |
| 65 | 423905 | AW579960 | Hs.135150 | lung type-I cell membrane-associated gly | 4.0 | 3.6 |
| | 437095 | D14661 | Hs.119 | Wilms' tumour 1-associated protein | 4.0 | 10.0 |
| | 425332 | AA633306 | Hs.127279 | ESTs | 4.0 | 10.9 |
| | 431556 | AF016028 | Hs.260039 | sarcospan (Kras oncogene-associated gene | 4.0 | 3.8 |
| | 427209 | H06509 | Hs.92423 | KIAA1566 protein | 4.0 | 3.1 |
| 70 | 435468 | AW362803 | Hs.166271 | ESTs | 4.0 | 2.2 |
| | 416773 | AK000340 | Hs.79828 | hypothetical protein FLJ20333 | 4.0 | 2.6 |
| | 440483 | AI200836 | Hs.150386 | ESTs | 4.0 | 2.5 |
| | 444821 | AA053564 | Hs.12040 | STE20-like kinase | 4.0 | 10.4 |
| | 433873 | AW156913 | Hs.150478 | ESTs, Weakly similar to KIAA0987 protein | 4.0 | 2.3 |
| 75 | 420028 | AB014680 | Hs.8786 | carbohydrate (chondroitin 6/keratan) sul | 3.9 | 2.8 |
| | 445706 | AW807631 | Hs.190488 | hypothetical protein FLJ10120 | 3.9 | 3.8 |
| | 424530 | AI632083 | Hs.28511 | ESTs | 3.9 | 2.2 |
| | 446851 | AW007332 | Hs.16261 | Homo sapiens cDNA: FLJ22063 fis, clone H | 3.9 | 16.0 |
| | 424720 | M89907 | Hs.152292 | SWI/SNF related, matrix associated, acti | 3.9 | 4.5 |
| | 409456 | U34962 | Hs.54473 | cardiac-specific homeo box | 3.9 | 8.0 |
| 80 | 420439 | AW270041 | Hs.193053 | eukaryotic translation initiation factor | 3.9 | 7.9 |
| | 447340 | AW961327 | Hs.280833 | ESTs | 3.9 | 2.1 |
| | 430887 | N66801 | Hs.260287 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 3.9 | 2.5 |
| | 409361 | NM_005982 | Hs.54416 | sine oculis homeobox (Drosophila) homolo | 3.9 | 4.6 |

| | | | | | | |
|----|--------|-----------|-----------|--|-----|------|
| 5 | 426509 | M31166 | Hs.2050 | pentaxin-related gene, rapidly induced b | 3.9 | 4.0 |
| | 410079 | U94362 | Hs.58589 | glycogenin 2 | 3.9 | 18.3 |
| | 426818 | AA554827 | Hs.124841 | ESTs, Weakly similar to ALU5_HUMAN ALU S | 3.9 | 3.0 |
| | 435232 | NM_001262 | Hs.4854 | cyclin-dependent kinase inhibitor 2C (p1 | 3.8 | 4.0 |
| | 427228 | AA115770 | Hs.174051 | small nuclear ribonucleoprotein 70kD pol | 3.8 | 7.9 |
| 10 | 443801 | AW206942 | Hs.253594 | ESTs | 3.8 | 3.4 |
| | 450746 | D82673 | Hs.169921 | general transcription factor II, i, pseu | 3.8 | 2.2 |
| | 443837 | A1984625 | Hs.9884 | spindle pole body protein | 3.8 | 6.5 |
| | 435760 | AF231922 | Hs.213004 | chromosome 21 open reading frame 62 | 3.8 | 2.2 |
| | 426757 | AW205640 | Hs.158206 | ESTs | 3.7 | 3.1 |
| 15 | 443101 | A1268936 | Hs.129872 | sperm surface protein | 3.7 | 2.4 |
| | 440118 | AB040893 | Hs.6968 | KIAA1460 protein | 3.7 | 3.5 |
| | 410612 | AW502698 | Hs.118152 | ESTs | 3.7 | 22.5 |
| | 435869 | AF255910 | Hs.54650 | vascular endothelial junction-associated | 3.7 | 4.2 |
| | 433208 | AW002834 | Hs.24095 | ESTs | 3.7 | 16.0 |
| 20 | 432357 | AA452506 | Hs.274412 | similar to yeast Upt3, variant A | 3.7 | 2.6 |
| | 413916 | N49813 | Hs.75615 | apolipoprotein C-II | 3.7 | 5.4 |
| | 429766 | AA612710 | Hs.146140 | ESTs | 3.7 | 3.2 |
| | 437470 | AL390147 | Hs.134742 | hypothetical protein DKFZp547D065 | 3.7 | 6.4 |
| | 438459 | T49300 | Hs.35304 | Homo sapiens cDNA FLJ13655 fis, clone PL | 3.7 | 10.7 |
| 25 | 420361 | N92054 | Hs.206910 | ESTs | 3.7 | 18.7 |
| | 408819 | AW163483 | Hs.48320 | DKFZP566B1346 protein | 3.7 | 8.8 |
| | 411960 | R77776 | Hs.18103 | ESTs | 3.7 | 2.3 |
| | 435923 | BE301930 | Hs.5010 | Homo sapiens clone 24672 mRNA sequence | 3.7 | 2.2 |
| | 440145 | AW021433 | Hs.250863 | ESTs | 3.7 | 3.8 |
| 30 | 453740 | AL120295 | | gb:DKFZp761M067_s1 761 (synonym: hamy2) | 3.6 | 3.0 |
| | 440975 | AW499914 | Hs.7579 | hypothetical protein FLJ10402 | 3.6 | 2.0 |
| | 443135 | A1376331 | Hs.156103 | ESTs | 3.6 | 12.4 |
| | 419687 | A1638859 | Hs.227699 | ESTs, Weakly similar to Yhr217cp [S.cere | 3.6 | 2.7 |
| | 451029 | AA852097 | Hs.25829 | ras-related protein | 3.6 | 2.9 |
| 35 | 414512 | AL044336 | Hs.6831 | golgi resident protein GCP60 | 3.6 | 10.5 |
| | 410853 | H04588 | Hs.30469 | ESTs | 3.6 | 23.9 |
| | 419900 | A1469960 | Hs.170698 | ESTs | 3.6 | 3.6 |
| | 429673 | AA884407 | Hs.211595 | protein tyrosine phosphatase, non-recept | 3.6 | 7.5 |
| | 428290 | A1932995 | Hs.183475 | Homo sapiens clone 25061 mRNA sequence | 3.6 | 9.6 |
| 40 | 444381 | BE387335 | Hs.283713 | ESTs, Weakly similar to CA54_HUMAN COLLA | 3.6 | 4.9 |
| | 442104 | L20971 | Hs.188 | phosphodiesterase 4B, cAMP-specific (dun | 3.6 | 2.1 |
| | 441269 | AW015206 | Hs.178784 | ESTs | 3.6 | 2.8 |
| | 447961 | W32791 | Hs.170405 | ESTs | 3.5 | 4.6 |
| | 447735 | AA775268 | Hs.6127 | Homo sapiens cDNA: FLJ23020 fis, clone L | 3.5 | 2.1 |
| 45 | 437580 | AA761075 | Hs.293567 | ESTs | 3.5 | 3.5 |
| | 447710 | A1420523 | Hs.161282 | ESTs | 3.5 | 3.5 |
| | 436446 | AW016809 | Hs.119021 | ESTs | 3.5 | 2.2 |
| | 448412 | A1219083 | Hs.42532 | ESTs, Moderately similar to ALU8_HUMAN A | 3.5 | 4.1 |
| | 409712 | AA167385 | Hs.13583 | ESTs | 3.5 | 3.8 |
| 50 | 404048 | | | | 3.5 | 3.2 |
| | 440516 | S42303 | Hs.161 | cadherin 2, type 1, N-cadherin (neuronal | 3.5 | 5.1 |
| | 405342 | AU077058 | Hs.54089 | BRCA1 associated RING domain 1 | 3.5 | 10.6 |
| | 456508 | AA502764 | Hs.123469 | ESTs, Weakly similar to AF208855 1 BM-01 | 3.5 | 3.8 |
| | 426101 | AL049987 | Hs.166361 | Homo sapiens mRNA; cDNA DKFZp564F112 [fr | 3.5 | 32.2 |
| 55 | 436252 | A1539519 | Hs.120969 | Homo sapiens cDNA FLJ11562 fis, clone HE | 3.5 | 4.6 |
| | 433954 | AA610649 | | gb:np95c03.s1 NCI_CGAP_Thy1 Homo sapiens | 3.5 | 3.5 |
| | 408495 | W68796 | Hs.237731 | ESTs | 3.5 | 6.1 |
| | 418801 | AA228366 | Hs.115122 | ESTs | 3.5 | 5.1 |
| | 422493 | AW474183 | Hs.233816 | ESTs | 3.5 | 15.2 |
| 60 | 428141 | D50402 | Hs.182611 | solute carrier family 11 (proton-coupled | 3.5 | 2.4 |
| | 414591 | A1888490 | Hs.55902 | ESTs | 3.5 | 8.3 |
| | 439627 | BE621702 | Hs.29076 | Homo sapiens cDNA: FLJ21841 fis, clone H | 3.5 | 30.2 |
| | 444969 | AL203334 | Hs.160628 | ESTs | 3.5 | 3.1 |
| | 435370 | A1964074 | Hs.225838 | ESTs | 3.5 | 3.0 |
| 65 | 443228 | W24781 | Hs.293798 | ESTs | 3.4 | 4.6 |
| | 414612 | BE274552 | Hs.76578 | protein inhibitor of activated STAT3 | 3.4 | 5.0 |
| | 437410 | AW023340 | Hs.14880 | ESTs | 3.4 | 2.7 |
| | 444172 | BE147740 | Hs.104558 | ESTs | 3.4 | 12.9 |
| | 428484 | AF104032 | Hs.184601 | solute carrier family 7 (cationic amino | 3.4 | 2.8 |
| 70 | 437860 | AA333063 | Hs.279898 | Homo sapiens cDNA: FLJ23165 fis, clone L | 3.4 | 4.0 |
| | 428776 | AW016636 | Hs.155647 | ESTs, Highly similar to R29144 1 [H.sapi | 3.4 | 2.5 |
| | 409493 | AA386192 | Hs.193482 | ESTs | 3.4 | 3.4 |
| | 432559 | AW452948 | Hs.257631 | ESTs | 3.4 | 6.3 |
| | 451455 | A1937227 | Hs.8821 | liver-expressed antimicrobial peptide | 3.4 | 6.1 |
| 75 | 444153 | AK001610 | Hs.10414 | hypothetical protein FLJ10748 | 3.4 | 2.6 |
| | 422872 | BE326786 | Hs.187646 | ESTs | 3.4 | 2.2 |
| | 414761 | AL077228 | Hs.77256 | enhancer of zeste (Drosophila) homolog 2 | 3.4 | 2.6 |
| | 416131 | L03532 | Hs.79024 | heterogeneous nuclear ribonucleoprotein | 3.4 | 9.5 |
| | 408576 | NM_003542 | Hs.45423 | H4 histone family, member G | 3.4 | 3.4 |
| 80 | 431770 | BE221880 | Hs.268555 | 5'-3' exonuclease 2 | 3.4 | 21.2 |
| | 426030 | BE243933 | Hs.108642 | zinc finger protein 22 (KOX 15) | 3.4 | 2.1 |
| | 422573 | AW297985 | Hs.28777 | H2A histone family, member L | 3.4 | 3.7 |
| | 436865 | AW880358 | Hs.190488 | hypothetical protein FLJ10120 | 3.4 | 7.6 |
| | 442091 | AW770493 | Hs.195904 | guanine nucleotide binding protein (G pr | 3.4 | 2.9 |
| | 418699 | BE539639 | Hs.173030 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 3.4 | 5.5 |
| | 434577 | R37316 | Hs.179769 | Homo sapiens cDNA: FLJ22487 fis, clone H | 3.4 | 3.9 |
| | 430314 | AA369601 | Hs.239138 | pre-B-cell colony-enhancing factor | 3.4 | 16.8 |

| | | | | | | |
|----|--------|-----------|-----------|---|-----|------|
| 5 | 447279 | AA325308 | Hs.18016 | Homo sapiens mRNA; cDNA DKFZp586H0324 (f | 3.3 | 3.0 |
| | 410020 | T86315 | Hs.728 | ribonuclease, RNase A family, 2 (liver, | 3.3 | 5.8 |
| | 447272 | NM_014827 | Hs.17969 | KIAA0663 gene product | 3.3 | 13.4 |
| | 407656 | AW747986 | Hs.37443 | Homo sapiens mRNA; cDNA DKFZp434B2119 (f | 3.3 | 2.3 |
| | 435354 | AA678267 | Hs.117115 | ESTs | 3.3 | 5.5 |
| 10 | 443884 | N20617 | Hs.226527 | leptin receptor | 3.3 | 8.6 |
| | 444984 | H15474 | Hs.12214 | Homo sapiens clone 23716 mRNA sequence | 3.3 | 2.0 |
| | 431053 | S40369 | Hs.249141 | Glutamate receptor subunit | 3.3 | 2.4 |
| | 424682 | AW604804 | Hs.151717 | KIAA0437 protein | 3.3 | 13.7 |
| | 457972 | AI419060 | Hs.47448 | ESTs | 3.3 | 4.2 |
| 15 | 424762 | AL119442 | Hs.183684 | eukaryotic translation initiation factor | 3.3 | 3.2 |
| | 438666 | AW014493 | Hs.126727 | ESTs | 3.3 | 10.8 |
| | 447796 | AW953622 | Hs.223025 | RAB31, member RAS oncogene family | 3.3 | 4.2 |
| | 426751 | W92744 | Hs.22664 | ESTs | 3.3 | 2.6 |
| | 436251 | BE515065 | Hs.5092 | nucleolar protein (KKE/D repeat) | 3.3 | 3.9 |
| 20 | 452688 | AA721140 | Hs.49930 | ESTs, Weakly similar to B34087 hypotheri | 3.3 | 4.9 |
| | 416359 | ALD42210 | Hs.16493 | hypothetical protein DKFZp762N2316 | 3.3 | 4.2 |
| | 424090 | X99699 | Hs.139262 | XIAP associated factor-1 | 3.3 | 2.9 |
| | 434987 | AW975114 | Hs.293273 | ESTs | 3.3 | 2.2 |
| | 428642 | NM_014899 | Hs.188006 | KIAA0878 protein | 3.3 | 5.7 |
| 25 | 420372 | AW960049 | Hs.293660 | ESTs, Weakly similar to A49618 probable | 3.3 | 5.5 |
| | 422224 | NM_013982 | Hs.113264 | neuregulin 2 | 3.2 | 3.0 |
| | 432482 | L19267 | Hs.275924 | dystrophin myotonia-containing WD repea | 3.2 | 2.7 |
| | 439963 | AW247529 | Hs.6793 | platelet-activating factor acetylhydrola | 3.2 | 2.0 |
| | 428418 | AI368826 | Hs.30654 | ESTs | 3.2 | 2.4 |
| 30 | 416728 | AB024597 | Hs.79658 | casein kinase 1, epsilon | 3.2 | 2.8 |
| | 416224 | NM_002902 | Hs.79088 | reticulocalbin 2, EF-hand calcium bindin | 3.2 | 2.2 |
| | 429803 | W81489 | Hs.223025 | RAB31, member RAS oncogene family | 3.2 | 4.3 |
| | 431387 | AI878854 | Hs.252229 | v-maf musculoaponeurotic fibrosarcoma (a | 3.2 | 2.8 |
| | 404171 | | | | 3.2 | 35.8 |
| 35 | 435575 | AF213457 | Hs.44234 | triggering receptor expressed on myeloid | 3.2 | 2.6 |
| | 426421 | AW367884 | Hs.169832 | zinc finger protein 42 (myeloid-specific | 3.2 | 3.8 |
| | 445070 | NM_000677 | Hs.258 | adenosine A3 receptor | 3.2 | 7.6 |
| | 407047 | X65965 | | gb.Hs.sapiens SOD-2 gene for manganese su | 3.2 | 82.0 |
| | 446006 | NM_004403 | Hs.13530 | deafness, autosomal dominant 5 | 3.2 | 2.2 |
| 40 | 430890 | X54232 | Hs.2699 | glypican 1 | 3.2 | 4.3 |
| | 439807 | AA376417 | Hs.173501 | Homo sapiens mRNA for FLJ00008 protein, | 3.2 | 2.3 |
| | 430412 | AW341754 | Hs.189305 | ESTs | 3.2 | 2.0 |
| | 442807 | AL049274 | Hs.8736 | Homo sapiens mRNA; cDNA DKFZp564H203 (fr | 3.2 | 2.7 |
| | 420253 | AI656055 | Hs.96200 | neighbor of A-kinase anchoring protein 9 | 3.2 | 2.9 |
| 45 | 436042 | AF284422 | Hs.119178 | cation-chloride cotransporter-interactin | 3.2 | 4.6 |
| | 423422 | AC005175 | Hs.128425 | NY-REN-24 antigen | 3.2 | 4.0 |
| | 413020 | R98736 | | gb.yr31h09.r1 Soares fetal liver spleen | 3.2 | 4.1 |
| | 452877 | AI250789 | Hs.32478 | ESTs | 3.2 | 4.0 |
| | 418113 | AI272141 | Hs.83484 | SRY (sex determining region Y)-box 4 | 3.1 | 9.0 |
| 50 | 421097 | AI280112 | Hs.125232 | Homo sapiens cDNA FLJ13266 fis, clone OV | 3.1 | 2.0 |
| | 450219 | AI826999 | Hs.224624 | ESTs | 3.1 | 23.7 |
| | 434256 | AI378817 | Hs.191847 | ESTs | 3.1 | 3.4 |
| | 421407 | T82331 | Hs.127453 | ESTs | 3.1 | 3.9 |
| | 451198 | AW964541 | Hs.11500 | Homo sapiens cDNA: FLJ21127 fis, clone C | 3.1 | 3.9 |
| 55 | 445664 | AW968638 | Hs.237691 | ESTs | 3.1 | 7.9 |
| | 411089 | AA456454 | Hs.118637 | Homo sapiens cDNA FLJ13365 fis, clone PL | 3.1 | 6.0 |
| | 458050 | AA834708 | | gb:cd99d04.s1 NC1_CGAP_Ov2 Homo sapiens | 3.1 | 4.4 |
| | 454140 | AB040888 | Hs.41793 | hypothetical protein FLJ10474 | 3.1 | 2.7 |
| | 417270 | AA429615 | Hs.98593 | Homo sapiens cDNA: FLJ23233 fis, clone C | 3.1 | 2.4 |
| 60 | 427951 | AI826125 | Hs.43546 | ESTs | 3.1 | 2.3 |
| | 443693 | AI344782 | Hs.9683 | protein-kinase, interferon-inducible dou | 3.1 | 7.2 |
| | 413357 | NM_006517 | Hs.75317 | solute carrier family 16 (monocarboxylic | 3.1 | 2.6 |
| | 429402 | AF116571 | Hs.201671 | SRY (sex determining region Y)-box 13 | 3.1 | 6.5 |
| | 447752 | M73700 | Hs.347 | lactotransferrin | 3.1 | 19.4 |
| 65 | 408949 | AF189011 | Hs.49163 | putative ribonuclease III | 3.1 | 3.7 |
| | 418039 | R06859 | Hs.193172 | ESTs | 3.1 | 3.8 |
| | 447343 | AA256641 | Hs.236894 | ESTs, Highly similar to LRP1_HUMAN LOW-D | 3.1 | 2.2 |
| | 424441 | X14850 | Hs.147097 | H2A histone family, member X | 3.1 | 3.2 |
| | 435163 | AA668884 | Hs.19155 | ESTs | 3.1 | 2.1 |
| 70 | 428712 | AW085131 | Hs.190452 | KIAA0365 gene product | 3.1 | 2.7 |
| | 434542 | AA769310 | Hs.61260 | hypothetical protein FLJ13164 | 3.1 | 14.3 |
| | 428147 | AW629985 | Hs.234983 | ESTs | 3.1 | 2.7 |
| | 415825 | Y18024 | Hs.78877 | inositol 1,4,5-trisphosphate 3-kinase B | 3.1 | 2.5 |
| | 422170 | AI791949 | Hs.112432 | anti-Mullerian hormone | 3.1 | 8.1 |
| 75 | 448801 | N57423 | Hs.179898 | HSPC055 protein | 3.0 | 2.0 |
| | 413542 | BE295928 | Hs.75424 | inhibitor of DNA binding 1, dominant neg | 3.0 | 18.3 |
| | 431562 | AI884334 | Hs.11637 | ESTs | 3.0 | 3.9 |
| | 410274 | AA381807 | Hs.61762 | hypoxia-inducible protein 2 | 3.0 | 3.0 |
| | 458962 | NM_005859 | Hs.25180 | purine-rich element binding protein A | 3.0 | 3.0 |
| 80 | 436277 | R86520 | Hs.120917 | ESTs | 3.0 | 2.7 |
| | 453288 | AW583292 | Hs.274412 | similar to yeast Upt3, variant A | 3.0 | 3.0 |
| | 447471 | AF039843 | Hs.18676 | sprouty (Drosophila) homolog 2 | 3.0 | 4.1 |
| | 442554 | AW467376 | Hs.129640 | ESTs | 3.0 | 4.7 |
| | 441466 | AW673081 | Hs.54828 | ESTs | 3.0 | 3.0 |
| | 420297 | AI628272 | Hs.88323 | ESTs | 3.0 | 8.1 |
| | 445101 | T75202 | Hs.12314 | Homo sapiens mRNA; cDNA DKFZp586C1019 (f | 3.0 | 18.7 |
| | 453405 | AI567972 | Hs.49919 | ESTs | 3.0 | 9.6 |

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|----|--------|-----------|-----------|--|-----|------|
| | 434521 | NM_002267 | Hs.3886 | karyopherin alpha 3 (importin alpha 4) | | |
| | 447948 | AI620923 | Hs.46579 | ESTs | 3.0 | 9.3 |
| | 445756 | AA290690 | Hs.288493 | ESTs | 3.0 | 10.1 |
| 5 | 413243 | AA769266 | Hs.193657 | ESTs | 3.0 | 3.5 |
| | 422845 | AA317841 | Hs.301838 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.0 | 5.9 |
| | 419409 | AW237831 | Hs.143792 | ESTs | 3.0 | 2.2 |
| | 446441 | AK001782 | Hs.15093 | hypothetical protein | 3.0 | 2.1 |
| | 427150 | BE616183 | Hs.173737 | ras-related C3 botulinum toxin substrate | 3.0 | 2.1 |
| 10 | 421043 | BE379455 | Hs.89072 | ESTs | 3.0 | 4.1 |
| | 427239 | BE270447 | Hs.174070 | ubiquitin carrier protein | 3.0 | 3.0 |
| | 433312 | AI241331 | Hs.131765 | ESTs | 3.0 | 4.1 |
| | 415102 | M31899 | Hs.77929 | excision repair cross-complementing rode | 3.0 | 11.0 |
| | 414702 | L22005 | Hs.76932 | cell division cycle 34 | 3.0 | 6.0 |
| 15 | 428673 | AW601325 | Hs.274472 | high-mobility group (nonhistone chromoso | 3.0 | 3.3 |
| | 422676 | D28481 | Hs.1570 | histamine receptor H1 | 3.0 | 15.8 |
| | 451693 | BE220445 | Hs.279635 | ESTs | 3.0 | 2.1 |
| | 412420 | AL035668 | Hs.73853 | bone morphogenetic protein 2 | 3.0 | 2.3 |
| | 424005 | AB033041 | Hs.137507 | KIAA1215 protein | 3.0 | 10.5 |
| 20 | 440789 | BE561793 | | gb:601346842F1 NIH_MGC_8 Homo sapiens cD | 3.0 | 3.9 |
| | 428832 | AA578229 | | gb:ml22b12s1 NCI_CGAP_HSC1 Homo sapiens | 3.0 | 5.1 |
| | 430293 | AI416988 | Hs.238272 | inositol 1,4,5-triphosphate receptor, ty | 3.0 | 2.3 |
| | 450883 | NM_001348 | Hs.25619 | death-associated protein kinase 3 | 3.0 | 6.3 |
| | 407879 | AA045464 | Hs.6557 | ESTs | 3.0 | 5.6 |
| 25 | 426167 | AF039023 | Hs.167496 | Homo sapiens cDNA FLJ11120 fis, clone PL | 2.9 | 7.0 |
| | 435281 | AB020699 | Hs.4864 | KIAA0892 protein | 2.9 | 2.6 |
| | 432339 | AW411259 | Hs.25945 | ESTs | 2.9 | 3.9 |
| | 440524 | R71264 | Hs.16798 | ESTs | 2.9 | 2.9 |
| | 408083 | BE383668 | Hs.42484 | hypothetical protein FLJ10618 | 2.9 | 9.7 |
| 30 | 427729 | AB033100 | Hs.300646 | Homo sapiens cDNA FLJ11744 fis, clone HE | 2.9 | 4.4 |
| | 422072 | AB018255 | Hs.111138 | KIAA0712 gene product | 2.9 | 3.1 |
| | 435904 | AF261655 | Hs.8910 | 1,2-alpha-mannosidase IC | 2.9 | 2.9 |
| | 440100 | BE382685 | Hs.158549 | ESTs | 2.9 | 3.6 |
| 35 | 448356 | AL120837 | Hs.20993 | high-glucose-regulated protein 8 | 2.9 | 3.6 |
| | 428005 | AW302245 | Hs.181390 | casein kinase 1, gamma 2 | 2.9 | 13.9 |
| | 403019 | AA834626 | Hs.66718 | RAD54 (S.cerevisiae)-like | 2.9 | 3.7 |
| | 419175 | AW270037 | Hs.179507 | KIAA0779 protein | 2.9 | 5.8 |
| | 433592 | NM_004642 | Hs.3436 | deleted in oral cancer (mouse, homolog) | 2.9 | 2.3 |
| 40 | 413922 | AI535895 | Hs.221024 | ESTs | 2.9 | 2.3 |
| | 428593 | AW207440 | Hs.185973 | degenerative spermatocyte (homolog Dros | 2.9 | 2.8 |
| | 441789 | D52059 | Hs.7972 | KIAA0871 protein | 2.9 | 3.3 |
| | 459107 | AA811881 | Hs.28505 | ubiquitin-conjugating enzyme E2H (homolo | 2.9 | 2.1 |
| | 448560 | BE613183 | Hs.23213 | ESTs | 2.9 | 2.8 |
| 45 | 425304 | AA463844 | Hs.31339 | fibroblast growth factor 11 | 2.9 | 3.0 |
| | 434946 | AW295389 | Hs.119768 | ESTs | 2.9 | 3.3 |
| | 408146 | R45821 | Hs.81057 | ESTs, Moderately similar to CL3BC [R,nor | 2.9 | 5.1 |
| | 446644 | NM_003272 | Hs.15791 | transmembrane 7 superfamily member 1 (up | 2.9 | 5.1 |
| | 446808 | AA703226 | Hs.16193 | Homo sapiens mRNA; cDNA DKFZp586B211 (fr | 2.9 | 2.8 |
| 50 | 433017 | Y15067 | Hs.279914 | zinc finger protein 232 | 2.9 | 8.5 |
| | 429500 | X78565 | Hs.289114 | hexabrachion (tenascin C, cytactin) | 2.9 | 2.2 |
| | 444706 | AK000398 | Hs.11747 | hypothetical protein FLJ20391 | 2.9 | 4.5 |
| | 407925 | BE002320 | Hs.287864 | Homo sapiens cDNA FLJ14030 fis, clone HE | 2.9 | 3.6 |
| | 431730 | AF208856 | Hs.268122 | hypothetical protein | 2.9 | 2.1 |
| | 447118 | AB014599 | Hs.17411 | KIAA0699 protein | 2.9 | 2.5 |
| 55 | 453496 | AA442103 | Hs.33084 | solute carrier family 2 (facilitated glu | 2.8 | 2.1 |
| | 425227 | H84455 | Hs.40639 | ESTs | 2.8 | 7.4 |
| | 456534 | X91195 | Hs.100623 | phospholipase C, beta 3, neighbor pseudo | 2.8 | 2.3 |
| | 421465 | AK001020 | Hs.104627 | Homo sapiens cDNA FLJ10158 fis, clone HE | 2.8 | 76.2 |
| 60 | 409095 | AW337272 | Hs.293656 | ESTs | 2.8 | 6.1 |
| | 424066 | Z99348 | Hs.112461 | ESTs | 2.8 | 34.0 |
| | 432945 | AL043683 | Hs.271357 | ESTs, Weakly similar to unnamed protein | 2.8 | 2.1 |
| | 414079 | H19184 | Hs.205230 | ESTs | 2.8 | 11.9 |
| | 414359 | M62194 | Hs.75929 | cadherin 11, type 2, OB-cadherin (osteob | 2.8 | 2.1 |
| 65 | 438890 | AA827756 | Hs.135049 | ESTs | 2.8 | 3.9 |
| | 430354 | AA954810 | Hs.239784 | human homolog of Drosophila Scribble | 2.8 | 4.9 |
| | 458367 | AA088470 | Hs.83135 | p53-responsive gene 6 | 2.8 | 5.2 |
| | 412014 | AI620650 | Hs.43761 | ESTs | 2.8 | 4.4 |
| | 428727 | AF078847 | Hs.191356 | general transcription factor IIH, polype | 2.8 | 4.8 |
| | 447942 | F12628 | Hs.155470 | zinc finger protein 38 (KOX 25) | 2.8 | 6.7 |
| 70 | 426432 | AF001601 | Hs.169857 | paraoxonase 2 | 2.8 | 2.2 |
| | 439189 | AI951185 | Hs.144630 | nuclear receptor subfamily 2, group F, m | 2.8 | 3.5 |
| | 446756 | AW028485 | Hs.26136 | ESTs | 2.8 | 2.5 |
| | 432148 | AW504912 | Hs.81907 | ESTs, Moderately similar to ALU4_HUMAN A | 2.8 | 4.1 |
| | 405649 | | | | 2.8 | 2.6 |
| 75 | 414473 | BE302693 | | gb:ba74c02y1 NIH_MGC_20 Homo sapiens cD | 2.8 | 3.8 |
| | 443839 | AW139834 | Hs.143321 | ESTs | 2.8 | 2.4 |
| | 448804 | AW512213 | Hs.42500 | ADP-ribosylation factor-like 5 | 2.8 | 2.1 |
| | 426825 | AL133415 | Hs.2064 | vimentin | 2.8 | 2.7 |
| | 417528 | H47315 | Hs.27519 | ESTs | 2.8 | 25.0 |
| 80 | 453657 | W23237 | Hs.296162 | ESTs | 2.8 | 11.6 |
| | 432714 | Y12059 | Hs.278675 | bromodomain-containing 4 | 2.8 | 3.2 |
| | 441072 | AW275480 | Hs.39504 | ESTs | 2.8 | 6.7 |
| | 441297 | AW403084 | Hs.7765 | ubiquitin-conjugating enzyme E2E 1 (homo | 2.7 | 2.7 |
| | 443849 | BE566066 | Hs.9893 | ASB-3 protein | 2.7 | 2.2 |
| | | | | | 2.7 | 3.0 |

| | | | | | | |
|----|--------|----------|-----------|--|-----|------|
| | 408243 | Y00787 | Hs.624 | interleukin 8 | 2.7 | 3.8 |
| | 446243 | BE296396 | Hs.14512 | Homo sapiens cDNA FLJ11761 fis, clone HE | 2.7 | 3.3 |
| | 432238 | AL133057 | Hs.274135 | Homo sapiens mRNA; cDNA DKFZp434K1815 (f | 2.7 | 3.0 |
| 5 | 433944 | AL117518 | Hs.3588 | KIAA0978 protein | 2.7 | 3.1 |
| | 411400 | AA311919 | Hs.69851 | GAR1 protein | 2.7 | 16.0 |
| | 436840 | AW450376 | Hs.130803 | ESTs, Highly similar to T00367 hypotheti | 2.7 | 4.1 |
| | 428281 | AA194554 | Hs.183434 | ATPase, H+ transporting, lysosomal (vacu | 2.7 | 3.2 |
| | 426340 | Z97989 | Hs.169370 | FYN oncogene related to SRC, FGR, YES | 2.7 | 2.0 |
| 10 | 408320 | AI125867 | Hs.20734 | ESTs | 2.7 | 4.7 |
| | 422363 | T55979 | Hs.115474 | replication factor C (activator 1) 3 (38 | 2.7 | 2.2 |
| | 436440 | AI471862 | Hs.196008 | Homo sapiens cDNA FLJ11723 fis, clone HE | 2.7 | 4.7 |
| | 408912 | AB011084 | Hs.48924 | KIAA0512 gene product | 2.7 | 2.1 |
| | 419304 | AI271326 | Hs.146101 | ESTs | 2.7 | 3.4 |
| 15 | 415045 | AA321559 | Hs.38270 | Homo sapiens cDNA: FLJ20984 fis, clone C | 2.7 | 2.3 |
| | 441872 | BE567100 | Hs.154938 | hypothetical protein MDS025 | 2.7 | 2.3 |
| | 422343 | AI628633 | | gb:U77005.x1 NCL CGAP_Kid11 Homo sapien | 2.7 | 2.5 |
| | 415539 | AI733881 | Hs.72472 | ESTs | 2.7 | 2.7 |
| | 443823 | BE089782 | Hs.9877 | hypothetical protein | 2.7 | 4.7 |
| 20 | 419881 | AA329340 | Hs.44649 | ESTs | 2.7 | 3.3 |
| | 429155 | BE242291 | Hs.197540 | hypoxia-inducible factor 1, alpha subuni | 2.7 | 5.5 |
| | 431319 | AA873350 | | gb:oh64h02.s1 NCL CGAP_Kid5 Homo sapiens | 2.7 | 65.9 |
| | 430219 | X99209 | Hs.235887 | HMT1 (hnRNP methyltransferase, S. cerevi | 2.7 | 3.1 |
| | 421016 | AA504583 | Hs.101047 | transcription factor 3 (E2A immunoglobul | 2.7 | 5.2 |
| 25 | 417259 | AW903838 | Hs.81800 | chondroitin sulfate proteoglycan 2 (vers | 2.7 | 10.7 |
| | 431747 | AW979134 | Hs.10700 | hypothetical protein | 2.7 | 2.9 |
| | 408085 | N25929 | Hs.42500 | ADP-ribosylation factor-like 5 | 2.7 | 7.8 |
| | 426218 | AF119043 | Hs.168005 | transcriptional intermediary factor 1 ga | 2.7 | 4.5 |
| | 434845 | BE267057 | Hs.4200 | hypothetical protein R32184_1 | 2.7 | 4.6 |
| 30 | 451644 | N23235 | Hs.30567 | ESTs | 2.7 | 2.3 |
| | 428408 | W74437 | Hs.188757 | Homo sapiens mRNA; cDNA DKFZp564M113 (fr | 2.7 | 5.7 |
| | 446627 | AI973016 | Hs.15725 | hypothetical protein SBB148 | 2.7 | 2.9 |
| | 450167 | AA446404 | Hs.24563 | NTF2-related export protein 1 | 2.7 | 9.9 |
| | 408821 | AL050385 | Hs.48332 | NIMA (never in mitosis gene a)-related k | 2.7 | 2.1 |
| 35 | 452068 | W76412 | Hs.57877 | ESTs | 2.7 | 2.1 |
| | 431129 | AL137751 | Hs.263571 | Homo sapiens mRNA; cDNA DKFZp434I0812 (f | 2.7 | 6.2 |
| | 429025 | AI399910 | Hs.4842 | ESTs | 2.7 | 2.9 |
| | 421114 | AW975051 | Hs.293156 | ESTs | 2.7 | 8.8 |
| | 428755 | D87454 | Hs.192966 | KIAA0265 protein | 2.7 | 3.0 |
| 40 | 416391 | AI878927 | Hs.79284 | mesoderm specific transcript (mouse) hom | 2.7 | 5.7 |
| | 414283 | AW960011 | Hs.154993 | ESTs | 2.7 | 5.9 |
| | 425262 | D87119 | Hs.155418 | GS3955 protein | 2.7 | 3.7 |
| | 447726 | AL137638 | Hs.19388 | Homo sapiens mRNA; cDNA DKFZp434J065 (fr | 2.7 | 14.3 |
| | 424623 | AW963062 | Hs.165809 | ESTs | 2.7 | 5.6 |
| 45 | 444772 | AW450800 | Hs.176859 | ESTs | 2.7 | 2.7 |
| | 428419 | U49436 | Hs.286236 | eukaryotic translation initiation factor | 2.7 | 4.6 |
| | 441049 | W88920 | Hs.29341 | hypothetical protein FLJ22376 | 2.7 | 4.5 |
| | 412758 | Y07818 | Hs.74566 | dihydropyrimidinase-like 3 | 2.6 | 5.1 |
| | 447720 | AL038765 | Hs.161304 | ESTs | 2.6 | 3.2 |
| 50 | 419708 | AK000753 | Hs.92374 | hypothetical protein | 2.6 | 3.0 |
| | 445502 | AW379160 | Hs.12813 | DKFZP434J214 protein | 2.6 | 5.0 |
| | 437370 | AL359567 | Hs.161962 | Homo sapiens mRNA; cDNA DKFZp547D023 (fr | 2.6 | 2.9 |
| | 444147 | AB002306 | Hs.10351 | KIAA0308 protein | 2.6 | 6.8 |
| | 433193 | AB040881 | Hs.32580 | Homo sapiens cDNA FLJ13122 fis, clone NT | 2.6 | 3.2 |
| 55 | 445439 | BE243084 | Hs.12719 | regulator of nonsense transcripts 1 | 2.6 | 3.9 |
| | 450309 | W61348 | Hs.4864 | KIAA0892 protein | 2.6 | 3.8 |
| | 422092 | AB007883 | Hs.111373 | KIAA0423 protein | 2.6 | 2.3 |
| | 424118 | BE269041 | Hs.140452 | cargo selection protein (mannose 6 phosp | 2.6 | 5.5 |
| | 407618 | AW054922 | Hs.53478 | Homo sapiens cDNA FLJ12366 fis, clone MA | 2.6 | 2.9 |
| | 446493 | AK001389 | Hs.15144 | hypothetical protein DKFZp564O043 | 2.6 | 3.2 |
| 60 | 442878 | AI868648 | Hs.22315 | ESTs | 2.6 | 4.7 |
| | 448771 | BE315511 | Hs.296244 | SNARE protein | 2.6 | 5.0 |
| | 416611 | AA568308 | Hs.192789 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 2.6 | 7.7 |
| | 409348 | AI401535 | Hs.146090 | ESTs | 2.6 | 3.5 |
| | 439349 | AI660898 | Hs.195602 | ESTs | 2.6 | 3.2 |
| 65 | 428433 | AA521410 | Hs.41371 | ESTs | 2.6 | 7.9 |
| | 436565 | BE547674 | Hs.204169 | ESTs | 2.6 | 3.0 |
| | 438662 | AA223599 | Hs.6351 | cleavage and polyadenylation specific fa | 2.6 | 2.6 |
| | 429362 | T25833 | Hs.200478 | ubiquitin-conjugating enzyme E2M (homolo | 2.6 | 2.3 |
| 70 | 459035 | AW291109 | Hs.208787 | ESTs | 2.6 | 2.6 |
| | 451814 | AA847992 | Hs.137003 | ESTs | 2.6 | 19.1 |
| | 452331 | AA598509 | Hs.29117 | H.sapiens mRNA for pur alpha extended 3' | 2.6 | 2.2 |
| | 438461 | AW075485 | Hs.285049 | phosphoserine aminotransferase | 2.6 | 2.1 |
| | 424362 | AL137646 | Hs.146001 | Homo sapiens mRNA; cDNA DKFZp585F0824 (f | 2.6 | 4.9 |
| 75 | 423699 | H41850 | Hs.131846 | PCAF associated factor 65 alpha | 2.6 | 3.7 |
| | 441226 | BE563042 | Hs.118820 | ESTs | 2.6 | 2.5 |
| | 444940 | AK002148 | Hs.12151 | hypothetical protein FLJ11286 | 2.6 | 3.4 |
| | 448731 | AI522273 | Hs.42640 | ESTs | 2.6 | 3.2 |
| | 424250 | AF073310 | Hs.143648 | insulin receptor substrate 2 | 2.6 | 2.5 |
| 80 | 433468 | AA832055 | Hs.232217 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.6 | 3.3 |
| | 419925 | AA159850 | Hs.93765 | lipoma HMGIC fusion partner | 2.6 | 4.6 |
| | 441364 | AW450466 | Hs.126830 | ESTs | 2.6 | 2.6 |
| | 425922 | AL157466 | Hs.162751 | Homo sapiens mRNA; cDNA DKFZp761E2423 (f | 2.5 | 2.7 |
| | 434974 | AA778711 | Hs.4310 | eukaryotic translation initiation factor | 2.5 | 2.5 |

| | | | | | | |
|----|--------|-----------|-----------|--|-----|------|
| 5 | 408392 | U28831 | Hs.44566 | KIAA1641 protein | 2.5 | 25.4 |
| | 432426 | AW973152 | Hs.31050 | ESTs | 2.5 | 10.0 |
| | 436623 | AI417073 | Hs.107265 | ESTs | 2.5 | 2.1 |
| | 452683 | AI089575 | Hs.9071 | progesterone membrane binding protein | 2.5 | 2.6 |
| | 410582 | AW867197 | Hs.14562 | Homo sapiens cDNA: FLJ21616 fis, clone C | 2.5 | 3.7 |
| 10 | 441328 | AI982794 | Hs.159473 | ESTs | 2.5 | 9.2 |
| | 453983 | H94997 | Hs.16450 | ESTs | 2.5 | 26.1 |
| | 438826 | R26709 | Hs.10095 | hypothetical protein from EUROIMAGE 1669 | 2.5 | 2.3 |
| | 427899 | AA829286 | Hs.181062 | serum amyloid A1 | 2.5 | 20.3 |
| | 427820 | BE222494 | Hs.180919 | inhibitor of DNA binding 2, dominant neg | 2.5 | 3.5 |
| 15 | 458933 | AI638429 | Hs.24763 | RAN binding protein 1 | 2.5 | 3.5 |
| | 444871 | U46386 | Hs.12102 | sorting nexin 3 | 2.5 | 2.3 |
| | 411329 | AL360265 | Hs.69554 | hypothetical protein FLJ20552 | 2.5 | 2.9 |
| | 424074 | AI902456 | Hs.210761 | ESTs | 2.5 | 4.0 |
| | 438988 | H30039 | Hs.107674 | ESTs | 2.5 | 2.7 |
| 20 | 412836 | AA121384 | Hs.191446 | ESTs | 2.5 | 5.7 |
| | 430189 | AI298841 | Hs.135133 | ESTs, Weakly similar to ORF YNL310c [S.c | 2.5 | 3.0 |
| | 432841 | M93425 | Hs.62 | protein tyrosine phosphatase, non-recept | 2.5 | 13.4 |
| | 416926 | H03109 | Hs.108920 | HT018 protein | 2.5 | 2.8 |
| | 451429 | AA525993 | Hs.173699 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.5 | 3.9 |
| 25 | 416388 | AI417358 | Hs.73677 | ESTs | 2.5 | 4.2 |
| | 421561 | Z45399 | Hs.105779 | protein inhibitor of activated STAT prot | 2.5 | 7.5 |
| | 436480 | AJ271643 | Hs.87469 | putative acid-sensing ion channel | 2.5 | 2.6 |
| | 416273 | AW575691 | Hs.79123 | KIAA0084 protein | 2.5 | 2.6 |
| | 427149 | H94688 | Hs.173737 | ras-related C3 botulinum toxin substrate | 2.5 | 2.6 |
| 30 | 453041 | AI680737 | Hs.289068 | transcription factor 4 | 2.5 | 2.2 |
| | 446899 | NM_005397 | Hs.16426 | podocalyxin-like | 2.5 | 4.7 |
| | 447301 | AW958124 | Hs.142442 | HP1-BP74 | 2.5 | 3.2 |
| | 447769 | AW873704 | Hs.48764 | ESTs | 2.5 | 2.4 |
| | 447754 | AW073310 | Hs.163533 | Homo sapiens cDNA FLJ14142 fis, clone MA | 2.5 | 2.5 |
| 35 | 427087 | BE073913 | Hs.173515 | uncharacterized hypothalamus protein HT0 | 2.5 | 23.6 |
| | 440903 | AI468079 | Hs.126623 | ESTs | 2.5 | 2.3 |
| | 432353 | NM_016558 | Hs.274411 | SCAN domain-containing 1 | 2.5 | 4.1 |
| | 408196 | AL034548 | Hs.43527 | SRY (sex determining region Y)-box 22 | 2.5 | 2.5 |
| | 411373 | BE326276 | Hs.8861 | ESTs | 2.5 | 3.9 |
| 40 | 452402 | AI138530 | Hs.22216 | peroxisome proliferative activated recep | 2.5 | 2.4 |
| | 429998 | AI458063 | Hs.57841 | ESTs | 2.5 | 2.6 |
| | 421772 | Z24958 | Hs.108139 | zinc finger protein 212 | 2.5 | 3.7 |
| | 442573 | H93366 | Hs.7557 | Homo sapiens cDNA: FLJ21962 fis, clone H | 2.5 | 2.1 |
| | 444677 | AL110212 | Hs.9242 | purine-rich element binding protein B | 2.5 | 3.4 |
| 45 | 441887 | AW967865 | Hs.92145 | ESTs | 2.5 | 3.3 |
| | 451031 | AI360187 | Hs.4254 | ESTs | 2.5 | 4.8 |
| | 432450 | AI990739 | Hs.77868 | ORF | 2.5 | 2.4 |
| | 415860 | D56051 | Hs.78888 | diazepam binding inhibitor (GABA recepto | 2.5 | 4.8 |
| | 439530 | AA313607 | Hs.58633 | Homo sapiens cDNA: FLJ22145 fis, clone H | 2.4 | 2.3 |
| 50 | 428607 | AB002353 | Hs.186840 | KIAA0355 gene product | 2.4 | 4.0 |
| | 415402 | AA164687 | Hs.297889 | ESTs | 2.4 | 2.5 |
| | 446888 | AL030996 | Hs.16411 | hypothetical protein LOC57187 | 2.4 | 2.2 |
| | 439208 | AK000299 | Hs.180952 | dynactin p62 subunit | 2.4 | 2.4 |
| | 452900 | AA626794 | Hs.250655 | prothymosin, alpha (gene sequence 28) | 2.4 | 3.4 |
| 55 | 408657 | AA782601 | Hs.173328 | protein phosphatase 2, regulatory subuni | 2.4 | 3.6 |
| | 439143 | AI359214 | Hs.179260 | ESTs | 2.4 | 2.5 |
| | 439867 | AA847510 | Hs.161292 | ESTs | 2.4 | 9.3 |
| | 408138 | AA535740 | Hs.301967 | Homo sapiens mRNA; cDNA DKFZp434M196 (fr | 2.4 | 5.6 |
| | 428386 | R17298 | Hs.295923 | seven in absentia (Drosophila) homolog 1 | 2.4 | 4.2 |
| 60 | 417289 | D86962 | Hs.81875 | growth factor receptor-bound protein 10 | 2.4 | 2.2 |
| | 405268 | | | | 2.4 | 3.1 |
| | 439734 | AC005013 | Hs.149 | cAMP response element-binding protein CR | 2.4 | 3.6 |
| | 445378 | AV653564 | Hs.226946 | ESTs | 2.4 | 2.4 |
| | 454085 | D82418 | Hs.29626 | ESTs, Weakly similar to unknown [D.melan | 2.4 | 22.0 |
| 65 | 427354 | T57896 | Hs.191095 | ESTs | 2.4 | 3.6 |
| | 452906 | BE207039 | Hs.75621 | serine (or cysteine) proteinase inhibito | 2.4 | 2.2 |
| | 450065 | AL050107 | Hs.301558 | DKFZP586I1419 protein | 2.4 | 3.6 |
| | 451091 | AA810932 | Hs.131899 | ESTs, Weakly similar to coded for by C. | 2.4 | 2.7 |
| | 414839 | X63692 | Hs.77462 | DNA (cytosine-5)-methyltransferase 1 | 2.4 | 2.6 |
| 70 | 420303 | AA258282 | Hs.278436 | KIAA1474 protein | 2.4 | 2.0 |
| | 437068 | AA743643 | Hs.291427 | ESTs | 2.4 | 2.6 |
| | 417446 | AL118671 | Hs.82163 | monoamine oxidase B | 2.4 | 4.4 |
| | 421454 | AI660389 | Hs.286108 | chorionic somatomammotropin hormone 1 (p | 2.4 | 3.5 |
| | 434943 | AI929819 | Hs.320 | xeroderma pigmentosum, complementation g | 2.4 | 6.4 |
| 75 | 446342 | BE298665 | Hs.14846 | Homo sapiens mRNA; cDNA DKFZp564D016 (fr | 2.4 | 3.0 |
| | 452847 | AK000857 | Hs.30783 | hypothetical protein FLJ20850 | 2.4 | 2.1 |
| | 422506 | R20909 | Hs.117816 | scorin | 2.4 | 2.2 |
| | 405204 | | | | 2.4 | 4.3 |
| | 419441 | AW023731 | Hs.274368 | Homo sapiens mRNA; cDNA DKFZp586I1524 (f | 2.4 | 11.7 |
| 80 | 442293 | AW292634 | Hs.150358 | ESTs | 2.4 | 2.1 |
| | 451484 | AV648896 | Hs.26461 | hypothetical protein | 2.4 | 2.0 |
| | 438545 | AB032977 | Hs.6298 | KIAA1151 protein | 2.4 | 2.1 |
| | 442724 | AA355525 | Hs.159604 | cysteinyt-IRNA synthetase | 2.4 | 2.8 |
| | 405517 | | | | 2.4 | 6.6 |
| 80 | 413822 | R08950 | Hs.272044 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.4 | 3.8 |
| | 445679 | AI343868 | Hs.58800 | Homo sapiens cDNA FLJ12488 fis, clone NT | 2.4 | 2.3 |
| | 408636 | BE294925 | Hs.46680 | CGI-12 protein | 2.4 | 8.1 |

| | | | | | | |
|----|--------|-----------|-----------|---|-----|-------|
| 5 | 409142 | AL136877 | Hs.50758 | chromosome-associated polypeptide C | 2.4 | 2.4 |
| | 422043 | AL133649 | Hs.110953 | Homo sapiens mRNA; cDNA DKFZp434A139 (tr | 2.4 | 2.1 |
| | 424687 | J05070 | Hs.151738 | matrix metalloproteinase 9 (gelatinase B | 2.4 | 2.6 |
| | 442560 | AA365042 | Hs.228598 | ESTs | 2.4 | 4.9 |
| | 418126 | T91451 | Hs.86538 | ESTs | 2.4 | 11.7 |
| 10 | 413313 | NM_002047 | Hs.75280 | glycyl-tRNA synthetase | 2.4 | 2.1 |
| | 415167 | AA160784 | Hs.26410 | ESTs | 2.4 | 4.4 |
| | 440040 | BE219431 | Hs.300713 | ESTs | 2.4 | 3.4 |
| | 443595 | AF169312 | Hs.9613 | PPAR(gamma) angiotensin related protein | 2.4 | 10.7 |
| | 438977 | AA482026 | Hs.298625 | ESTs | 2.4 | 2.8 |
| 15 | 452066 | AA772149 | Hs.16979 | ESTs | 2.4 | 5.4 |
| | 428500 | AI815395 | Hs.184641 | delta-6 fatty acid desaturase | 2.4 | 2.2 |
| | 408503 | AW119059 | Hs.63163 | ESTs, Weakly similar to UDP-GalNAc:polyp | 2.4 | 2.7 |
| | 433401 | AF039698 | Hs.284217 | serologically defined colon cancer antig | 2.4 | 4.8 |
| | 412676 | NM_000165 | Hs.74471 | gap junction protein, alpha 1, 43kD (con | 2.4 | 2.2 |
| 20 | 453753 | BE252983 | Hs.35086 | ubiquitin specific protease 1 | 2.4 | 2.8 |
| | 424050 | AA211218 | Hs.138361 | farnesyltransferase, CAAAX box, alpha | 2.4 | 3.9 |
| | 440225 | BE295782 | Hs.159 | tumor necrosis factor receptor superfam | 2.4 | 76.7 |
| | 430512 | AF182294 | Hs.241578 | U6 snRNA-associated Sm-like protein LSm8 | 2.4 | 12.3 |
| | 415156 | X84908 | Hs.78060 | phosphorylase kinase, beta | 2.4 | 10.4 |
| 25 | 435975 | AL118990 | Hs.41997 | alpha-1-B glycoprotein | 2.4 | 7.7 |
| | 429831 | AA564489 | Hs.137526 | ESTs | 2.4 | 4.1 |
| | 407373 | AA031576 | Hs.143812 | Homo sapiens cDNA FLJ12956 fis, clone NT | 2.4 | 3.3 |
| | 422221 | AA306649 | Hs.168213 | gbt:EST177656 Jurkat T-cells VI Homo sapi | 2.4 | 3.8 |
| | 451351 | AW058261 | Hs.158311 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.4 | 3.3 |
| 30 | 410082 | AA081594 | Hs.238927 | Musashi (Drosophila) homolog 1 | 2.4 | 2.5 |
| | 430304 | AL122071 | Hs.25566 | Homo sapiens mRNA; cDNA DKFZp434H1235 (f | 2.4 | 6.5 |
| | 418863 | AL135743 | Hs.21145 | ESTs | 2.4 | 5.2 |
| | 448414 | BE391820 | Hs.183779 | Homo sapiens cDNA: FLJ22489 fis, clone H | 2.4 | 3.7 |
| | 428351 | AK001701 | Hs.159455 | Homo sapiens cDNA FLJ10590 fis, clone NT | 2.4 | 6.2 |
| 35 | 425750 | AL050276 | Hs.75839 | zinc finger protein 288 | 2.4 | 5.1 |
| | 426295 | AW367283 | Hs.254562 | zinc finger protein 6 (CMPX1) | 2.4 | 113.6 |
| | 408772 | W88532 | Hs.294084 | ESTs | 2.4 | 12.3 |
| | 426307 | F24978 | Hs.252748 | ESTs | 2.4 | 4.0 |
| | 405203 | | Hs.156089 | ESTs | 2.4 | 2.5 |
| 40 | 453537 | AA036755 | Hs.283681 | ESTs | 2.4 | 3.6 |
| | 431427 | AK000401 | Hs.143851 | Homo sapiens cDNA FLJ20394 fis, clone KA | 2.4 | 6.2 |
| | 458021 | AI885190 | Hs.87627 | ESTs, Weakly similar to KIAA1339 protein | 2.4 | 4.3 |
| | 453928 | BE222198 | Hs.111911 | ESTs | 2.4 | 2.6 |
| | 446853 | AV660630 | Hs.13999 | disrupter of silencing 10 | 2.3 | 9.7 |
| 45 | 441626 | AA281167 | Hs.104557 | ESTs | 2.3 | 23.0 |
| | 446138 | AW504182 | Hs.3337 | KIAA0700 protein | 2.3 | 2.2 |
| | 452568 | AA805634 | Hs.22862 | transmembrane 4 superfamily member 1 | 2.3 | 22.2 |
| | 417665 | AW852858 | Hs.298033 | ESTs | 2.3 | 8.0 |
| | 420088 | AC006486 | Hs.14947 | Homo sapiens cDNA: FLJ22286 fis, clone H | 2.3 | 5.1 |
| 50 | 421456 | AW579842 | Hs.182828 | hypothetical protein FLJ10697 | 2.3 | 2.5 |
| | 412093 | BE242691 | Hs.25010 | ESTs | 2.3 | 31.4 |
| | 428172 | U09367 | Hs.173840 | zinc finger protein 136 (clone pHZ-20) | 2.3 | 4.9 |
| | 450447 | AF212223 | Hs.249889 | hypothetical protein P15-2 | 2.3 | 2.3 |
| | 436001 | AW903849 | Hs.34401 | HUEL (C4orf1)-interacting protein | 2.3 | 4.1 |
| 55 | 414786 | AI246482 | Hs.30332 | ESTs | 2.3 | 2.1 |
| | 459284 | AF155660 | Hs.14791 | mitochondrial solute carrier | 2.3 | 2.9 |
| | 452701 | NM_005110 | Hs.29468 | glutamine-fructose-6-phosphate transamin | 2.3 | 2.6 |
| | 446320 | AF126245 | Hs.239720 | acyl-Coenzyme A dehydrogenase family, me | 2.3 | 3.9 |
| | 446669 | AW972832 | Hs.301805 | ESTs | 2.3 | 3.8 |
| 60 | 434616 | D79338 | Hs.16542 | CCR4-NOT transcription complex, subunit | 2.3 | 3.6 |
| | 452135 | AI492175 | Hs.184013 | ESTs | 2.3 | 2.3 |
| | 408696 | AW958157 | Hs.92381 | ESTs, Highly similar to unnamed protein | 2.3 | 2.8 |
| | 436176 | AL121422 | Hs.55501 | ESTs | 2.3 | 3.2 |
| | 419713 | AW968058 | Hs.54982 | nudix (nucleoside diphosphate linked moi | 2.3 | 17.0 |
| 65 | 414197 | W44877 | Hs.73793 | ESTs | 2.3 | 11.8 |
| | 445270 | AI762154 | Hs.170098 | Homo sapiens cDNA FLJ14014 fis, clone HE | 2.3 | 4.2 |
| | 412247 | AF022375 | | vascular endothelial growth factor | 2.3 | 5.1 |
| | 426494 | AL119528 | | KIAA0372 gene product | 2.3 | 4.4 |
| | 405687 | | | | 2.3 | 2.2 |
| 70 | 417410 | AF063020 | Hs.82110 | PC4 and SFRS1 interacting protein 1 | 2.3 | 2.0 |
| | 450747 | AI064821 | Hs.48306 | ESTs, Highly similar to EWS_HUMAN RNA-BI | 2.3 | 3.8 |
| | 433680 | AI805366 | Hs.199945 | ESTs | 2.3 | 6.7 |
| | 420025 | AF184939 | Hs.94392 | LDL induced EC protein | 2.3 | 2.4 |
| | 413407 | AI356293 | Hs.75339 | inositol polyphosphate phosphatase-like | 2.3 | 3.1 |
| 75 | 452908 | AB001451 | Hs.30965 | neuronal Shc adaptor homolog | 2.3 | 3.0 |
| | 424414 | AI361002 | Hs.94814 | Homo sapiens cDNA FLJ12168 fis, clone MA | 2.3 | 2.0 |
| | 435791 | AA243086 | Hs.25204 | chondroitin 4-O-sulfotransferase 2 | 2.3 | 2.4 |
| | 457635 | AV660976 | Hs.3569 | hypothetical protein | 2.3 | 6.9 |
| | 427985 | AI770170 | Hs.65583 | ESTs | 2.3 | 2.3 |
| 80 | 445498 | AV654019 | Hs.180402 | Homo sapiens cDNA: FLJ23506 fis, clone L | 2.3 | 2.3 |
| | 410310 | J02931 | Hs.62192 | coagulation factor III (thromboplastin, | 2.3 | 4.1 |
| | 450368 | AU077158 | Hs.24930 | tubulin-specific chaperone a | 2.3 | 3.5 |
| | 444614 | R44284 | Hs.2730 | heterogeneous nuclear ribonucleoprotein | 2.3 | 2.6 |
| | 448607 | AL042506 | Hs.21599 | Homo sapiens cDNA FLJ10107 fis, clone HE | 2.3 | 2.8 |
| | 447975 | BE378418 | Hs.127240 | ESTs | 2.3 | 2.2 |
| | 429767 | AW793022 | Hs.218329 | hypothetical protein | 2.3 | 11.5 |
| | 408877 | AA479033 | Hs.130315 | ESTs | 2.3 | 2.3 |

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|----|--------|-----------|-----------|---|-----|-------|
| | 448481 | W15284 | Hs.74832 | ESTs | | |
| | 452833 | BE559681 | Hs.30736 | KIAA0124 protein | 2.3 | 3.3 |
| | 421057 | T58283 | Hs.42679 | ESTs | 2.3 | 2.8 |
| 5 | 408885 | C02741 | Hs.48712 | hypothetical protein FLJ20736 | 2.3 | 11.0 |
| | 427615 | BE410107 | Hs.179817 | CGI-82 protein | 2.3 | 4.6 |
| | 448861 | AL049951 | Hs.22370 | Homo sapiens mRNA; cDNA DKFZp564O0122 (f | 2.3 | 2.3 |
| | 430154 | AW583058 | Hs.234726 | serine (or cysteine) proteinase inhibitor | 2.3 | 6.3 |
| | 428494 | AA233439 | Hs.184634 | hypothetical protein FLJ20005 | 2.3 | 34.6 |
| 10 | 422987 | AW407887 | Hs.301772 | serine/threonine kinase 11 (Peutz-Jegher | 2.3 | 10.2 |
| | 408216 | AA741038 | Hs.6670 | ESTs | 2.3 | 3.2 |
| | 407862 | BE548267 | Hs.50724 | Homo sapiens cDNA FLJ10934 fs, clone OV | 2.3 | 3.3 |
| | 432215 | AU076609 | Hs.2934 | ribonucleotide reductase M1 polypeptide | 2.3 | 5.7 |
| | 410086 | AI268405 | Hs.13467 | Homo sapiens BAC clone RP11-121A8 from 7 | 2.3 | 2.1 |
| 15 | 444853 | AW576245 | Hs.149740 | Homo sapiens mRNA for FLJ00028 protein, | 2.3 | 2.2 |
| | 413284 | AU077055 | Hs.289107 | baculoviral IAP repeat-containing 2 | 2.3 | 4.5 |
| | 445547 | D86181 | Hs.273 | galactosylceramidase (Krabbe disease) | 2.3 | 4.8 |
| | 420258 | AA477514 | Hs.96247 | translin-associated factor X | 2.3 | 2.5 |
| | 437223 | C15105 | Hs.107884 | ESTs | 2.3 | 3.5 |
| 20 | 437353 | AA749195 | Hs.143746 | ESTs | 2.3 | 2.7 |
| | 426224 | BE085860 | Hs.168075 | karyopherin (importin) beta 2 | 2.3 | 2.6 |
| | 402575 | Z23024 | Hs.138860 | Rho GTPase activating protein 1 | 2.3 | 36.1 |
| | 430712 | AW044647 | Hs.196284 | ESTs | 2.3 | 3.1 |
| | 452036 | NM_003966 | Hs.27621 | sema domain, seven thrombospondin repeat | 2.3 | 2.4 |
| 25 | 425180 | U00115 | Hs.155024 | B-cell CLL/lymphoma 6 (zinc finger prote | 2.3 | 2.4 |
| | 441648 | H05734 | Hs.30559 | ESTs | 2.3 | 4.3 |
| | 424130 | AL050136 | Hs.140945 | Homo sapiens mRNA; cDNA DKFZp586L141 (f | 2.3 | 2.1 |
| | 414682 | AL021154 | Hs.76884 | inhibitor of DNA binding 3, dominant neg | 2.3 | 2.9 |
| | 423814 | AF105020 | Hs.132999 | putative protein O-mannosyltransferase | 2.3 | 12.2 |
| 30 | 421641 | AI638184 | Hs.106334 | Homo sapiens clone Z3836 mRNA sequence | 2.3 | 3.7 |
| | 427882 | AA640987 | Hs.193767 | ESTs | 2.3 | 2.3 |
| | 442159 | AW163390 | Hs.8123 | chromobox homolog 3 (Drosophila HP1 gamm | 2.3 | 10.2 |
| | 412541 | BE009398 | Hs.74002 | nuclear receptor coactivator 1 | 2.3 | 4.4 |
| | 447217 | BE465754 | Hs.17778 | neuropilin 2 | 2.3 | 2.4 |
| 35 | 452336 | AA960961 | Hs.29147 | hypothetical protein FLJ11015 | 2.3 | 3.0 |
| | 423913 | NM_016436 | Hs.301055 | hepatocellular carcinoma-associated anti | 2.3 | 4.1 |
| | 411737 | AW160339 | Hs.71791 | hypothetical protein | 2.3 | 3.4 |
| | 412276 | BE262621 | Hs.73798 | macrophage migration inhibitory factor (| 2.2 | 2.0 |
| | 456974 | M12529 | Hs.169401 | apolipoprotein E | 2.2 | 2.4 |
| 40 | 416033 | NM_012201 | Hs.78979 | Golgi apparatus protein 1 | 2.2 | 2.6 |
| | 406739 | AI566709 | Hs.182426 | ribosomal protein S2 | 2.2 | 10.4 |
| | 448646 | AU077149 | Hs.21704 | transcription factor 12 (HTF4, helix-loo | 2.2 | 115.3 |
| | 437371 | AK000868 | Hs.5570 | hypothetical protein FLJ10006 | 2.2 | 4.2 |
| | 451413 | AA448974 | Hs.26367 | PC3-96 protein | 2.2 | 3.6 |
| 45 | 408665 | T88845 | Hs.112200 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 2.2 | 6.2 |
| | 437548 | AI701596 | Hs.121592 | ESTs | 2.2 | 3.2 |
| | 452053 | AI750575 | Hs.173933 | nuclear factor I/A | 2.2 | 3.0 |
| | 428303 | AW974476 | Hs.183601 | regulator of G-protein signalling 16 | 2.2 | 3.3 |
| 50 | 441376 | H94227 | Hs.6592 | ESTs, Weakly similar to salivary proline | 2.2 | 3.4 |
| | 413399 | BE091833 | Hs.22564 | gb:IL2-BT0731-260400-076-F04 BT0731 Homo | 2.2 | 2.5 |
| | 448913 | AA194422 | Hs.22564 | myosin VI | 2.2 | 2.1 |
| | 439053 | BE244588 | Hs.6456 | chaperonin-containing TCP1, subunit 2 (b | 2.2 | 2.4 |
| | 428065 | AI634046 | Hs.157313 | ESTs | 2.2 | 3.1 |
| | 425846 | AA102174 | Hs.159629 | myosin IXB | 2.2 | 3.5 |
| 55 | 426404 | AA377607 | Hs.273138 | ESTs | 2.2 | 7.1 |
| | 423464 | NM_016240 | Hs.128856 | CSR1 protein | 2.2 | 3.3 |
| | 436135 | D85390 | Hs.5057 | carboxypeptidase D | 2.2 | 2.1 |
| | 450476 | AL045285 | Hs.246849 | ESTs, Moderately similar to ALU6_HUMAN A | 2.2 | 9.1 |
| | 420798 | W93774 | Hs.99936 | keratin 10 (epidermolytic hyperkeratosis | 2.2 | 2.5 |
| 60 | 433530 | BE349534 | Hs.281789 | ESTs | 2.2 | 2.8 |
| | 436297 | AI084582 | Hs.5105 | hypothetical protein FLJ10569 | 2.2 | 2.1 |
| | 433058 | H86865 | Hs.280666 | Homo sapiens chromosome 19, cosmid R3218 | 2.2 | 2.4 |
| | 435924 | AW029203 | Hs.191952 | ESTs | 2.2 | 2.3 |
| | 417125 | AW181998 | Hs.81248 | CUG triplet repeat, RNA-binding protein | 2.2 | 3.2 |
| 65 | 449338 | H73444 | Hs.394 | adrenomedullin | 2.2 | 2.3 |
| | 446065 | AA085191 | Hs.6949 | ESTs, Weakly similar to T2D3_HUMAN TRANS | 2.2 | 18.3 |
| | 410668 | BE379794 | Hs.65403 | hypothetical protein | 2.2 | 3.1 |
| | 424992 | AW290893 | Hs.96918 | Homo sapiens cDNA: FLJ21561 fs, clone C | 2.2 | 2.6 |
| 70 | 437801 | AA613866 | Hs.5848 | Homo sapiens mRNA; cDNA DKFZp564L222 (f | 2.2 | 10.8 |
| | 412491 | W31589 | Hs.73957 | RAB5A, member RAS oncogene family | 2.2 | 2.5 |
| | 446392 | AF142419 | Hs.15020 | homolog of mouse quaking QKI (KH domain | 2.2 | 2.4 |
| | 450503 | R35917 | Hs.25042 | Homo sapiens mRNA full length insert cDN | 2.2 | 3.4 |
| | 432476 | T94344 | | gb:ye31h10.s1 Stratagene lung (937210) H | 2.2 | 2.8 |
| | 424251 | AA677466 | Hs.143696 | coactivator-associated arginine methyltr | 2.2 | 2.6 |
| 75 | 456619 | AV647917 | Hs.107153 | inhibitor of growth family, member 1-Rx | 2.2 | 5.0 |
| | 433411 | AI658666 | Hs.49994 | ESTs | 2.2 | 2.6 |
| | 424714 | AI114630 | Hs.208334 | Homo sapiens cDNA: FLJ21874 fs, clone H | 2.2 | 2.1 |
| | 416326 | AF186780 | Hs.79219 | RaiGDS-like gene; KIAA0959 protein | 2.2 | 2.7 |
| | 407696 | AI697340 | Hs.76549 | ATPase, Na+K+ transporting, alpha 1 pol | 2.2 | 2.2 |
| 80 | 445939 | BE018658 | Hs.141003 | Homo sapiens cDNA: FLJ21691 fs, clone C | 2.2 | 6.5 |
| | 414765 | X07854 | Hs.77269 | guanine nucleotide binding protein (G pr | 2.2 | 4.4 |
| | 407136 | T64896 | Hs.287420 | Homo sapiens cDNA FLJ11533 fs, clone HE | 2.2 | 6.2 |
| | 453665 | AA626250 | Hs.181185 | eukaryotic translation elongation factor | 2.2 | 2.8 |
| | 433608 | AW340005 | Hs.164485 | ESTs | 2.2 | 2.3 |
| | | | | | 2.2 | 2.1 |

| | | | | | | |
|----|--------|-----------|-----------|--|-----|-------|
| 5 | 447646 | BE619752 | Hs.66053 | ESTs, Weakly similar to S22126 finger pr | 2.2 | 4.1 |
| | 433139 | AB029826 | Hs.47649 | 3-methylcrotonyl-CoA carboxylase biotin- | 2.2 | 11.7 |
| | 413433 | NM_003199 | Hs.289068 | transcription factor 4 | 2.2 | 2.2 |
| | 421535 | AB002359 | Hs.105478 | phosphonobosylformylglycinamide synthase | 2.2 | 2.2 |
| | 428591 | BE313029 | Hs.185807 | Homo sapiens clone 24758 mRNA sequence | 2.2 | 4.8 |
| 10 | 417248 | AA329449 | Hs.247302 | twisted gastrulation | 2.2 | 2.5 |
| | 403966 | | | | 2.2 | 5.2 |
| | 437112 | AA744692 | Hs.166539 | ESTs | 2.2 | 3.0 |
| | 414799 | AI752416 | Hs.77326 | insulin-like growth factor binding prote | 2.2 | 4.9 |
| | 431049 | AA846576 | Hs.103267 | hypothetical protein FLJ22548 similar to | 2.2 | 4.4 |
| 15 | 422100 | AI096988 | Hs.111554 | ADP-ribosylation factor-like 7 | 2.2 | 2.5 |
| | 426543 | AV650198 | Hs.170311 | heterogeneous nuclear ribonucleoprotein | 2.2 | 2.4 |
| | 423720 | AL044191 | Hs.23388 | Homo sapiens cDNA: FLJ21310 fis, clone C | 2.2 | 4.2 |
| | 443804 | AL135352 | Hs.255883 | ESTs | 2.2 | 2.2 |
| | 435080 | AI831760 | Hs.155111 | ESTs | 2.2 | 2.5 |
| 20 | 452808 | AF244135 | Hs.30670 | hepatocellular carcinoma-associated anti | 2.2 | 7.1 |
| | 433934 | AW273261 | Hs.216292 | ESTs | 2.2 | 2.1 |
| | 432004 | BE018302 | Hs.2894 | placental growth factor, vascular endoth | 2.2 | 4.4 |
| | 452518 | AA280722 | Hs.24758 | ESTs | 2.2 | 3.0 |
| | 409600 | AJ011679 | Hs.55099 | Homo sapiens mRNA; cDNA DKFZp586D2123 (f | 2.2 | 2.3 |
| 25 | 448965 | AF092134 | Hs.22679 | CGI-24 protein | 2.2 | 4.0 |
| | 444954 | AW247076 | Hs.12163 | eukaryotic translation initiation factor | 2.2 | 5.3 |
| | 458894 | AW292171 | Hs.23978 | scaffold attachment factor B | 2.2 | 2.5 |
| | 402269 | | | | 2.2 | 2.2 |
| | 423798 | AF047033 | Hs.301617 | Homo sapiens mRNA full length insert cDN | 2.2 | 4.0 |
| 30 | 413836 | W92003 | Hs.70614 | ESTs | 2.2 | 3.6 |
| | 432231 | AA339977 | Hs.274127 | CLST 11240 protein | 2.1 | 2.1 |
| | 412204 | AI125507 | Hs.130829 | ESTs | 2.1 | 3.0 |
| | 438807 | AA848011 | Hs.124570 | ESTs, Weakly similar to reverse transcri | 2.1 | 2.2 |
| | 404170 | | | | 2.1 | 41.6 |
| 35 | 434858 | AW979012 | Hs.134462 | ESTs | 2.1 | 2.2 |
| | 426882 | AA149707 | Hs.173091 | ubiquitin-like 3 | 2.1 | 2.1 |
| | 421939 | BE169531 | Hs.109727 | TAK1-binding protein 2; KIAA0733 protein | 2.1 | 26.5 |
| | 442432 | BE093589 | Hs.38178 | Homo sapiens cDNA: FLJ23468 fis, clone H | 2.1 | 3.7 |
| | 424950 | AA602917 | Hs.158974 | ESTs | 2.1 | 19.9 |
| 40 | 418123 | AA669830 | Hs.83530 | hypothetical protein | 2.1 | 4.6 |
| | 440467 | AK001519 | Hs.7194 | CGI-74 protein | 2.1 | 5.3 |
| | 437092 | AA744292 | Hs.181244 | major histocompatibility complex, class | 2.1 | 3.0 |
| | 421579 | NM_002975 | Hs.105927 | stem cell growth factor; lymphocyte secr | 2.1 | 3.3 |
| | 428953 | AA306610 | Hs.194676 | DKFZP434C013 protein | 2.1 | 5.0 |
| 45 | 457313 | AF047002 | Hs.241520 | transcriptional coactivator | 2.1 | 3.5 |
| | 420570 | AI453665 | Hs.290870 | ESTs, Weakly similar to S23650 retroviru | 2.1 | 2.1 |
| | 446918 | AL135125 | Hs.13913 | KIAA1577 protein | 2.1 | 2.3 |
| | 427567 | N24236 | Hs.179662 | nucleosome assembly protein 1-like 1 | 2.1 | 2.8 |
| | 446363 | AL117440 | Hs.301967 | Homo sapiens mRNA; cDNA DKFZp434M196 (fr | 2.1 | 4.0 |
| 50 | 428482 | AI290352 | Hs.184592 | KIAA0344 gene product | 2.1 | 2.8 |
| | 456559 | AI336273 | Hs.102548 | glucocorticoid receptor DNA binding fact | 2.1 | 2.3 |
| | 442819 | BE622721 | Hs.301766 | ESTs, Weakly similar to hypothetical pro | 2.1 | 27.1 |
| | 428808 | AA436007 | Hs.188780 | ESTs | 2.1 | 5.0 |
| | 414893 | AA215295 | Hs.77578 | ubiquitin specific protease 9, X chromos | 2.1 | 15.9 |
| 55 | 447023 | AA356764 | Hs.17109 | integral membrane protein 2A | 2.1 | 3.0 |
| | 402250 | AV655272 | Hs.20252 | novel Ras family protein | 2.1 | 4.2 |
| | 429952 | AF080158 | Hs.226573 | inhibitor of kappa light polypeptide gen | 2.1 | 7.9 |
| | 420006 | H14429 | Hs.94300 | serologically defined colon cancer antig | 2.1 | 5.6 |
| | 407316 | AA031663 | Hs.28802 | centaurin-alpha 2 protein | 2.1 | 4.4 |
| 60 | 417139 | M69043 | Hs.81328 | nuclear factor of kappa light polypeptid | 2.1 | 103.2 |
| | 414774 | X02419 | Hs.77274 | plasminogen activator, urokinase | 2.1 | 29.9 |
| | 430488 | D19589 | Hs.4220 | ESTs, Moderately similar to tetracycline | 2.1 | 2.1 |
| | 428680 | U69199 | Hs.90259 | ESTs, Weakly similar to alpha 1 [H.sapie | 2.1 | 2.5 |
| | 448501 | AA332316 | Hs.4273 | hypothetical protein FLJ13159 | 2.1 | 2.0 |
| 65 | 422552 | N39729 | Hs.118243 | deoxyribonuclease II, lysosomal | 2.1 | 2.9 |
| | 419476 | AW953030 | Hs.59425 | Homo sapiens cDNA: FLJ23323 fis, clone H | 2.1 | 3.1 |
| | 408681 | AW953853 | Hs.292833 | ESTs | 2.1 | 3.9 |
| | 417353 | AA375752 | Hs.76362 | general transcription factor IIA, 2 (12k | 2.1 | 4.1 |
| | 422070 | AF149785 | Hs.111126 | pituitary tumor-transforming 1 interacti | 2.1 | 4.9 |
| 70 | 442711 | AF151073 | Hs.8645 | hypothetical protein | 2.1 | 2.2 |
| | 450139 | AK001838 | Hs.296323 | Homo sapiens cDNA FLJ10976 fis, clone PL | 2.1 | 7.4 |
| | 452897 | BE066058 | Hs.269233 | ESTs | 2.1 | 4.2 |
| | 409147 | AI889208 | Hs.17283 | hypothetical protein FLJ10890 | 2.1 | 4.5 |
| | 433028 | AI199144 | Hs.283737 | AD-017 protein | 2.1 | 2.6 |
| 75 | 407831 | BE613377 | Hs.15580 | Homo sapiens cDNA: FLJ22276 fis, clone H | 2.1 | 8.5 |
| | 417871 | AA521368 | Hs.24252 | ESTs | 2.1 | 2.9 |
| | 428754 | AI521102 | Hs.301374 | ESTs, Moderately similar to ALU5_HUMAN A | 2.1 | 5.3 |
| | 430127 | AA219498 | Hs.233952 | proteasome (prosome, macropain) subunit, | 2.1 | 4.3 |
| | 442622 | NM_000435 | Hs.8546 | Notch (Drosophila) homolog 3 | 2.1 | 8.5 |
| 80 | 414242 | AA749230 | Hs.22666 | ESTs | 2.1 | 2.8 |
| | 433323 | AA805132 | Hs.30701 | ESTs | 2.1 | 5.0 |
| | 439022 | AA356599 | Hs.173904 | ESTs | 2.1 | 6.4 |
| | 443357 | AW016773 | Hs.75615 | apolipoprotein C-II | 2.1 | 2.0 |
| | 449103 | T24968 | Hs.23038 | HSPC071 protein | 2.1 | 2.7 |
| | 427512 | AB018322 | Hs.179507 | KIAA0779 protein | 2.1 | 2.0 |
| | 426728 | NM_007118 | Hs.171957 | triple functional domain (PTPRF interact | 2.1 | 2.9 |
| | 440112 | AA099014 | Hs.231029 | ESTs | 2.1 | 2.3 |

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|--------|-----------|-----------|--|-----|------|
| 446920 | BE397649 | Hs.31257 | Homo sapiens cDNA FLJ13634 fis, clone PL | 2.1 | 4.8 |
| 428459 | D44650 | Hs.184411 | gene with multiple splice variants near | 2.1 | 2.9 |
| 432842 | AW674093 | Hs.279525 | hypothetical protein PRO2605 | 2.1 | 2.3 |
| 438829 | AA826926 | Hs.204214 | ESTs | 2.1 | 2.7 |
| 411442 | N25956 | Hs.101810 | Homo sapiens cDNA FLJ14232 fis, clone NT | 2.1 | 2.2 |
| 409423 | AI969783 | Hs.43071 | ESTs, Weakly similar to AF151900.1 CGI-1 | 2.1 | 2.2 |
| 456804 | AI421645 | Hs.139851 | caveolin 2 | 2.1 | 15.2 |
| 434536 | H14486 | Hs.3903 | Cdc42 effector protein 4; binder of Rho | 2.1 | 2.8 |
| 447126 | AW150632 | Hs.62954 | ferritin, heavy polypeptide 1 | 2.1 | 25.0 |
| 442328 | AI952430 | Hs.265237 | ESTs | 2.1 | 2.1 |
| 444488 | AW192879 | Hs.184796 | ESTs, Weakly similar to PET2_HUMAN OLIGO | 2.1 | 2.9 |
| 438874 | H02780 | | gb:bj41a11.1 Soares placenta Nb2HP Homo | 2.1 | 10.6 |
| 412805 | AW954569 | Hs.296287 | ESTs | 2.1 | 4.6 |
| 446334 | U52427 | Hs.14839 | polymerase (RNA) II (DNA directed) polyp | 2.1 | 2.3 |
| 427201 | AB037860 | Hs.173933 | nuclear factor IIA | 2.1 | 5.1 |
| 436997 | AA741151 | Hs.137323 | ESTs | 2.1 | 3.0 |
| 426369 | AF134157 | Hs.169487 | Kreisler (mouse) maf-related leucine zip | 2.1 | 2.3 |
| 453613 | F06838 | Hs.14763 | ESTs | 2.1 | 2.4 |
| 413276 | Z24725 | Hs.75260 | mitogen inducible 2 | 2.1 | 5.5 |
| 422050 | AA302741 | Hs.25786 | ESTs | 2.1 | 4.0 |
| 424797 | AA622394 | Hs.153177 | ribosomal protein S28 | 2.1 | 2.1 |
| 437365 | AW965771 | Hs.91065 | hypothetical protein DKFZp761B2423 | 2.1 | 3.0 |
| 412482 | AI499930 | Hs.181043 | KIAA0788 protein | 2.1 | 2.7 |
| 418662 | AI801098 | Hs.151500 | ESTs | 2.1 | 2.1 |
| 404030 | | | | 2.1 | 2.1 |
| 437802 | AI475995 | Hs.122910 | ESTs | 2.1 | 3.8 |
| 441130 | AI160734 | Hs.283429 | SMC (mouse) homolog, X chromosome | 2.1 | 3.5 |
| 416084 | L16991 | Hs.79006 | deoxythymidylate kinase (thymidylate kin | 2.1 | 7.4 |
| 409944 | BE297925 | Hs.57687 | four and a half LIM domains 3 | 2.1 | 6.3 |
| 425421 | L11669 | Hs.157145 | tetracycline transporter-like protein | 2.1 | 7.1 |
| 428399 | NM_006276 | Hs.184167 | splicing factor, arginine/serine-rich 7 | 2.1 | 2.7 |
| 421313 | NM_014923 | Hs.103329 | KIAA0970 protein | 2.1 | 2.6 |
| 445229 | BE276013 | Hs.172364 | Homo sapiens mRNA for FLJ00086 protein, | 2.1 | 4.7 |
| 401001 | | | | 2.1 | 14.7 |
| 425159 | NM_004341 | Hs.154868 | carbamoyl-phosphate synthetase 2, aspart | 2.1 | 7.2 |
| 438855 | AW946276 | Hs.6441 | tissue inhibitor of metalloproteinase 2 | 2.1 | 4.9 |
| 433369 | Z49254 | Hs.3254 | mitochondrial ribosomal protein L23 | 2.1 | 25.0 |
| 433228 | F28212 | Hs.284247 | KIAA1491 protein | 2.1 | 5.1 |
| 445392 | AA057478 | Hs.23272 | ESTs | 2.0 | 2.3 |
| 433891 | AA613792 | | gb:nc097h03.s1 NCI_CGAP_Pr2 Homo sapiens | 2.0 | 2.5 |
| 432572 | AI660840 | Hs.191202 | ESTs, Weakly similar to ALUE_HUMAN !!! | 2.0 | 2.9 |
| 448474 | AI792014 | Hs.13809 | ESTs | 2.0 | 12.1 |
| 427045 | H86504 | Hs.173328 | protein phosphatase 2, regulatory subuni | 2.0 | 2.9 |
| 444916 | AB028956 | Hs.12144 | KIAA1033 protein | 2.0 | 4.2 |
| 439177 | AW820275 | Hs.76611 | ESTs | 2.0 | 3.3 |
| 423533 | NM_014339 | Hs.129751 | interleukin 17 receptor | 2.0 | 5.0 |
| 430057 | AW450303 | Hs.2534 | bone morphogenetic protein receptor, typ | 2.0 | 2.3 |
| 424429 | U63830 | Hs.146847 | TRAF family member-associated NFkB activ | 2.0 | 12.7 |
| 428385 | AF112213 | Hs.184062 | putative Rab5-interacting protein | 2.0 | 4.6 |
| 458946 | AA009716 | Hs.42311 | ESTs | 2.0 | 16.4 |
| 444816 | Z48633 | Hs.283742 | H.sapiens mRNA for retrotransposon | 2.0 | 4.9 |
| 426829 | AI761241 | Hs.301719 | ESTs | 2.0 | 2.4 |
| 433619 | AW965275 | Hs.284288 | hqp0256 protein | 2.0 | 4.4 |
| 421985 | AK001779 | Hs.110445 | CGI-97 protein | 2.0 | 3.8 |
| 439895 | AB037773 | Hs.6762 | hypothetical protein FLJ10595 | 2.0 | 2.2 |
| 449188 | AW072939 | Hs.23200 | myotubularin related protein 1 | 2.0 | 2.2 |
| 404820 | | | | 2.0 | 2.7 |
| 425811 | AL039104 | Hs.159557 | karyopherin alpha 2 (RAG cohort 1, impor | 2.0 | 2.5 |
| 422163 | AF027208 | Hs.297332 | Homo sapiens cDNA: FLJ21471 fis, clone C | 2.0 | 3.7 |
| 431172 | AI125639 | Hs.250666 | hairy (Drosophila)-homolog | 2.0 | 10.2 |
| 415200 | AL040328 | Hs.301912 | Homo sapiens cDNA: FLJ22920 fis, clone K | 2.0 | 2.1 |
| 458176 | AI961519 | Hs.140309 | ESTs, Weakly similar to KIAA0681 protein | 2.0 | 5.0 |
| 407895 | R44203 | Hs.265540 | HSPC042 protein | 2.0 | 4.6 |
| 449816 | AI701457 | Hs.38694 | ESTs | 2.0 | 2.0 |
| 422976 | AU076657 | Hs.1600 | sec61 homolog | 2.0 | 5.7 |
| 430220 | BE378277 | Hs.152230 | ESTs | 2.0 | 11.7 |
| 435446 | AA682305 | Hs.133268 | ESTs | 2.0 | 4.2 |
| 431031 | AA830335 | Hs.105273 | ESTs | 2.0 | 14.1 |
| 425233 | Z17861 | Hs.155218 | E1B-55kDa-associated protein 5 | 2.0 | 5.6 |
| 426458 | D83032 | Hs.169984 | nuclear protein | 2.0 | 5.9 |
| 421965 | AA301100 | | gb:EST14128 Testis tumor Homo sapiens cD | 2.0 | 2.1 |
| 427128 | AW301984 | Hs.173685 | Homo sapiens cDNA FLJ12619 fis, clone NT | 2.0 | 6.3 |
| 449722 | BE280074 | Hs.23960 | cyclin B1 | 2.0 | 2.1 |
| 450816 | BE271927 | Hs.87385 | ESTs | 2.0 | 2.4 |
| 453507 | AF083217 | Hs.33085 | WD repeat domain 3 | 2.0 | 13.1 |
| 422801 | AF125672 | Hs.287994 | nuclear receptor co-repressor 2 | 2.0 | 3.5 |
| 418178 | AA043951 | Hs.83715 | Sjogren syndrome antigen B (autoantigen | 2.0 | 3.9 |
| 417819 | AI253112 | Hs.133540 | ESTs | 2.0 | 4.0 |
| 414787 | AL049332 | Hs.77311 | BTG family, member 3 | 2.0 | 4.0 |
| 447032 | AK000310 | Hs.17138 | hypothetical protein FLJ20303 | 2.0 | 7.0 |
| 431742 | NM_016652 | Hs.268281 | CGI-201 protein | 2.0 | 2.5 |
| 448431 | BE613061 | Hs.300697 | ESTs, Weakly similar to CA13_HUMAN COLLA | 2.0 | 6.5 |
| 456444 | AA884517 | Hs.31856 | ESTs, Weakly similar to KIAA1453 protein | 2.0 | 2.5 |

| | | | | | | |
|----|--------|-----------|-----------|--|-----|------|
| 5 | 419178 | NM_006284 | Hs.89657 | TATA box binding protein (TBP)-associate | 2.0 | 6.0 |
| | 446437 | AW014360 | Hs.202119 | ESTs, Weakly similar to A46010 X-linked | 2.0 | 2.2 |
| | 449910 | AI074585 | Hs.58440 | ESTs | 2.0 | 2.1 |
| | 435963 | AF271212 | Hs.87627 | disrupter of silencing 10 | 2.0 | 2.1 |
| | 421283 | AI760018 | Hs.205071 | ESTs | 2.0 | 2.6 |
| | 414482 | S57498 | Hs.76252 | endothelin receptor type A | 2.0 | 2.4 |
| | 450960 | AB013897 | Hs.25722 | Homo sapiens mRNA for HKR1, partial cds | 2.0 | 2.1 |
| | 438644 | AI126162 | Hs.129037 | ESTs | 2.0 | 2.1 |
| 10 | 458343 | AI004775 | Hs.205091 | ESTs, Weakly similar to WW domain bindin | 2.0 | 6.5 |
| | 412574 | BE410731 | Hs.74050 | follicular lymphoma variant translocatio | 2.0 | 12.4 |
| | 458079 | AI795870 | Hs.54277 | ESTs | 2.0 | 3.8 |
| | 450582 | AI339732 | Hs.13144 | HSPC180 protein | 2.0 | 2.8 |
| | 409936 | AK001691 | Hs.57655 | hypothetical protein FLJ10829 | 2.0 | 3.1 |
| 15 | 426865 | D63476 | Hs.172813 | PAK-interacting exchange factor beta | 2.0 | 3.3 |
| | 446430 | AA346837 | Hs.15075 | hypothetical protein DKFZp434E2216 | 2.0 | 2.0 |

Table 4B:

| | |
|-------------|---------------------------------------|
| Pkey: | Unique Eos probeset identifier number |
| CAT number: | Gene cluster number |
| Accession: | Genbank accession numbers |

| | | | |
|----|--------|------------|---|
| 20 | Pkey | CAT Number | Accession |
| | 447197 | 2176805_1 | R36075 R36167 AI366546 |
| | 407192 | 2200202_1 | AA602964 AA609200 |
| 25 | 429007 | 327976_1 | AA443145 BF958169 AW904500 AL119015 D80642 |
| | 429163 | 1238297_1 | AW974271 AA592975 AA447312 AA884766 |
| | 439579 | 24302_1 | AF086400 W73990 W79232 |
| | 432060 | 1235850_1 | AA525021 AW971364 AA570759 |
| 30 | 416913 | 924456_1 | AW934714 AW749864 AW749902 BE162498 BE161005 BE162499 BE161006 AA190449 AW513465 BE162500 BE161007 |
| | 426413 | 372468_1 | AW954494 AA377823 BG219617 BG195685 BG616269 AI022688 |
| | 433586 | 32908_1 | BC011194 AW517087 AA601054 T85512 |
| | 448451 | 7632_32 | AW000978 R39988 AW015994 AI598202 BF821479 AI521706 |
| | 442495 | 928718_1 | AI184717 AW518883 AF121173 |
| 35 | 439566 | 23928_1 | AF086387 W72711 W77884 |
| | 407939 | 600387_1 | AW118352 AW196215 W05608 |
| | 453740 | 612139_1 | AL120295 BG291384 T88779 |
| | 433854 | 899720_1 | BG675161 H59558 AI699484 AA610649 AI937812 |
| | 413020 | 1485885_1 | BE048113 R98736 Z42904 |
| 40 | 458050 | 61684_1 | AK057874 AW901381 AW901380 AV730240 T50211 AA828756 AA834708 |
| | 440769 | 21430_5 | BG419454 BF924037 R13764 AW793200 BE561793 BG698295 BE270077 |
| | 428832 | 1137866_1 | BI008687 AA481363 AA436432 BI008686 AA578229 AA481375 |
| | 414473 | 35761_3 | BG392866 BE302693 |
| | 422343 | 786037_1 | AW561833 AA309282 AA551780 AI628633 AA551995 AW378461 |
| 45 | 431319 | 122030_1 | BG435498 BG924768 AV718536 AA873350 T82428 T82429 AU185416 AA658442 |
| | 422221 | 319_18 | BG910399 BE826714 BF905312 AA305649 Z40822 N76633 |
| | 413399 | 1511159_1 | BE091833 BE091874 BE091871 |
| | 432476 | 1237465_1 | AW973269 AA548913 T94344 AA834800 AA857492 |
| | 438874 | 52147_1 | AF075017 R66779 R22463 H02780 |
| 50 | 433891 | 647290_1 | AW182329 AA613792 T05304 AW858385 |
| | 421965 | 1883_13 | BC022394 AI742351 BE676249 AI742341 AW572776 AI566256 AI538553 BI837905 AA301100 AA620903 AI142397 AW082310 AI147387 BF509145 |
| | | | AW968207 AA468415 AU185163 AW450843 AI568752 AW137191 |

TABLE 4C:

| | | |
|----|--------------|---|
| 55 | Pkey: | Unique number corresponding to an Eos probeset |
| | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. |
| | Strand: | Indicates DNA strand from which exons were predicted. |
| | NL_position: | Indicates nucleotide positions of predicted exons. |

| | | | | |
|----|--------|---------|--------|-------------------------------------|
| 60 | Pkey | Ref | Strand | NL_position |
| | 400859 | 9757499 | Minus | 91888-92018,98131-98294,99474-99570 |
| | 405238 | 7249119 | Minus | 51728-51836 |
| | 400992 | 8096828 | Plus | 140390-140822 |
| 65 | 400860 | 9757499 | Minus | 151830-152104,152649-152744 |
| | 402524 | 9798518 | Minus | 20529-21096 |
| | 404210 | 5006246 | Plus | 169926-170121 |
| | 402604 | 9909420 | Plus | 20393-20767 |
| | 402855 | 9662953 | Minus | 59763-59909 |
| 70 | 404029 | 7671252 | Plus | 108716-111112 |
| | 402605 | 9909420 | Minus | 47680-47973 |
| | 404049 | 3688074 | Minus | 75765-78155 |
| | 403549 | 8081591 | Minus | 137150-137362 |
| | 404048 | 3688074 | Minus | 54421-56808 |
| | 404171 | 9930793 | Plus | 173667-173783,176876-177055 |
| 75 | 405649 | 4926908 | Minus | 50032-50132,50624-50764 |
| | 405268 | 4156151 | Minus | 24404-24521 |
| | 405204 | 7230116 | Plus | 126569-126754 |
| | 405517 | 9454624 | Plus | 114757-114877 |
| | 405203 | 7230116 | Plus | 125295-125463 |
| 80 | 405687 | 6249568 | Minus | 54787-54891,55844-55917 |
| | 403966 | 8568881 | Plus | 158193-158277,160116-160290 |
| | 402269 | 3128156 | Minus | 1168-1324,5492-5611,23445-23851 |
| | 404170 | 9930793 | Plus | 168836-169248 |

404030 7671252 Plus 149362-151749
 401001 7229886 Minus 113631-113762
 404820 4678240 Plus 20475-21085

5

TABLE 5A: ABOUT 43 GENES UPREGULATED IN GLIOBLASTOMA THAT ENCODE PREDICTED MEMBRANE PROTEINS

| Pkey: | Unique Eos probeset identifier number | | | | |
|----------------|---|-----------|--|------|------|
| ExAccn: | Exemplar Accession number, Genbank accession number | | | | |
| UnigeneID: | Unigene number | | | | |
| Unigene Title: | Unigene gene title | | | | |
| R1: | Ratio of brain tumor to body atlas | | | | |
| R2: | Ratio of brain tumor to normal brain | | | | |
| Pkey | ExAccn | UnigeneID | Unigene title | R1 | R2 |
| 415817 | U88967 | Hs.78857 | protein tyrosine phosphatase, receptor-1 | 72.0 | 11.3 |
| 447072 | D61594 | Hs.17279 | tyrosylprotein sulfotransferase 1 | 54.2 | 7.1 |
| 451099 | R52795 | Hs.25954 | interleukin 13 receptor, alpha 2 | 22.0 | 7.6 |
| 415910 | U20350 | Hs.78913 | chemokine (C-X3-C) receptor 1 | 21.2 | 3.0 |
| 412986 | X81120 | Hs.75110 | cannabinoid receptor 1 (brain) | 18.6 | 18.6 |
| 417355 | D13168 | Hs.82002 | endothelin receptor type B | 16.4 | 16.4 |
| 419721 | NM_001650 | Hs.288550 | aquaporin 4 | 16.2 | 4.4 |
| 452355 | N54926 | Hs.29202 | G protein-coupled receptor 34 | 13.9 | 13.9 |
| 410227 | AB009284 | Hs.61152 | exostosins (multiple)-like 2 | 11.9 | 2.9 |
| 419723 | AL120193 | Hs.92614 | Homo sapiens growth differentiation factor | 7.4 | 3.5 |
| 414825 | X06370 | Hs.77432 | epidermal growth factor receptor (avian | 6.9 | 6.4 |
| 443898 | AW804296 | Hs.9950 | Sec61 gamma | 4.8 | 7.2 |
| 422033 | AW245805 | Hs.110903 | claudin 5 (transmembrane protein deleted | 4.3 | 6.1 |
| 414821 | M63835 | Hs.77424 | Fc fragment of IgG, high affinity Ia, re | 4.2 | 34.8 |
| 431556 | AF016028 | Hs.260039 | sarcompan (Kras oncogene-associated gene | 4.0 | 3.8 |
| 435869 | AF255910 | Hs.54550 | vascular endothelial junction-associated | 3.7 | 4.2 |
| 440516 | S42303 | Hs.161 | cadherin 2, type 1, N-cadherin (neuronal | 3.5 | 5.1 |
| 428141 | D50402 | Hs.182611 | solute carrier family 11 (proton-coupled | 3.5 | 2.4 |
| 428484 | AF104032 | Hs.184601 | solute carrier family 7 (cationic amino | 3.4 | 2.8 |
| 431053 | S40369 | Hs.249141 | Glutamate receptor subunit | 3.3 | 2.4 |
| 445070 | NM_000677 | Hs.258 | adenosine A3 receptor | 3.2 | 7.6 |
| 430890 | X54232 | Hs.2699 | glypican 1 | 3.2 | 4.3 |
| 423422 | AC005175 | Hs.128425 | NY-REN-24 antigen | 3.1 | 2.6 |
| 413367 | NM_006517 | Hs.75317 | solute carrier family 16 (monocarboxylic | 3.0 | 4.1 |
| 447471 | AF039843 | Hs.18676 | sprouty (Drosophila) homolog 2 | 3.0 | 4.1 |
| 427150 | BE616183 | Hs.173737 | ras-related C3 botulinum toxin substrate | 3.0 | 2.1 |
| 422676 | D28481 | Hs.1570 | histamine receptor H1 | 3.0 | 6.3 |
| 430293 | AI416988 | Hs.238272 | inositol 1,4,5-trisphosphate receptor, ty | 2.8 | 7.4 |
| 453496 | AA442103 | Hs.33084 | solute carrier family 2 (facilitated glu | 2.7 | 3.2 |
| 428281 | AA194554 | Hs.183434 | ATPase, H+ transporting, lysosomal (vacu | 2.4 | 4.4 |
| 417446 | AL118671 | Hs.82163 | monoamine oxidase B | 2.4 | 2.2 |
| 412676 | NM_000165 | Hs.74471 | gap junction protein, alpha 1, 43kD (con | 2.4 | 76.7 |
| 440225 | BE295782 | Hs.159 | tumor necrosis factor receptor superfam | 2.3 | 2.3 |
| 450447 | AF212223 | Hs.25010 | hypothetical protein P15-2 | 2.3 | 4.1 |
| 410310 | J02931 | Hs.62192 | coagulation factor III (thromboplastin, | 2.3 | 2.4 |
| 452036 | NM_003966 | Hs.27621 | sema domain, seven thrombospondin repeat | 2.3 | 3.0 |
| 447217 | BE465754 | Hs.17778 | neuropilin 2 | 2.1 | 3.0 |
| 447023 | AA356764 | Hs.17109 | integral membrane protein 2A | 2.1 | 4.9 |
| 422070 | AF149785 | Hs.111126 | pituitary tumor-transforming 1 interacti | 2.1 | 15.2 |
| 456804 | AI421645 | Hs.139851 | caveolin 2 | 2.1 | 2.3 |
| 430057 | AW450303 | Hs.2534 | bone morphogenetic protein receptor, typ | 2.0 | 3.7 |
| 422163 | AF027208 | Hs.297332 | Homo sapiens cDNA: FLJ21471 fis, clone C | 2.0 | 2.4 |
| 414482 | S57498 | Hs.76252 | endothelin receptor type A | | |

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TABLE 6A: ABOUT 397 GENES DOWNREGULATED IN GLIOBLASTOMA

| Pkey: | Unique Eos probeset identifier number | | | | |
|----------------|---|--|--|--|--|
| ExAccn: | Exemplar Accession number, Genbank accession number | | | | |
| UnigeneID: | Unigene number | | | | |
| Unigene Title: | Unigene gene title | | | | |
| R1: | Ratio of normal brain to body atlas | | | | |
| R2: | Ratio of normal brain to brain tumor | | | | |

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| Pkey | Ex Accn | UnigeneID | Title | R1 | R2 |
|--------|------------|-----------|--|-------|-------|
| 439340 | AB032436 | Hs.6535 | brain-specific Na-dependent inorganic ph | 4.47 | 77.82 |
| 424846 | AU077324 | Hs.1832 | neuropeptide Y | 4.49 | 55.32 |
| 428874 | W32133 | Hs.194366 | transferrin (prealbumin, amyloidosis I | 7.06 | 45.64 |
| 416836 | D54745 | Hs.80247 | cholecystokinin | 9.45 | 44.59 |
| 401412 | c14p3_2958 | | exon | 3.20 | 32.56 |
| 451835 | T63543 | Hs.209715 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 3.21 | 28.93 |
| 412768 | AW996044 | Hs.26239 | ESTs | 3.16 | 28.12 |
| 415448 | T68645 | Hs.952 | solute carrier family 10 (sodium/bile ac | 3.27 | 27.04 |
| 411305 | BE241596 | Hs.69547 | myelin basic protein | 13.80 | 25.92 |
| 438054 | AA776626 | Hs.62183 | ESTs | 3.59 | 25.06 |
| 410837 | BE145698 | | gb:LLQ-HT0205-231199-145-a07 HT0205 Homo | 3.05 | 24.43 |
| 425121 | AI797511 | Hs.154679 | synaptotagmin 1 | 6.92 | 23.67 |
| 456763 | AJ271351 | Hs.128180 | B-cell translocation gene 4 | 3.29 | 23.32 |
| 429656 | X05608 | Hs.211584 | neurofilament, light polypeptide (68kD) | 8.03 | 22.56 |
| 451892 | AI821302 | Hs.167834 | ESTs | 4.12 | 21.82 |

| | | | | | | |
|----|--------|------------|-----------|---|------|-------|
| 5 | 424922 | BE386547 | Hs.217112 | ESTs, Weakly similar to Similarity to Ye | 4.41 | 21.28 |
| | 411666 | AF106564 | Hs.71346 | neurofilament 3 (150kD medium) | 5.27 | 21.20 |
| | 432247 | AA531287 | Hs.105805 | ESTs | 3.25 | 21.14 |
| | 436812 | AW298067 | | gb:U1-H-BWD-ajp-g-09-0-UI.s1 NCI_CGAP_Su | 3.02 | 21.12 |
| | 422234 | AF119818 | Hs.113287 | discs, large (Drosophila) homolog-associ | 3.38 | 20.50 |
| 10 | 435708 | AI362949 | Hs.75169 | ESTs | 8.79 | 20.45 |
| | 423135 | N67655 | Hs.26411 | ESTs | 6.82 | 20.28 |
| | 440600 | AI807691 | Hs.126351 | ESTs | 3.56 | 20.09 |
| | 405230 | cNp1_7656 | | exon | 3.31 | 19.95 |
| | 456915 | N55540 | Hs.78026 | ESTs, Weakly similar to similar to ankyr | 3.14 | 19.40 |
| 15 | 425130 | AA448208 | Hs.99163 | ESTs | 3.53 | 19.20 |
| | 416812 | H91010 | Hs.44940 | ESTs | 3.54 | 19.08 |
| | 454171 | AW854832 | | gb:QV2-CT0261-201099-011-f05 CT0261 Homo | 3.78 | 19.04 |
| | 457463 | AW877031 | Hs.272321 | Homo sapiens cDNA FLJ12571 fis, clone NT | 3.13 | 18.91 |
| | 454589 | AW809699 | | gb:MR4-ST0124-241199-026-e12 ST0124 Homo | 4.10 | 18.60 |
| 20 | 418104 | T05726 | Hs.177130 | ESTs | 3.17 | 18.41 |
| | 416357 | T82050 | Hs.268907 | ESTs | 3.11 | 18.13 |
| | 414683 | S78296 | Hs.76888 | interneuron neuronal intermediate filamen | 5.55 | 18.13 |
| | 447694 | AI420083 | Hs.170303 | ESTs | 3.56 | 17.79 |
| | 427627 | R87582 | Hs.179915 | guanine nucleotide binding protein (G pr | 4.63 | 17.65 |
| 25 | 428010 | AA806554 | Hs.185375 | ESTs | 3.03 | 17.40 |
| | 417159 | R01761 | | gb:ye81f10.s1 Soares fetal liver spleen | 3.23 | 17.38 |
| | 436788 | AA766908 | Hs.259047 | ESTs | 3.16 | 17.21 |
| | 459349 | AW749381 | | gb:QV3-BT0381-170100-060-c02 BT0381 Homo | 3.26 | 17.10 |
| | 450214 | BE439763 | Hs.227571 | regulator of G-protein signalling 4 | 3.86 | 17.04 |
| 30 | 438068 | AI927209 | Hs.283089 | HMT1 (hnRNP methyltransferase, S. cerevi | 3.54 | 16.48 |
| | 437268 | AI754847 | Hs.227571 | regulator of G-protein signalling 4 | 5.63 | 16.92 |
| | 435315 | AA700240 | Hs.165402 | ESTs | 4.06 | 16.12 |
| | 424240 | AB023185 | Hs.143535 | calcium/calmodulin-dependent protein kin | 4.69 | 15.92 |
| | 412446 | AI768015 | Hs.92127 | ESTs | 5.44 | 15.75 |
| 35 | 449714 | AB033015 | Hs.23941 | KIAA1189 protein | 4.59 | 15.43 |
| | 435832 | AA425688 | Hs.41641 | Bruno (Drosophila) -like 4, RNA binding | 4.63 | 14.97 |
| | 437397 | AA349847 | Hs.4221 | hypothetical protein DKFZp761H039 | 5.93 | 14.81 |
| | 435502 | L13266 | Hs.105 | glutamate receptor, ionotropic, N-methyl | 3.29 | 14.61 |
| | 414187 | BE312141 | | gb:601145962F1 NIH_MGC_19 Homo sapiens c | 3.37 | 14.46 |
| 40 | 417868 | AI078534 | Hs.122592 | ESTs | 7.57 | 14.22 |
| | 428536 | AI143139 | Hs.2288 | visinin-like 1 | 5.16 | 13.98 |
| | 402125 | c18p3_155 | | exon | 3.11 | 13.94 |
| | 440503 | NM_006539 | Hs.7235 | calcium channel, voltage-dependent, gamma | 3.49 | 13.92 |
| | 419090 | T85201 | Hs.188468 | ESTs | 3.25 | 13.79 |
| 45 | 437665 | AA765417 | Hs.292053 | ESTs | 3.07 | 13.79 |
| | 457113 | AI734016 | Hs.270508 | ESTs | 3.50 | 13.69 |
| | 424933 | AW999974 | Hs.5181 | proliferation-associated 2G4, 38kD | 3.59 | 13.48 |
| | 443489 | AI073512 | Hs.133916 | ESTs | 3.24 | 13.20 |
| | 404289 | c6p3_5821 | | exon | 3.99 | 13.12 |
| 50 | 406534 | ph2_4616 | | exon | 3.89 | 13.10 |
| | 423280 | AA324037 | | gb:EST26901 Cerebellum II Homo sapiens c | 3.38 | 13.03 |
| | 455421 | AW937661 | Hs.288324 | Homo sapiens cDNA FLJ13283 fis, clone OV | 3.04 | 12.93 |
| | 433725 | AF063559 | Hs.283919 | Homo sapiens clone HQ0117 PRO0117 mRNA, | 3.71 | 12.85 |
| | 416660 | R98905 | Hs.35992 | ESTs | 3.92 | 12.74 |
| 55 | 407593 | AW044083 | Hs.237008 | ESTs | 3.85 | 12.67 |
| | 451734 | NM_006176 | Hs.26944 | neurogranin (protein kinase C substrate, | 7.41 | 12.59 |
| | 410366 | AI267589 | Hs.25214 | hypothetical protein | 7.89 | 12.50 |
| | 405348 | cNp3_13716 | | exon | 3.45 | 12.42 |
| | 442338 | AI761976 | Hs.156080 | ESTs | 3.69 | 12.35 |
| 60 | 424458 | M29273 | Hs.1780 | myelin associated glycoprotein | 4.72 | 12.31 |
| | 431400 | AA504607 | | gb:aa63a02.s1 NCI_CGAP_GCB1 Homo sapiens | 3.42 | 12.29 |
| | 417754 | R13027 | Hs.268703 | ESTs | 3.35 | 12.18 |
| | 440184 | AB002297 | Hs.7022 | dedicator of cyto-kinesis 3 | 6.15 | 12.11 |
| | 431339 | AA506294 | Hs.257266 | ESTs | 3.50 | 11.97 |
| 65 | 452265 | BE501516 | Hs.114772 | ESTs | 3.82 | 11.96 |
| | 419297 | AA446040 | Hs.98640 | Homo sapiens cDNA: FLJ21069 fis, clone C | 3.16 | 11.86 |
| | 424991 | AA775471 | Hs.241467 | ESTs | 3.03 | 11.64 |
| | 431988 | AC002302 | Hs.77202 | protein kinase C, beta 1 | 3.78 | 11.62 |
| | 450987 | AA017202 | Hs.32794 | ESTs | 3.28 | 11.61 |
| 70 | 440607 | AA894559 | Hs.192097 | ESTs | 3.11 | 11.60 |
| | 454566 | AW807605 | | gb:MR4-ST0098-120100-001-b06 ST0098 Homo | 3.26 | 11.54 |
| | 442000 | H38671 | Hs.8071 | KIAA0735 gene product; synaptic vesicle | 3.44 | 11.51 |
| | 437948 | AA772920 | | gb:ae73c09.s1 Stratagene schizo brain S1 | 3.16 | 11.46 |
| | 401081 | c11p3_921 | | exon | 3.18 | 11.35 |
| 75 | 438919 | AW979114 | | gb:EST391224 MAGE resequences, MAGP Homo | 4.16 | 11.35 |
| | 454578 | AW809178 | | gb:MR4-ST0118-261099-012-c07 ST0118 Homo | 3.02 | 11.27 |
| | 422279 | H69644 | Hs.114231 | C-type lectin-like receptor-2 | 3.35 | 11.13 |
| | 453101 | AW952776 | Hs.94943 | ESTs | 3.21 | 11.07 |
| | 455836 | BE145795 | | gb:MR0-HT0208-101299-103-a12 HT0208 Homo | 3.61 | 10.83 |
| 80 | 413324 | V00571 | Hs.75294 | corticotropin releasing hormone | 3.72 | 10.71 |
| | 412266 | N59006 | Hs.26133 | ESTs | 3.80 | 10.60 |
| | 436887 | AW953157 | Hs.193235 | ESTs | 7.24 | 10.56 |
| | 454968 | AW849046 | | gb:IL3-CT0214-150300-085-H06 CT0214 Homo | 3.05 | 10.53 |
| | 418162 | T11958 | | gb:A802R Heart Homo sapiens cDNA clone A | 3.07 | 10.50 |
| | 425537 | AB007913 | Hs.158291 | KIAA0444 protein | 3.07 | 10.46 |
| | 436230 | AI248723 | Hs.17711 | ESTs | 3.09 | 10.45 |
| | 431169 | AW971240 | | gb:EST383329 MAGE resequences, MAGL Homo | 3.02 | 10.43 |

| | | | | | | |
|----|--------|------------|-----------|---|------|-------|
| | 447359 | NM_012093 | Hs.18268 | adenylate kinase 5 | 5.91 | 10.40 |
| | 457187 | AA443927 | Hs.144360 | EST | 3.30 | 10.39 |
| | 407539 | X91103 | | gb:H.sapiens mRNA for Hs44 protein. | 3.02 | 10.35 |
| 5 | 452855 | R17746 | Hs.84469 | ESTs | 3.02 | 10.26 |
| | 440352 | AI692322 | Hs.65373 | ESTs | 3.03 | 10.20 |
| | 456116 | Z28528 | Hs.172004 | titin | 3.11 | 10.17 |
| | 458172 | BE007237 | | gb:PMO-BN0139-050500-003-g09 BN0139 Homo | 3.32 | 10.14 |
| | 445881 | AI263029 | Hs.210689 | ESTs | 3.04 | 10.11 |
| 10 | 454059 | NM_003154 | Hs.37048 | statherin | 3.27 | 9.97 |
| | 402624 | c1p1_2660 | | exon | 3.05 | 9.94 |
| | 441539 | AA937200 | Hs.192939 | ESTs | 3.27 | 9.82 |
| | 412172 | N76794 | | gb:yv45g07.r1 Soares fetal liver spleen | 3.03 | 9.78 |
| | 427942 | AA417856 | | gb:zv01d05.r1 NCI_CGAP_GCB1 Homo sapiens | 4.09 | 9.73 |
| 15 | 438867 | BE041837 | Hs.120316 | ESTs | 3.25 | 9.73 |
| | 454688 | AW814472 | | gb:MR3-ST0203-010200-109-b06 ST0203 Homo | 3.41 | 9.73 |
| | 446122 | AI362790 | Hs.181801 | ESTs | 3.40 | 9.71 |
| | 420480 | AL137361 | Hs.98173 | hypothetical protein | 3.03 | 9.56 |
| | 433447 | U29195 | Hs.3281 | neuronal pentraxin II | 3.72 | 9.54 |
| 20 | 407178 | AA195651 | Hs.104106 | ESTs | 3.89 | 9.47 |
| | 415614 | F12926 | Hs.165998 | DKFZP564M2423 protein | 3.06 | 9.45 |
| | 450518 | BE245175 | Hs.270893 | ESTs | 3.99 | 9.39 |
| | 455675 | BE065984 | | gb:RC3-BT0319-120200-014-a06 BT0319 Homo | 3.46 | 9.32 |
| | 456459 | AA253074 | Hs.146261 | ESTs | 4.08 | 9.30 |
| 25 | 423420 | AI571364 | Hs.128382 | Homo sapiens mRNA; cDNA DKFZp76111224 (f | 5.18 | 9.23 |
| | 455644 | BE064521 | | gb:RC4-BT0311-250200-014-d02 BT0311 Homo | 3.02 | 9.20 |
| | 419800 | AA282392 | Hs.191525 | ESTs | 3.28 | 9.16 |
| | 430964 | Y10929 | Hs.248167 | zinc finger protein 186 (Kruppel type) | 3.04 | 9.00 |
| | 409716 | AL117454 | Hs.56027 | Homo sapiens mRNA; cDNA DKFZp586J1717 (f | 3.02 | 9.00 |
| 30 | 412962 | AW839578 | Hs.18160 | Homo sapiens cDNA FLJ11550 fis, clone HE | 3.33 | 8.99 |
| | 445040 | AW444934 | Hs.195929 | ESTs, Weakly similar to pre-serum amyloid | 3.50 | 8.96 |
| | 451496 | AW503407 | | gb:UL-HF-BN0-akw-d-11-0-UL.r1 NIH_MGC_50 | 3.17 | 8.94 |
| | 424617 | AA344151 | | gb:EST50059 Gall bladder I Homo sapiens | 3.25 | 8.91 |
| | 441914 | AA971496 | Hs.128465 | ESTs | 3.42 | 8.88 |
| 35 | 405320 | cNp3_12168 | | exon | 3.30 | 8.84 |
| | 449179 | AI633785 | Hs.196561 | ESTs | 3.43 | 8.84 |
| | 400335 | Y13187 | Hs.248066 | Homo sapiens dmd gene, intron 11 | 3.13 | 8.78 |
| | 454962 | AW847645 | | gb:IL3-CT0213-280100-055-A04 CT0213 Homo | 4.16 | 8.74 |
| | 407803 | AW081681 | Hs.269064 | ESTs | 3.09 | 8.73 |
| 40 | 455260 | AW878317 | | gb:MR3-OT0007-260300-206-e09 OT0007 Homo | 3.78 | 8.70 |
| | 431096 | AA324358 | Hs.249227 | Homo sapiens DNA, cosmid clones TN62 and | 4.01 | 8.67 |
| | 424481 | R19453 | Hs.1787 | proteolipid protein (Pelizaeus-Merzbache | 8.12 | 8.63 |
| | 407616 | AW054849 | Hs.245831 | ESTs, Weakly similar to CIKG_HUMAN VOLTA | 3.08 | 8.53 |
| | 434589 | AF147363 | | gb:Homo sapiens full length insert cDNA | 3.26 | 8.51 |
| 45 | 439239 | AI031540 | Hs.235331 | ESTs | 5.78 | 8.48 |
| | 410926 | AW810708 | | gb:MR2-ST0129-051099-007-g07 ST0129 Homo | 3.34 | 8.47 |
| | 430004 | U27768 | Hs.227571 | regulator of G-protein signalling 4 | 4.26 | 8.45 |
| | 409623 | AW449185 | | gb:UL-H-BI3-akg-e-05-0-UL.s1 NCI_CGAP_Su | 3.32 | 8.43 |
| | 420156 | AW449258 | Hs.6187 | ESTs | 3.40 | 8.38 |
| 50 | 411555 | AF113537 | Hs.70669 | HMP19 protein | 5.85 | 8.34 |
| | 408509 | AA497035 | Hs.110502 | ESTs | 3.17 | 8.34 |
| | 442368 | AI698577 | Hs.202481 | ESTs | 3.02 | 8.33 |
| | 457870 | AA732217 | Hs.294054 | ESTs | 3.04 | 8.32 |
| | 437254 | AA831258 | | gb:oc73f04.s1 NCI_CGAP_GCB1 Homo sapiens | 3.35 | 8.24 |
| 55 | 415508 | R39236 | | gb:yc91d03.s1 Soares infant brain 1NIB H | 3.07 | 8.22 |
| | 409483 | U49379 | Hs.54506 | diacylglycerol kinase, epsilon (64kD) | 3.31 | 8.20 |
| | 435229 | AA676556 | Hs.269515 | ESTs, Moderately similar to ALUB_HUMAN ! | 3.21 | 8.19 |
| | 458120 | W21398 | Hs.54523 | ESTs, Weakly similar to cytochrome P-450 | 3.22 | 8.17 |
| | 444613 | H29627 | Hs.79092 | ESTs | 3.78 | 8.16 |
| 60 | 417050 | N39540 | Hs.108029 | ESTs | 4.06 | 8.14 |
| | 425607 | U09860 | Hs.158333 | protease, serine, 7 (enterokinase) | 3.68 | 8.06 |
| | 413263 | BE075131 | | gb:PM1-BT0585-110200-003-g03 BT0585 Homo | 3.40 | 8.04 |
| | 424549 | AI873205 | Hs.183114 | Homo sapiens cDNA FLJ14236 fis, clone NT | 3.27 | 8.03 |
| | 452689 | F33868 | Hs.284176 | transferrin | 3.03 | 8.01 |
| 65 | 405476 | cNp3_19940 | | exon | 3.28 | 8.00 |
| | 403932 | cSp1_533 | | exon | 3.58 | 7.99 |
| | 407095 | AF011757 | Hs.105937 | RAGE binding protein | 3.32 | 7.96 |
| | 415967 | H11124 | | gb:ym14h07.s1 Soares infant brain 1NIB H | 3.10 | 7.96 |
| | 417555 | H65366 | | gb:yr67c10.r1 Soares fetal liver spleen | 3.05 | 7.95 |
| 70 | 448985 | AA324885 | Hs.22777 | carbonic anhydrase XI | 5.30 | 7.79 |
| | 428689 | NM_014351 | Hs.189810 | sulfotransferase-related protein | 3.87 | 7.74 |
| | 424140 | Z48051 | Hs.141308 | myelin oligodendrocyte glycoprotein | 4.68 | 7.74 |
| | 441099 | AW339393 | Hs.126573 | ESTs | 3.08 | 7.74 |
| | 448589 | AFD17090 | Hs.21554 | KIAA1107 protein | 3.10 | 7.73 |
| 75 | 406112 | ph0_24243 | | exon | 3.22 | 7.70 |
| | 458439 | AV647220 | Hs.282889 | ESTs, Weakly similar to strong similarit | 3.22 | 7.69 |
| | 429859 | NM_007050 | Hs.225952 | protein tyrosine phosphatase, receptor I | 3.15 | 7.68 |
| | 412090 | AW955826 | Hs.12396 | ESTs, Weakly similar to ALU6_HUMAN ALU S | 3.01 | 7.67 |
| | 413547 | BE147440 | | gb:RC1-HT0229-080100-015-f09 HT0229 Homo | 3.01 | 7.66 |
| 80 | 447772 | AI924558 | Hs.161399 | ESTs | 3.04 | 7.63 |
| | 411132 | AW819191 | | gb:CM1-ST0283-071299-061-d08 ST0283 Homo | 3.72 | 7.61 |
| | 425490 | NM_002248 | Hs.158173 | potassium intermediate/small conductance | 3.15 | 7.60 |
| | 454568 | BE141434 | | gb:MRO-HT0079-051099-002-d01 HT0079 Homo | 3.16 | 7.59 |
| | 439099 | AB037800 | Hs.6462 | KIAA1379 protein | 3.40 | 7.57 |

| | | | | | | |
|----|--------|------------|-----------|---|------|------|
| | 415669 | NM_005025 | Hs.78589 | serine (or cysteine) proteinase inhibitor | 5.71 | 7.57 |
| | 428175 | AJ810774 | Hs.98376 | ESTs | 3.04 | 7.55 |
| | 413162 | BE068115 | | gb:CM1-BT0368-061299-060-g07 BT0368 Homo | 3.43 | 7.54 |
| 5 | 451361 | AA053854 | Hs.235390 | Homo sapiens mRNA; cDNA DKFZp761B101 (fr | 3.11 | 7.53 |
| | 442527 | AF150289 | Hs.205436 | ESTs | 3.31 | 7.53 |
| | 450407 | NM_000810 | Hs.24969 | gamma-aminobutyric acid (GABA) A recepto | 5.24 | 7.53 |
| | 456966 | AI589569 | Hs.190082 | ESTs | 3.13 | 7.47 |
| | 441799 | AW292276 | Hs.127872 | ESTs | 3.38 | 7.41 |
| 10 | 424185 | AA279752 | Hs.142570 | Homo sapiens clone 24629 mRNA sequence | 3.16 | 7.40 |
| | 429783 | AA811987 | Hs.125779 | ESTs | 3.13 | 7.38 |
| | 429268 | AA205386 | Hs.198481 | RAR-related orphan receptor B | 3.48 | 7.38 |
| | 400708 | c11p1_1292 | | exon | 3.33 | 7.35 |
| | 402598 | BE314624 | Hs.3128 | polymerase (RNA) II (DNA directed) polyp | 3.04 | 7.33 |
| 15 | 455377 | AW905347 | | gb:QV2-NN1073-220400-159-f06 NN1073 Homo | 3.03 | 7.33 |
| | 435070 | AI821270 | Hs.116930 | ESTs | 3.03 | 7.33 |
| | 405427 | cNp3_17682 | | exon | 3.03 | 7.25 |
| | 455149 | AW861879 | | gb:CM0-CT0341-260100-160-h12 CT0341 Homo | 3.56 | 7.24 |
| | 402816 | c1p3_2531 | | exon | 3.13 | 7.21 |
| 20 | 422890 | Z43784 | Hs.78713 | solute carrier family 25 (mitochondrial | 3.40 | 7.15 |
| | 422297 | AW961290 | Hs.155615 | ESTs | 3.44 | 7.10 |
| | 412686 | AW984068 | | gb:RC0-HN0006-160300-011-e06 HN0006 Homo | 3.91 | 7.09 |
| | 436383 | BE065178 | | gb:RC1-BT0314-020200-012-h01 BT0314 Homo | 3.09 | 7.09 |
| | 412290 | BE069037 | | gb:QV3-BT0379-161299-040-e12 BT0379 Homo | 3.04 | 7.08 |
| 25 | 415486 | H12214 | Hs.13284 | ESTs | 4.22 | 7.07 |
| | 407728 | AW071502 | Hs.175931 | ESTs | 3.05 | 7.06 |
| | 448548 | R13209 | Hs.21413 | solute carrier family 12, (potassium-chl | 5.93 | 7.05 |
| | 417275 | X63578 | Hs.81849 | parvalbumin | 4.08 | 7.04 |
| | 418425 | AI871247 | Hs.6262 | ESTs | 4.10 | 7.04 |
| 30 | 440558 | AA889574 | Hs.177511 | ESTs | 3.28 | 7.04 |
| | 411427 | AW846080 | | gb:MR3-CT0176-081099-002-b09 CT0176 Homo | 3.11 | 7.03 |
| | 422272 | AI452421 | Hs.77965 | Clk-associating RS-cyclophilin | 3.39 | 7.03 |
| | 410816 | AW806175 | | gb:MR1-UM0108-130400-003-a06 UM0108 Homo | 3.30 | 7.02 |
| | 418375 | NM_003081 | Hs.84389 | synaposomal-associated protein, 25kD | 9.93 | 7.01 |
| 35 | 421627 | AI138551 | Hs.97318 | ESTs | 3.10 | 7.01 |
| | 447258 | BE047911 | | gb:tz44a05.y1 NCL_CGAP_Bm52 Homo sapien | 3.09 | 6.99 |
| | 455547 | AW994078 | | gb:RC3-BN0036-090200-011-h02 BN0036 Homo | 3.35 | 6.98 |
| | 432209 | AW971278 | | gb:EST383367 MAGE resequences, MAGL Homo | 3.49 | 6.92 |
| | 404541 | c8p1_6409 | | exon | 4.62 | 6.89 |
| 40 | 451539 | AA059467 | Hs.218933 | ESTs | 3.01 | 6.88 |
| | 429954 | AI918130 | Hs.21374 | ESTs | 3.82 | 6.87 |
| | 411138 | AW819500 | | gb:RC5-ST0293-180100-012-c07 ST0293 Homo | 3.08 | 6.87 |
| | 447464 | AW444957 | Hs.201897 | ESTs, Weakly similar to ALU4_HUMAN ALU S | 3.33 | 6.85 |
| | 454713 | AW815111 | | gb:QV4-ST0212-091199-023-c09 ST0212 Homo | 3.16 | 6.84 |
| 45 | 415734 | NM_014747 | Hs.78748 | KIAA0237 gene product | 5.00 | 6.84 |
| | 429667 | AA456275 | Hs.44841 | ESTs | 3.09 | 6.80 |
| | 403008 | c21p3_2374 | | exon | 3.04 | 6.78 |
| | 446079 | T56522 | Hs.154030 | ESTs | 3.11 | 6.75 |
| | 441869 | NM_003947 | Hs.8004 | huntingtin-associated protein interacti | 4.49 | 6.75 |
| 50 | 437804 | AA828257 | Hs.124324 | ESTs | 3.42 | 6.73 |
| | 436454 | AA757615 | Hs.291509 | ESTs | 3.01 | 6.72 |
| | 416334 | H53139 | Hs.36271 | ESTs | 3.12 | 6.70 |
| | 455955 | BE167014 | | gb:CM2-HT0502-140200-088-d08 HT0502 Homo | 3.05 | 6.68 |
| | 445085 | AI569295 | Hs.179285 | ESTs | 3.19 | 6.68 |
| 55 | 445611 | AW418497 | Hs.145583 | ESTs | 3.61 | 6.68 |
| | 437762 | T78028 | Hs.154679 | synaptotagmin 1 | 7.21 | 6.68 |
| | 416268 | H49111 | | gb:yo21c07.r1 Soares adult brain N2b5HB5 | 3.02 | 6.67 |
| | 449766 | AI668690 | Hs.54773 | ESTs | 3.25 | 6.64 |
| | 443100 | AI033188 | | gb:ow94e08.s1 Soares_fetal_liver_spleen_ | 3.07 | 6.64 |
| 60 | 408070 | AW148852 | | gb:xf05d05.x1 NCL_CGAP_Bm35 Homo sapien | 3.12 | 6.60 |
| | 451602 | AW008846 | Hs.60857 | ESTs | 3.05 | 6.59 |
| | 441447 | AA934077 | Hs.126980 | ESTs | 4.06 | 6.59 |
| | 445078 | AI869975 | Hs.4775 | junctional protein 3 | 4.25 | 6.59 |
| | 434501 | AF143878 | Hs.194152 | Homo sapiens clone IMAGE:115304 mRNA seq | 3.25 | 6.58 |
| 65 | 415960 | R49020 | Hs.24974 | ESTs | 3.34 | 6.59 |
| | 403395 | c3p1_11541 | | exon | 3.59 | 6.57 |
| | 403061 | c2p1_10450 | | exon | 3.06 | 6.56 |
| | 419232 | AI382037 | Hs.87421 | ESTs | 3.28 | 6.56 |
| | 425984 | AW836277 | Hs.165636 | hypothetical protein DKFZp761C07121 | 6.50 | 6.56 |
| 70 | 403717 | c4p1_3133 | | exon | 3.52 | 6.53 |
| | 452178 | AW043576 | Hs.171929 | ESTs | 3.38 | 6.53 |
| | 455758 | R15709 | Hs.284231 | Novel human gene mapping to chromosome 22 | 4.42 | 6.52 |
| | 433858 | N69243 | Hs.192974 | Homo sapiens cDNA FLJ12735 fs, clone NT | 3.58 | 6.52 |
| | 425440 | AA357518 | | gb:EST66256 LNCAP cells 1 Homo sapiens c | 3.15 | 6.49 |
| 75 | 419412 | AW161058 | Hs.90297 | synuclein, beta | 5.60 | 6.47 |
| | 423678 | AW963357 | Hs.7847 | ESTs | 3.47 | 6.47 |
| | 416625 | R97839 | Hs.35758 | ESTs | 3.10 | 6.46 |
| | 451854 | T92536 | Hs.194096 | ESTs | 3.28 | 6.46 |
| | 406732 | AA487229 | Hs.2064 | vimentin | 3.71 | 6.44 |
| | 434619 | H43163 | Hs.32810 | ESTs | 3.05 | 6.44 |
| 80 | 413797 | BE167274 | Hs.5996 | ESTs | 3.23 | 6.44 |
| | 438612 | AW977980 | Hs.292129 | ESTs | 3.39 | 6.42 |
| | 412317 | AW991979 | | gb:RC1-BN0014-210100-012-f05 BN0014 Homo | 3.46 | 6.42 |
| | 422159 | N76767 | Hs.153406 | ESTs | 3.03 | 6.41 |

| | | | | | | |
|----|--------|------------|-----------|--|------|------|
| | 429290 | AF203032 | Hs.198760 | neurofilament, heavy polypeptide (200kD) | 3.46 | 6.35 |
| | 427334 | R44789 | Hs.119486 | ESTs, Weakly similar to transmembrane re | 3.93 | 6.35 |
| | 453839 | AL138417 | | gb:DKFZp434B1729_r1 434 (synonym: htes3) | 3.06 | 6.34 |
| 5 | 429096 | AB011106 | Hs.196012 | KIAA0534 protein | 3.12 | 6.33 |
| | 444609 | AW571659 | Hs.278081 | ESTs | 3.30 | 6.33 |
| | 419515 | S81944 | Hs.90791 | gamma-aminobutyric acid (GABA) A recepto | 3.11 | 6.33 |
| | 418900 | BE207357 | Hs.301709 | ESTs | 3.14 | 6.30 |
| | 437979 | AA774318 | Hs.121708 | ESTs | 3.25 | 6.29 |
| 10 | 410359 | R38624 | Hs.106313 | ESTs | 4.74 | 6.28 |
| | 415990 | R76929 | Hs.29633 | ESTs | 3.39 | 6.28 |
| | 419392 | W28573 | | gb:51f10 Human retina cDNA randomly prim | 3.00 | 6.28 |
| | 424312 | AB013452 | Hs.144931 | ATPase, aminophospholipid transporter (A | 3.06 | 6.26 |
| | 444762 | AI733700 | Hs.143883 | ESTs | 3.09 | 6.25 |
| 15 | 447785 | AL041765 | Hs.161423 | ESTs | 3.05 | 6.22 |
| | 418199 | AA884555 | Hs.86603 | ESTs | 3.55 | 6.22 |
| | 440582 | AA993337 | Hs.129082 | ESTs | 3.73 | 6.21 |
| | 457766 | AL119470 | Hs.145631 | ESTs | 3.69 | 6.21 |
| | 426814 | AF036943 | Hs.172619 | KIAA1106 protein | 4.71 | 6.21 |
| 20 | 412018 | BE148152 | | gb:RC4-HT0231-041199-012-b04 HT0231 Homo | 3.36 | 6.21 |
| | 414699 | AI815523 | Hs.76930 | synuclein, alpha (non A4 component of am | 3.68 | 6.19 |
| | 420127 | AA360399 | Hs.44811 | ESTs | 3.54 | 6.18 |
| | 418833 | AW974899 | Hs.292776 | ESTs | 3.08 | 6.18 |
| | 441265 | AA927180 | Hs.153261 | ESTs | 3.21 | 6.17 |
| 25 | 413408 | R51793 | Hs.21745 | ESTs | 3.56 | 6.15 |
| | 434512 | AW139932 | Hs.188941 | ESTs | 3.56 | 6.15 |
| | 422253 | W81526 | Hs.118329 | ESTs | 5.04 | 6.10 |
| | 439950 | AW937417 | Hs.293561 | ESTs | 3.24 | 6.10 |
| | 417210 | N99228 | Hs.49162 | ESTs | 3.54 | 6.10 |
| 30 | 414306 | BE272198 | Hs.283869 | Human DNA sequence from clone RP5-1013A2 | 3.35 | 6.10 |
| | 411265 | AW834695 | | gb:RC0-LT0001-261199-031-D05 LT0001 Homo | 3.07 | 6.10 |
| | 412734 | AW993498 | | gb:RC2-BN0033-170300-019-b08 BN0033 Homo | 3.36 | 6.09 |
| | 425172 | AA447729 | Hs.12714 | ESTs | 5.40 | 6.06 |
| | 451759 | W23161 | Hs.32886 | ESTs | 3.21 | 6.02 |
| 35 | 432154 | AI701523 | Hs.112577 | ESTs | 3.50 | 6.02 |
| | 401313 | c13p1_435 | | exon | 3.92 | 5.96 |
| | 446951 | AI350575 | Hs.156730 | ESTs | 3.20 | 5.95 |
| | 440917 | AA909651 | Hs.160025 | ESTs | 3.06 | 5.94 |
| | 405961 | ph0_14521 | | exon | 3.12 | 5.91 |
| 40 | 428737 | AA984728 | Hs.192760 | kinesin family member 5A | 3.05 | 5.90 |
| | 417292 | N69197 | Hs.191361 | ESTs | 3.62 | 5.89 |
| | 448681 | AL109781 | Hs.21754 | Homo sapiens mRNA full length insert cDN | 3.52 | 5.88 |
| | 452524 | AW136499 | Hs.29796 | Homo sapiens mRNA; cDNA DKFZp434D1319 (f | 3.07 | 5.88 |
| | 426575 | M74826 | Hs.170808 | glutamate decarboxylase 2 (pancreatic is | 4.08 | 5.87 |
| 45 | 423641 | AL137256 | Hs.130489 | Homo sapiens mRNA; cDNA DKFZp761K0912 (f | 3.28 | 5.87 |
| | 420755 | AI699437 | Hs.165268 | ESTs | 3.17 | 5.86 |
| | 448116 | AW352276 | Hs.170700 | ESTs | 3.28 | 5.86 |
| | 412694 | AW984373 | | gb:PM3-HN0011-200300-001-f01 HN0011 Homo | 3.00 | 5.83 |
| | 437612 | AA827715 | Hs.105153 | Homo sapiens cDNA FLJ14230 fis, clone NT | 3.09 | 5.82 |
| 50 | 411522 | AW850286 | | gb:IL3-CT0219-161199-031-H11 CT0219 Homo | 3.26 | 5.81 |
| | 456910 | BE185921 | Hs.98073 | ESTs | 3.20 | 5.80 |
| | 439915 | AI521791 | Hs.252358 | ESTs | 3.55 | 5.80 |
| | 404403 | c8p1_1094 | | exon | 3.23 | 5.80 |
| | 405332 | cNp3_13017 | | exon | 3.51 | 5.78 |
| 55 | 411167 | AW820204 | | gb:QV2-ST0296-190100-029-c11 ST0296 Homo | 3.04 | 5.78 |
| | 416139 | H21109 | Hs.172853 | ESTs | 3.63 | 5.77 |
| | 434222 | AF119886 | Hs.283941 | Homo sapiens PRO2591 mRNA, complete cds | 3.65 | 5.77 |
| | 415247 | F02431 | Hs.6581 | ESTs | 3.08 | 5.75 |
| | 446037 | AI076806 | Hs.282965 | ESTs | 3.42 | 5.75 |
| 60 | 450478 | AW451709 | Hs.271200 | ESTs | 3.80 | 5.72 |
| | 446588 | AV659343 | Hs.282954 | ESTs | 3.29 | 5.72 |
| | 413118 | BE065939 | | gb:RC3-BT0319-100100-012-c11 BT0319 Homo | 3.03 | 5.72 |
| | 416946 | NM_012324 | Hs.80545 | mitogen-activated protein kinase 8 inter | 3.91 | 5.72 |
| | 454751 | AW819132 | | gb:RC3-ST0281-240400-015-c10 ST0281 Homo | 3.06 | 5.72 |
| 65 | 457194 | H20669 | Hs.35406 | ESTs, Highly similar to unnamed protein | 3.54 | 5.71 |
| | 438601 | AA811713 | Hs.163222 | ESTs | 3.26 | 5.71 |
| | 439032 | AA829487 | Hs.274412 | similar to yeast Upf3, variant A | 3.10 | 5.67 |
| | 408940 | M58583 | Hs.662 | cerebellin 1 precursor | 3.32 | 5.67 |
| | 437700 | AA766060 | Hs.122848 | ESTs | 3.23 | 5.66 |
| 70 | 416061 | R45516 | Hs.26119 | ESTs | 3.85 | 5.65 |
| | 452851 | BE177663 | | gb:RC1-HT0598-020300-011-h11 HT0598 Homo | 3.04 | 5.64 |
| | 430330 | AA476583 | Hs.132981 | ESTs | 3.51 | 5.63 |
| | 435312 | AJ243396 | Hs.4865 | voltage-gated sodium channel beta-3 subu | 5.67 | 5.62 |
| | 400710 | c11p1_1297 | | exon | 3.04 | 5.61 |
| 75 | 457130 | NM_005651 | Hs.183671 | tryptophan 2,3-dioxygenase | 3.31 | 5.60 |
| | 434513 | AF143888 | Hs.18213 | Homo sapiens clone IMAGE:121736 mRNA seq | 3.93 | 5.60 |
| | 434277 | X77748 | Hs.3786 | glutamate receptor, metabotropic 3 | 3.67 | 5.58 |
| | 440854 | AW444900 | Hs.246715 | ESTs | 3.30 | 5.58 |
| | 457086 | AA412591 | Hs.204685 | ESTs | 3.37 | 5.57 |
| 80 | 431883 | AA731404 | Hs.105510 | ESTs | 3.67 | 5.56 |
| | 400758 | AA158742 | Hs.225084 | Homo sapiens cDNA FLJ14280 fis, clone PL | 3.43 | 5.55 |
| | 455374 | AW904039 | | gb:CM3-NN1040-200400-156-d03 NN1040 Homo | 3.36 | 5.52 |
| | 440750 | AW105131 | Hs.245405 | ESTs | 3.10 | 5.50 |
| | 451865 | H43737 | Hs.33186 | ESTs, Weakly similar to unknown protein | 3.38 | 5.50 |

| | | | | | | |
|----|--------|------------|-----------|---|------|------|
| 5 | 453100 | AW806871 | Hs.224786 | ESTs | 3.30 | 5.49 |
| | 433940 | H05129 | Hs.7459 | cyclic AMP-regulated phosphoprotein, 21 | 3.24 | 5.49 |
| | 454935 | AW846075 | | gb:MR3-CT0176-081099-002-b02 CT0176 Homo | 3.26 | 5.48 |
| | 435447 | A1872932 | Hs.142442 | HP1-BP74 | 3.89 | 5.47 |
| | 402953 | c20p3_3451 | | exon | 3.28 | 5.47 |
| | 456233 | AA203339 | | gb:zx56a01.r1 Soares_fetal_liver_spleen_ | 3.02 | 5.47 |
| | 407718 | AW070784 | Hs.243243 | EST | 3.30 | 5.45 |
| | 417429 | A1950529 | Hs.286237 | Homo sapiens cDNA FLJ111841 fis, clone HE | 3.31 | 5.38 |
| 10 | 446408 | A1797169 | Hs.208486 | ESTs | 3.07 | 5.37 |
| | 441792 | AW873635 | Hs.143962 | ESTs | 3.19 | 5.35 |
| | 450661 | AW952160 | Hs.32916 | ESTs | 3.70 | 5.35 |
| | 433932 | AW954599 | Hs.169330 | neuronal protein | 6.78 | 5.33 |
| | 427002 | AA524093 | Hs.23158 | ESTs | 4.00 | 5.32 |
| 15 | 428741 | AA461386 | | gb:zx70h06.r1 Soares_tatal_fetus_Nb2HF8_ | 3.10 | 5.32 |
| | 446383 | T05816 | Hs.92511 | EST | 3.39 | 5.30 |
| | 442988 | A1026130 | Hs.131683 | ESTs | 3.07 | 5.29 |
| | 426713 | A1655299 | Hs.130055 | ESTs | 3.33 | 5.29 |
| | 421294 | AA713486 | Hs.180291 | ESTs | 3.44 | 5.28 |
| 20 | 406462 | ph2_21981 | | exon | 3.20 | 5.28 |
| | 423508 | AW604297 | Hs.129711 | hepatitis A virus cellular receptor 1 | 3.26 | 5.27 |
| | 442114 | BE217975 | Hs.157021 | ESTs | 3.32 | 5.26 |
| | 432508 | A1808915 | Hs.190201 | ESTs | 3.46 | 5.26 |
| | 425604 | U94320 | Hs.158330 | neuropeptide Y receptor Y5 | 3.26 | 5.23 |
| 25 | 417925 | R26789 | Hs.23995 | ESTs | 3.08 | 5.23 |
| | 444448 | H66317 | Hs.143660 | ESTs | 3.81 | 5.22 |
| | 413024 | AF036268 | Hs.75149 | SH3-domain GRB2-like 2 | 3.71 | 5.22 |
| | 437911 | AA848010 | Hs.124250 | ESTs | 3.11 | 5.18 |
| | 435406 | F26698 | Hs.4884 | calcium/calmodulin-dependent protein kin | 4.95 | 5.17 |
| 30 | 407131 | R98679 | | gb:yr31c03.s1 Soares fetal liver spleen | 3.30 | 5.16 |
| | 435776 | A1537162 | Hs.263988 | ESTs | 3.14 | 5.13 |
| | 455532 | AW984828 | | gb:RC1-HN0015-120400-021-h11 HN0015 Homo | 3.14 | 5.13 |
| | 457352 | AA489099 | | gb:aa56h09.s1 NCI_CGAP_GCB1 Homo sapiens | 3.48 | 5.12 |
| 35 | 428670 | AA431682 | Hs.134832 | ESTs | 3.17 | 5.12 |
| | 445962 | A1268410 | Hs.201386 | ESTs | 3.14 | 5.12 |
| | 418153 | R13696 | Hs.112830 | ESTs | 3.16 | 5.10 |
| | 440565 | AW103823 | Hs.131586 | ESTs | 3.08 | 5.10 |
| | 431446 | AW294929 | Hs.255369 | Homo sapiens cDNA FLJ10265 fis, clone HE | 3.42 | 5.09 |
| 40 | 456036 | BE536554 | Hs.75839 | zinc finger protein 6 (CMPX1) | 3.21 | 5.09 |
| | 420883 | A1735488 | Hs.111436 | ESTs | 3.17 | 5.08 |
| | 455528 | AW984757 | | gb:RC1-HN0015-040400-011-g10 HN0015 Homo | 3.35 | 5.08 |
| | 408442 | R59608 | Hs.21435 | ESTs | 3.10 | 5.07 |
| | 446093 | A1345849 | Hs.145896 | ESTs | 3.30 | 5.06 |
| 45 | 403489 | c3p1_2255 | | exon | 3.43 | 5.05 |
| | 405278 | clp3_1070 | | exon | 3.05 | 5.03 |
| | 412804 | H18857 | Hs.22547 | ESTs | 3.63 | 5.03 |
| | 458407 | W90022 | Hs.186809 | ESTs, Highly similar to LECT2 precursor | 3.52 | 5.03 |
| | 407367 | AA130773 | | gb:zo13d01.r1 Stratagene colon (937204) | 3.51 | 5.02 |
| 50 | 439108 | AW163034 | Hs.6467 | synaptogyrin 3 | 5.63 | 5.01 |
| | 445335 | A1220339 | Hs.166775 | ESTs | 3.21 | 5.01 |
| | 435404 | A1240661 | Hs.124995 | ESTs | 3.99 | 5.00 |

TABLE 6B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

| Pkey | CAT Number | Accession |
|--------|------------|--|
| 410837 | 282574_1 | AW806917 AW866469 BF898475 BF898476 AW866540 AW866614 BE145698 AW866675 |
| 436812 | 659779_1 | AW978773 AW298067 AA810101 AW194180 AA731645 AI690573 |
| 454171 | 1049240_1 | AW854832 AW854798 AW854857 AW854816 AW854834 AW854817 |
| 454589 | 28039_6 | BG574750 BF374578 AW810080 AW810106 AW810084 BF374755 AW809621 BF374734 BF374590 BF374594 AW809699 BF374588 AW810437 |
| | | AW810161 AW809662 AW810151 |
| 417159 | 2075888_1 | R01760 N49787 R01761 |
| 459349 | 1027822_1 | AW749381 H93337 |
| 65 | 414187 | BE259777 BE312141 BF942980 |
| | 423280 | AW955178 H86636 AA324037 |
| | 431400 | AW969094 AA504607 AA504705 |
| 70 | 454566 | AW807605 AW807690 AW807677 AW807752 AW807673 AW807900 AW807955 AW807679 AW807615 AW807917 AW807849 AW807832 AW807821 |
| | | AW807842 AW807827 AW807754 AW807830 AW807829 AW807825 AW807819 AW807769 AW807685 AW807603 AW807763 AW807612 AW807840 |
| | | AW807908 AW807684 AW807609 AW807596 AW807595 AW807593 AW807907 AW807902 AW807846 AW807756 AW807687 AW807836 AW807835 |
| | | AW807770 AW807753 AW807669 AW807678 AW807686 AW807680 AW807688 AW807847 AW807957 AW807674 AW807602 AW807617 AW807921 |
| | | AW807667 AW807952 AW807918 AW807670 AW807760 AW807956 AW807608 AW807683 AW807839 AW807601 AW807822 AW807898 |
| | | AA772920 D59870 D61151 AI591331 BF960996 |
| 75 | 437948 | AW979114 AA828060 AA837606 AA829203 |
| | 1242618_1 | BE150647 AW971143 AW809224 AW809221 BF753820 AW809220 AW809178 AW809150 AW809195 AW809175 |
| | 1670_3 | BE145800 BE145921 BE145873 BE145871 BE145930 BE145797 BE145795 |
| | 455836 | AW848279 AW849039 AW847956 AW847957 AW849046 AW848698 AW849034 AW849033 |
| | 454968 | T11756 T20135 T19729 T11958 T11816 R45874 |
| | 418162 | AW971240 AA493723 AA493843 |
| 80 | 431169 | BE007237 BE546311 AA984819 BI256810 W19919 BE007263 BG000322 BF327011 AA890198 BE007496 |
| | 458172 | W04156 AW897535 N94221 |
| | 427942 | BE543651 AA417856 AV756446 BG505084 BI460307 BI460993 BG613293 |
| | 454688 | BF375123 AW814472 AW814474 AW813343 AW816161 AW813380 AW813300 |

| | | | |
|----|--------------|---|--|
| 5 | 455675 | 1490763_1 | BE065984 BE066085 BE065942 BE065955 |
| | 455644 | 1489581_1 | BE064521 BE064441 BE064426 BE064285 BE064286 |
| | 451496 | 85420_1 | AA046879 BF327988 AW503407 AA018131 |
| | 424617 | 895912_1 | AW963059 AA344151 AA344472 |
| | 454862 | 323094_1 | AW853945 AW854083 BF962818 AW847791 BI035483 AW847645 BF961514 BF963484 BF952264 BF963521 |
| | 455260 | 231032_1 | BE161805 AW878317 BE161759 BF870032 BF869588 |
| | 434589 | 14676_1 | AF147363 T47219 T47218 |
| | 410926 | 1064369_1 | AW810708 AW810808 AW810771 AW810924 |
| 10 | 409623 | 830636_1 | AW449665 BE220971 AW449185 |
| | 437254 | 1239876_1 | AW976161 AA831258 AA765857 AA747712 AI784019 |
| | 415508 | 1874742_1 | R45579 F10822 R39236 |
| | 413263 | 1497122_1 | BE075132 BE075131 BE075130 D60395 BF688035 |
| | 415967 | 1899490_1 | H49130 H11230 BF363165 H49061 H11124 |
| | 417555 | 1978200_1 | AA203678 AL597143 H65366 |
| 15 | 413547 | 1520005_1 | BE147456 BE147563 BE147708 BE147440 |
| | 411132 | 1070974_1 | AW819177 AW819242 AW819191 AW819175 AW819252 AW819244 AW819265 AW819269 AW819190 AW819268 AW819183 AW819246 AW819194 |
| | | | AW819249 AW819186 AW819180 AW819188 BE158470 AW819251 BE152602 AW819263 |
| 20 | 454568 | 1061859_1 | AW807909 AW807824 AW807826 AW807903 AW807766 AW807750 AW807911 BE141434 AW807611 AW807837 AW807899 BF374481 |
| | 413162 | 1492355_1 | BE068104 BE068096 BE068198 BE068115 BE068102 BE068154 BE068103 |
| | 455377 | 154707_1 | BF947516 AW905291 BF947512 BF952606 BF952706 BF952525 BF952524 BF952619 BF947500 BF952608 BF952523 BF952532 BF952344 |
| | | | BF746516 BF947614 BF746511 BF952358 AW905400 AW905300 BF947617 AW905349 BF952531 AW905403 BF952528 BE081655 BF746513 |
| | | | AW905286 BF952868 BF947513 BF947510 BF947618 BF947619 AW905347 |
| | | | AW861879 AW861948 AW858447 AW861873 AW858418 AW861871 |
| 25 | 412686 | 1243154_1 | AW984068 AW984077 AW984072 |
| | 436383 | 46767_1 | AJ227879 BE065178 BE065329 |
| | 412290 | 1163352_1 | BE069037 BE069178 AW936034 AW936025 |
| | 411427 | 1083097_1 | AW846080 AW846074 AW846118 AW846130 |
| | 410816 | 1060611_1 | AW806175 AW806176 AW806170 AW806156 |
| | 447258 | 1485710_1 | BE617316 BE047911 AA984167 |
| 30 | 455547 | 1245954_1 | AW994078 BE176183 |
| | 432209 | 1235790_1 | AW971278 AA528270 AA553447 AW971281 |
| | 411138 | 1071173_1 | AW819500 AW819503 AW819481 AW819459 BF375618 |
| | 454713 | 1067889_1 | AW815111 AW815094 AW815218 |
| 35 | 455965 | 1555935_1 | BE167014 BE167058 BE167062 |
| | 416268 | 1959926_1 | H41854 H49111 H46317 |
| | 443100 | 416959_1 | BE004743 AW804074 BE089437 BE089439 BE089378 BE089438 BE004795 W02375 A1033188 BF332422 BF332418 BE178660 |
| | 408070 | 632273_1 | AW148852 BG994152 |
| | 425440 | 1228191_1 | AW962960 AA357518 AA360531 |
| 40 | 412317 | 1164038_1 | AW991979 AW991981 AW991983 AW936856 AW991977 AW991971 AW936852 |
| | 453839 | 3209657_1 | AL138417 AL138418 |
| | 419392 | 215562_2 | W28573 W27418 |
| | 412018 | 147109_1 | BE148133 BE148132 BF736564 BE148152 BE148159 BF893700 |
| | 411265 | 1074383_1 | AW834695 AW834717 AW834714 |
| 45 | 412734 | 1245451_1 | AW993498 AW993484 AW993490 BF512974 |
| | 412694 | 1243393_1 | AW984388 AW984392 AW984379 AW984351 AW984381 AW984377 AW984366 AW984348 AW984391 AW984373 AW984372 AW984353 AW984362 |
| | 411522 | 1089092_1 | BE143505 BF374194 BF374190 AW850286 |
| | 411167 | 1071740_1 | AW820323 AW820314 AW820321 |
| | 413118 | 1490760_1 | BE066079 BE065939 BE065956 |
| 50 | 454751 | 1070838_1 | AW819132 AW819122 AW819018 AW819135 AW819126 AW819024 AW819012 AW819141 |
| | 452861 | 319757_1 | BE177663 AW994738 A1923735 BF948431 BF948329 |
| | 455374 | 1161013_1 | AW904029 AW904030 AW904039 AW904031 AW904032 AW904046 |
| | 454935 | 1083098_1 | AW846075 AW846103 BF333976 AW846077 AW846122 AW846129 AW846095 AW846076 BF333979 BF333978 AW846092 |
| | 456233 | 2635744_1 | AA203339 AA906160 AA929005 |
| 55 | 428741 | 1384399_1 | AA461386 AA433841 AA433845 |
| | 455532 | 1243692_1 | AW984828 AW984787 AW984806 AW984817 AW984826 AW984822 AW984773 AW984786 AW984803 AW984796 |
| | 457352 | 1233795_1 | AW968968 AA489099 N72933 AA489184 |
| | 455528 | 1243660_1 | AW984734 AW984757 AW984797 AW984745 |
| | 407367 | 4907_1 | AF085963 H72550 H72951 AA130773 |
| 60 | TABLE 6C: | | |
| | Pkey: | Unique number corresponding to an Eos probeset | |
| | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. | |
| | Strand: | Indicates DNA strand from which exons were predicted. | |
| 65 | NL_position: | Indicates nucleotide positions of predicted exons. | |
| | Pkey | Ref | Strand NL_position |
| 70 | 401412 | 7940103 | Minus 43347-45776 |
| | 405230 | 7249032 | Minus 97493-97682 |
| | 402125 | 4033680 | Plus 172732-172868 |
| | 404289 | 2769644 | Plus 15049-15286,30267-30457 |
| | 406534 | 7711477 | Plus 40463-40586,41191-41336,41856-41986,4300 |
| | 406348 | 2914717 | Minus 43310-43462 |
| 75 | 401081 | 3478647 | Plus 105163-105305 |
| | 402624 | 7885063 | Minus 31308-31439 |
| | 405320 | 3478667 | Minus 118511-118926,119175-119331 |
| | 405476 | 2121229 | Plus 69890-70883 |
| | 403932 | 7454203 | Minus 8142-8753 |
| 80 | 406112 | 9133145 | Plus 61863-62028 |
| | 400708 | 7249204 | Plus 118115-119445 |
| | 405427 | 7243901 | Minus 6509-6729 |
| | 402816 | 6723302 | Minus 25104-25291 |
| | 404541 | 8318559 | Plus 103456-103664 |

Transmembrane domains: none found
Cellular Localization: plasma membrane

1 11 21 31 41 51
5 MVGKLKQNL LACLVISSVT VFYLGQHAME CHHRIEERSQ PVKLESTRIT VRTGLDLKAN 60
KTPAYEKDMP LIFIGGVPRS GTTLMRAMLD AHPDIRCGEE TRVIPRILAL KQMSRSRSKE 120
KIRLDEAGVT DEVLDSAMQA FLLEIIVKHG EPAPYLCNKD PFALKSLTYL SRLFPNAKFL 180
LMVRDGRASV HSMISRKVIT AGFDLNSYRD CLTKWNRRAIE TMYNQCMVEG YKKCMVLVHYE 240
10 QLVLHPRWMM RTLLKFLQIP WNHSLVHHEE MIGKAGGVSL SKVERSTDQV IKPVNVGALS 300
KMWGKIPDPV LQDMAVIAPM LAKLGYPYA NPPNYGKPDF KIIENTRRVY KGEFQLPDFL 360
KEKPQTEQVE

DNA sequence 3

15 Gene name: interleukin 13 receptor, alpha 2
Unigene number: Hs.25954
Probeset Accession #: R52795
Nucleic Acid Accession #: NM_000640
Coding sequence: 94-1236

20 1 11 21 31 41 51
CGGATGAAGG CTATTGAAG TGGCCATAAC CTGGTCAGAA GTGTGCGCTGT CGGCGGGGAG 60
AGAGGCAATA TCAAGGTTT AAATCTCGGA GAAATGGCTT TCGTTTGCTT GGCTATCGGA 120
TGCTTATATA CTTTCTGAT AAGCACAACA TTTGGCTGTA CTTCACTCTC AGACACCGAG 180
25 ATAAAAGTTA ACCCTCCICA GGATTTTGAG ATAGTGGATC CCGGATACTT AGGTTATCTC 240
TATTTGCAAT GGCACACCCC ACTGTCTCTG GATCAITTTA AGGAATGCAC AGTGGAAATAT 300
GAACATAAAT ACCGAACAT TGGTAGTGAA ACATGGAAGA CCATCATTAC TAAGAATCTA 360
CATTACAAAG ATGGGTTTGA TCTTAACAAG GGCATTGAAG CGAAGATAACA CACGCTTTTA 420
CCATGGCAAT GCACAAATGG ATCAGAAGTT CAAAGTTCCT GGGCAGAAAC TACTTATTGG 480
30 ATATCACCAC AAGGAATTC AGAACTAAA GTTCAGGATA TGGATTGCGT ATATTACAAT 540
TGSCAATATT TACTCTGTTT TTGGAAACCT GGCATAGGTG TACTTCTTGA TACCAATTAC 600
AACTGTGTTT ACTGTATGTA GGGCTTGGAT CATGCATTAC AGTGTGTTGA TTACATCAAG 660
GCTGATGGAC AAAATATAGG ATGCAGATT CCCTATTGG AGGCATCAGA CTATAAAGAT 720
TTCTATATTT GTGTTAATGG ATCATCAGAG AACAGCCTA TCAGATCCAG TTATTTCACT 780
35 TTTCACTTC AAAATATAGT TAAACCTTTG CCGCCAGTCT ATCTTACTTT TACTCGGGAG 840
AGTTTCATGT AAATTAAGCT GAAATGGAGC ATACCTTTGG GACCTATTCC AGCAAGGTGT 900
TTTGATTATG AAATTGAGAT CAGAGAAGAT GATACTACCT TGGTGAAGTC TACAGTTGAA 960
AATGAAACAT ACACCTTGAA AACACAAAT GAAACCGAC AATTATGCTT TGTAGTAAGA 1020
AGCAAAAGTA ATATTATATG CTCAGATGAC GGAATTGTGA GTGAGTGGAG TGATAAACAA 1080
40 TGCTGGGAAG GTGAAGACCT ATCGAAGAAA ACTTTGCTAC GTTCTGGCT ACCATTGGT 1140
TTCATCTTAA TATTAGTTAT ATTGTAAACC GGTCTGCTTT TGCCTAAGCC AACACCTAC 1200
CCAAAATGA TTCAGAAAT TTTCTGTGAT ACATGAAGAC TTTCCATATC AAGAGACATG 1260
GTATTGACTC AACAGTTTCC AGTCATGGCC AAATGTTCAA TATGAGTCTC AATAAACTGA 1320
ATTTTCTCTG CGAAAAA AAAA AAAAAA AAAAAA AAAAAA AAAAAA 1380
AA

Protein sequence 3

50 Gene name: interleukin 13 receptor, alpha 2
Unigene number: Hs.25954
Probeset Accession #: R52795
Protein Accession # NP_000631
Signal sequence: 1-23
FN3 domain: 155-322

Transmembrane domains: 340-362
Cellular Localization: plasma membrane

55 1 11 21 31 41 51
MAFVCLAIGC LYTLISTTF GCTSSSDTEI KVNPPQDFEI VDPGYLGPLY LQWQPPLSLD 60
HFKECTVEYE LKYNIGSET WKTIIITKNLH YKDGFDLNGK IEAKIHTLLP WQCTNGSEVQ 120
60 SSWAETTYWI SPQIPETKV QDMDCVYVNW QYLLCSWKPG IGVLLDTNYN LFYWYEGLDH 180
ALQCVDYIKA DQGNIGCRFP YLEASDYKDF YICVNGSSEN KPIRSSYFTF QLQNIQKPLP 240
FVYLFTRES SCEIKLWISI PLGPPIPARCF DYEIEIREDD TTLVTATVEN ETYTLKTTNE 300
TRQLCFVVRV KVMYICSDDG IWSEWSDKQC WEGEDLSKKT LLRFWLPFGF ILILVIFVTG 360
LLLRKENTYP KMIPEFFCDT

DNA sequence 4

65 Gene name: chemokine (C-X3-C) receptor 1
Unigene number: Hs.78913
Probeset Accession #: U20350
Nucleic Acid Accession #: NM_001337
Coding sequence: 46-1113

70 1 11 21 31 41 51
GGGCGAGATC CAGATTCCTT TTGCAAGTCCA CGCCAGGCCT TCACCATGGA TCAGTTCCCT 60
GAATCAGTGA CAGAAAACCT TGAGTACGAT GATTGGCTG AGGCCTGTTA TATTGGGGAC 120
75 ATCGTGGTCT TTGGGACTGT GTTCTGTGTC ATATTCTACT CCGTCATCTT TGCCATTGGC 180
CTGGTGGGAA ATTGTTGGT AGTGTGTTGCC CTCACCAACA GCAAGAGACC CAAGAGTGTC 240
ACCGACATTT ACCTCCTGAA CCTGGCCTTG TCTGATCTGC TGTGTTAGC CACTTTGCC 300
TTCTGGAGTC ACTATTGAT AAATGAAAAG GGCCTCCACA ATGCCATGTG CAAATTCAT 360
80 ACCGCTTCT TCTTCATCGG CTTTCTTGGG AGCATATTCT TCATCACCGT CATCAGCATT 420
GATAGGTACC TGGCCATCGT CCTGGCGGCC AACTCCATGA ACAACCGGAC CGTGACGAT 480
GGCGTCACCA TCAGCCTAGG CGTCTGGGCA CGAGCCATT TGGTGGCAGC ACCCCAGTTC 540
ATGTTCAACA AGCAGAAAGA AAATGAATGC CTTGGTGACT ACCCCAGAGT CTTTCAGGAA 600
ATCTGGCCCG TGCTCGCAA TGTGGAACA AATTCTCTTG GCTTCTACT CCCCCTGCTC 660
ATTATGAGTT ATTGCTACT CAGATCATC CAGAGCGTGT TTTCTGCAA GAACCAAG 720

AAAGCCAAAG CCATTAAACT GATCCTTCTG GTGGTCATCG TGTITTTCTT CTCTGGACA 780
CCCTACAACG TTAGTATTTT CTTGGAGACG CTTAAGCTCT ATGACTTCTT TCCCAGTTGT 840
GACATGAGGA AGGATCTGAG GCTGGCCCTC AGTGTGACTG AGACGGTTGC ATTTAGCCAT 900
TGTTCCTGTA ATCCTCTCAT CTATGCATTG GCTGGGGAGA AGTTCAGAAG ATACCTTTTAC 960
CACCTGTATG GGAATGCCT GGCCTGCTCG TGTGGGCGCT CAGTCCACGT TGATTTCTCC 1020
TCATCTGAAT CACAAGGAG CAGGCATGGA AGTGTCTGTA GCAGCAATT TACTTACCAC 1080
ACGAGTGATG GAGATGCATT GCTCCTTCTC TGAAGGGAAT CCCAAGCCTT TGTGTCTACA 1140
GAGAACCCTG AGTTCCTGAA CCTGATGCTG ACTAGTGAGG AAGATTTTGT TTGTTATTTT 1200
TTACAGGCAC AAAATGATGG ACCCAATGCA CACAAAACAA CCTAGAGTGT TTGTTGAGAA 1260
TTGTGCTCAA AATTTGAAGA ATGAACAAAT TGAACCTCTT GAATGACAAA GAGTAGACAT 1320
TTCTCTTACT GCAAAATGTA TCAGAACTTT TTGGTTTGCA GATGACAAA ATTCAACTCA 1380
GACTAGTTTA GTTAAATGAG GGTGGTGAAT ATTGTTTATA TTGTGGCACA AGCAAAAAGG 1440
GTGTCGTAGC CCTCAAAGTG AGGGGAACCA GGGCCTGAGC CAAGCTA

Protein sequence 4

Gene name: chemokine (C-X3-C) receptor 1

Unigene number: Hs.78913

Protein Accession #: NP_001328

Signal sequence: 1-44

Pfam domain: 7tm_1 [48-293]

Cellular Localization: plasma membrane

1 11 21 31 41 51
MDQPPESVTE NFEYDDLAEA CYIGDIVVFG TVFLSIFYSV IFAIGLVGNL LVVFALTNSK 60
KPKSVTDIYL LNLALSDLFL VATLPFWTHY LINEKGLHNA MCKFTTAPFF IGFFGSIPFI 120
TVISIDRYLA IVLAANSMMN RTVQHGVTTIS LGVWAAAILV AAPQFMFTQ KENECLGDYP 180
EVLQEIWVPL RNVETNPLGF LLPLLIMSYC YFRIIQTLS CKNHKKAKAI KLILLVVIVF 240
FLFWTPYNVM IFLTELKLYD FFPSCDMRKD LRLALSVTET VAFSHCLNLP LIYAFAGEKF 300
RRYLHYLYGK CLAVLCGRSV HVDFSSSESQ RSRHGSVLSS NFTYHTSDGD ALLLL

DNA sequence 5

Gene name: cannabinoid receptor 1 (brain)

Unigene number: Hs.75110

Probeset Accession #: 412986

Nucleic Acid Accession #: NM_001840

Coding sequence: 92-1510

1 11 21 31 41 51
TCGGCTTATT TGTITTTCCCT CCTCTTAGGA TTGCCCCCTG TGGGTCACCT TCTCAGTCAT 60
TTTGAGCTCA GCCTAATCAA AGACTGAGGT TATGAAGTCG ATCTAGATG GCCTTGACAGA 120
TACCACCTTC CGCACCATCA CCACTGACCT CTTGTACGTG GGCTCAAATG ACATTAGTA 180
CGAAGACATC AAAGGTGACA TGGCATCCAA ATTAGGGTAC TTCCCAACAGA AATTCCCTTT 240
AACTTCCTTT AGGGGAAGTC CCTTCCAAGA GAAGATGACT GGGGAGACAC ACCCCAGCT 300
AGTCCACGCA GACCAGGTGA ACATTACAGA ATTTTACAAC AAGTCTCTCT CGTCCCTCAA 360
GGAGAATGAG GAGAACATCC AGTGTGGGGA GAACTTCATG GACATAGAGT GTTTCATGGT 420
CCTGAACCCC AGCCAGCAGC TGGCCATTGC AGTCTGTGCC CTCACGCTGG GCACCTTCAC 480
GGTCTCTGAG AACCTCCTGG TGCTGTGGGT CATCTCCAC TCCCGCAGCC TCCGCTGAC 540
GCCTTCCTAC CACTTCATCG GCAGCCTGGC GGTGGCAGAC CTCCTGGGGA GTGTCAATTT 600
TGCTACAGC TTCACTGACT TCCACGTGTT CCACGCAAA GATAGCCGCA ACGTGTCTCT 660
GTTCAAACCTG GGTGGGGTCA CGCCTCCTT CACTGCCTCC GTGGGCAGCC TGTTCCTCAC 720
AGCCATCGAC AGGTACATAT CCATTACAGG GCCCCTGGCC TATAAGAGGA TTGTACACCA 780
GCCCAAGGCC GTGGTGGCCT TTTGCCTGAT GTGGACATA GCCATTGTGA TCGCCGTGCT 840
GCCTCTCCTG GGCCTGGAAT GCGAGAAACT GCAATCTGTT TGCTCAGACA TTTTCCACAC 900
CATTGATGAA ACCTACCTGA TGTCTCTGAT CGGGGTCAAC AGCGTACTGC TTCTGTTTCT 960
CGTGTATGCG TACATGTATA TTCTCTGGAA GGCTCACAGC CACGCCGTCC GCATGATTCA 1020
GCGTGGCACC CAGAAGAGCA TCATCATCCA CAGCTCTGAG GATGGGAAGG TACAGGTGAC 1080
CCGGCCAGAC CAAGCCCGCA TGGACATTAG GTTAGCCAAG ACCCTGGTCC TGATCCTGGT 1140
GGTGTGATC ATCTGCTGGG GCCCTCTGCT TGCAATCATG GTGTATGATG TCTTTGGGAA 1200
GATGAACAGC CTCATTAAGA CGGTGTTTGC ATTCTGCAGT ATGCTCTGCC TGCTGAACTC 1260
CACCGTGAAC CCACTCATCT ATGCTCTGAG GAGTAAGGAC CTGCGACAGC CTTTCCGGAG 1320
CATGTTTCCC TCTTGTAAG GCACTGCGCA GCCTCTGGAT AACAGCATGG GGGACTCGGA 1380
CTGCCTGCAC AAACAGCGAA ACAATGCAGC CAGTGTTCAC AGGGCCGCGA AAAGCTGCAT 1440
CAAGAGCACA GTCAAGATTG CCAAGGTAAC CATGCTGTG TCCACAGACA CGTCTGCGGA 1500
GGCTCTGTGA GCCTGATGCC TCCCTGGCAG CACAGGAAAA GAATTTTTTT TTTTAAAGCTC 1560
AAAACTTAGA AGAGTCTATT GTCTCCTTGG TTATATTTTT TTAACCTTAC CATGCTCAAT 1620
GAAAAGGTGA TTGTACACAT GATCACTTAT CAGTTTGCTA ATGTTTCCAT AGTTTAGGTA 1680
CTCAAACTCC ATTCTCCAGG GGTTTACAGT GAAGAAAGCC TGTGTGTTAA GTGACTGAAC 1740
GATCCTTCAA AGTCTCAATG AAATAGGAGG GAAACCTTTG GCTACACAAT TGGAAAGTCTA 1800
AGAACCCATG GAAAAATGCC ATCAAATGAA TAATGCCTTT GTAACCAAA CTTTCACTAT 1860
AATGTGAAT GTAACGTGCC GTAGATACAG AGATGTCCAT TTTTACAAGT TATAGTACTA 1920
GAGATATTT GTAAAATGTA TTATGTCCTG TGAGATGTGT ATCAGTGTGT ATGTGCTATT 1980
AATATTTGTT TAGTTCAGCC AAACGTGAAAG GTAGACTTTT ATGAGAACAA TGGACAAGCA 2040
GTGGATACGT GTCAATGTGT GCACCTTTTT TCTATATTAT TGCCCATGAT ATAACCTTAG 2100
AAATAAACCT TAATATTTCT TCCCAAAAAA AAAAA

Protein sequence 5

Gene name: cannabinoid receptor 1 (brain)

Unigene number: Hs.75110

Protein Accession #: NP_001831

Signal sequence: none found

Pfam domain: 7tm_1 [133-397]

Transmembrane domains: 121-143, 156-178, 195-217, 237-259, 276-298, 344-366, 378-400

Cellular Localization: plasma membrane

1 11 21 31 41 51

5
GTTTATAGCA AACATGGGT ATGCTGTAGC TAACCTTATA AAAGTGAAT ATAACAATGT 4020
AAAAAATTAT ATATCTGGGA GGATTTTITG GTTGCCTAAA GTGGCTATAG TTACTGATT 4080
TTTATTATGT AAGCAAAACC AATAAAAAAT TAAGTTTTTT TAACCACTAC CTTATTTTTC 4140
ACTGTACAGA CACTAATTCA TTAATACTA ATTGATTGTT TAAAAGAAAT ATAAATGTGA 4200
CAAGTGGACA TTTATTTATG TAAATATACA ATTATCAAGC AAGTATGAAG TTATTCAATT 4260
AAAATGCCAC ATTTCTGGTC TCTGGG

Protein sequence 6

10
Gene name: endothelin receptor type B
Unigene number: Hs.82002
Protein Accession #: NP_000106
Signal sequence: 1-27
Pfam domain: 7tm_1 [118-386]
15
Transmembrane domains: 100-122, 138-160, 173-195, 221-243, 277-299, 325-347, 358-380
Cellular Localization: plasma membrane
1
11 21 31 41 51
MQPPPSLCGR ALVALVLACG LSRINGEERG FPDDRATPLL QTAEIMTPPT KTLWPKGSNA 60
SLARSLAPAE VPKGDRTAGS PPRTISPPPC QGPIEIKETF KYINTVVSCL VFVLGIIGNS 120
20
TLLRIIYKXN CMRNGPNILI ASLALGDLH IVIDIPINIV KLLAEDWPFQ AEMCKLVVFI 180
QKASVGTIVL SLICALSIDRY RAVASWSRIK GIGVPKWTAV EIVLIWVSV VLAAPPAIGF 240
DIITMDYKGS YLRICLLHFPV QKTAQMIFYK TAKDWLFSF YFCLPLAITA PFYTLMTCEM 300
LRKSKGMQIA LNDHLKORRE VAKTVFCLVL VFALCWLPLH LSRILKLTLY NQNDPNRCEL 360
LSFLVLVDYI GNMASLNSC INPIALYLVS KRKNCPKSC LCCWCQSFE QKSLEEKQSC 420
25
LKFKANDHGY DNFRSSNKYS SS

DNA sequence 7

30
Gene name: G protein-coupled receptor 34
Unigene number: Hs.29202
Probeset Accession #: N54926
Nucleic Acid Accession #: AF039686
Coding sequence: 79-1224
1
11 21 31 41 51
35
AAAAACCTGA AGACATAAGA ACTACACATG AGGAATATGT CATTTAGCAC TTTCACITTT 60
TGATCTCCAC AGAAGACAAT GAGAAGTCAT ACCATAACAA TGACGACAAC TTCAGTCAGC 120
AGCTGGCCTT ACTCCTCCCA CAGAATGCGC TTTATAACCA ATCATAGCGA CCAACCGCCA 180
CAAAACITCT CAGCAACACC AAATGTTACT ACCTGTCCCA TGGATGAAAA ATTGCTATCT 240
40
ACTGTGTTAA CCACATCCTA CTCGTATT TTCTCGTGG GACTGGTGG GAACATAATC 300
GCCCTCTATG TATTCTCTGG TATTCACCGT AAAAGAAATT CCATTCAAAT TTATCTACTT 360
AACGTAGCCA TGCAGACCT CCTACTCATC TTCTGCCTCC CTTCCGAAT CATGTATCAT 420
ATTAACCAAA ACAAGTGGAC ACTAGGTGTG ATTCTGTGCA AGGTGTGGG AACACTGTTT 480
TATATGAACA TGTACATTAG CATTATTTTG CTGGATTCA TCAGTTTGA TCGCTATATA 540
45
AAAATTAATC GGTCTATACA GCAACGGAAG GCAATAACAA CCAACAAAG TATTTATGTC 600
TGTGTATAG TATGGATGGT TGCTCTGGT GGATTCCTAA CTATGATTAT TTAACTACTT 660
AAGAAAGGAG GGCATAATTC CACAATGTGT TTCCATTACA GAGATAAGCA TAACGCAAAA 720
GGAGAAGCCA TTTTAACTCT CATTCTGTGT GATATGTTCT GGCTAATTTT CTACTAATA 780
ATCCTTTCAT ATATTAAGAT TGGGAAGAAT CTATTGAGGA TTTCTAAAAG GAGGTCAAAA 840
50
TTTCCTAAT CTGTAATAA TGCCACTACA GCTCGTAAC CTCTTATTGT ACTTATCATT 900
TTTACTATAT GTTTTGTTC CTATCATGCC TTTCGATTCA TCTACATTTC TTCACAGCTA 960
AATGTATCAT CTGCTACTG GAAAGAAATT GTTCACAAA CCAATGAGAT CATGCTGGTT 1020
CTCTCATCTT TCAATAGTGT CTTAGATCCA GTCATGTATT TCCTGATGTC CAGTAACATT 1080
CGCAAAATAA TGTGCCAAT TCTTTTGA GAATTCAAG GTGAACCAAG TAGGAGTGAA 1140
55
AGCACTTCAG AATTAAACC AGGATACTCC CTGCATGATA CATCTGTGGC AGTGAATAA 1200
CAGTCTAGTT CTAAGAGTAC TTGAGGTAAA CATACTAAAA TGAATTATAT AATGCAGCCT 1260
CTTAATCTCT TGAAGAACTA AAAAATTAGG AAACAAAGTT CTAGCATTTA CAAAACCTAG 1320
ATCTCAAGC TCTGCTGTGA TTTGTGATAT TTCAATTGCT TAACGTGAAA CCAT

Protein sequence 7

60
Gene name: G protein-coupled receptor 34
Unigene number: Hs.29202
Protein Accession #: AAD50531
Signal sequence: none found
65
Pfam domain: 7tm_1 [71-327]
Transmembrane domains: 90-112, 126-148, 171-193, 217-239, 263-285
Cellular Localization: plasma membrane
1
11 21 31 41 51
70
MRSHTITMT TSVSSWPYSS HRMRFITNHS DQPPQNFSA PNVITCPMDE KLLSTVLTS 60
YSVIPVGLV GNIALYVFL GIHRKRNSIQ IYLLNVAIAD LLLIFCLPFR IMYHINQKX 120
TLGVILCKVV GTLFVMMYI SIILLGFISL DRYIKINRSI QQRKAITTKQ SIYVCCIVWM 180
VALGGELTMI ILTLKKGHN STMCFYHRDK HNAKGEAIFN FILVVMFWLI FLLIILSYIK 240
IGKNLLRISK RRSKFPNSGK YATTARNFSI VLIIFTICFV PYHAFPIYI SSQNLVSSCY 300
75
WKEIVHKTNE IMLVLSFNS CLDPVVMFLM SSNIRKIMCQ LLFRRFQGEF SRSESTSEPK 360
PGYSLHDTSV AVKIQSSKS T

DNA SEQUENCE 8

80
Gene name: exostoses (multiple)-like 2
Unigene number: Hs.61152
Nucleic Acid Accession #: NM_001439
Coding sequence: 288-1280
1
11 21 31 41 51
CACTTTGCGG GCGGCACTTT TTCCAGGTG TTAATCCAGC TAATGGAGAA GGATAGATGC 60

| | |
|----|--|
| 5 | ACGCTACTTG GTTTAGAAAA AAAACAAAA ATGAGCAAAC GAGACGCCCC TTCOGTTTAA 120 |
| | TGATAACTAA GCTGCAGGGA AATAAATCGG CTGGCCCTAC TGCAATCTAC TGCACTCGAG 180 |
| | AAACATCACA GAAATTTCTT TGATTTATCT TAATAGTGAC AAGTGAGCCT GCTTCTGTCA 240 |
| | ATTACTGAAG CTATAAGGAG ATTTTTTAAA AATTAAACTT CAACACAATG AGGTGTTGCC 300 |
| | ACATCTGCAA ACTTCTCTGG AGAGTAATGG GGATTGAGT GCTTCGATTA TCTTTGGTGG 360 |
| | TCATCTCGT ATTTATCTAG GTAGCTGGTG CTTTGACTGC CTACTTCCC AGTGTTAAG 420 |
| | AAGACAAGAT GCTCATGTTG CGTAGGGAAA TAAATCCCA GGGCAAGTCC ACCATGGACT 480 |
| | CCTTTACTCT CATAATGCGA ACGTACAACA GAACAGATCT CTTATTGAAA CTTTAAATC 540 |
| 10 | ATTATCAGCG TGTACCAAT CTGCACAAAG TGATTGTGGT ATGGAACAAT ATTGGAGAGA 600 |
| | AGGCACCGA TGAATTATGG AATTCTCTAG GGGCCCAACC TATCCCTGTG ATCTTCAAC 660 |
| | AAACAGACAG AAACAGGATG AGAATCGAC TCCAGGTCTT TCCTGAATG GAAACCAATG 720 |
| | CAGTGTGGAT GGTAGATGAT GACACACTCA TCAGCACCCC AGAAGTGTG TTTGCTTTCT 780 |
| | CAGTTTGGCA GCAATTTCTT GATCAAAATG TAGGATTGTG TCCTAGAAAG CACGTCTCTA 840 |
| 15 | CTTCATCAGG TATCTACAGT TATGGAAGTT TTGAAATGCA AGCACCAGGG TCTGAAATG 900 |
| | GTGACCAGTA TCTATAGTGG CTGATTGGAG CCTCATTCTT CAATAGCAAA TATCTGAAT 960 |
| | TATTTAGAG GCAACCTGCA GCTGTCCATG CTTTATAGTA TGATACCTAA AACTGTGATG 1020 |
| | ATATTGCCAT GAATTTTATC ATTGCCAAGC ATATTGGCAA GACTTCAGGG ATATTGTGTA 1080 |
| | AGCCTGTAAA CATGACAAT TTGAAAAAAG AAACCAACAG TGGCTATTCT GGAATGTGGC 1140 |
| 20 | ATCGAGCTGA CAGAGGCTCG CAGAGGTCTT ATTGTATAAA TAAGCTTGTG AATATCTATG 1200 |
| | ATAGCATGCC CTAAAGATAC TCCACATTA TGATTCCCA GTTTGGTTT CCATATGCCA 1260 |
| | ACTCAAAAG AAAAATATAA AAGTAAAAA AACAATAACA AACCTGAAA CTGCTTGCCA 1320 |
| | TTTGAGTAGC TTCTCCATGC TATGATTTT TTTAAGCAAC ATCATGAAT TTATCTACTC 1380 |
| | CAGAAGTCTC TACAATAGAA AAAAAGTGC AGTCTTCTA GGATATAAAA TTCACATTAC 1440 |
| 25 | TTTTGAAGC CAAGAAGTTG GTCCTATCCA GTTAGGCTCT CTTATGAAGA GTTTTCATCC 1500 |
| | AGGGATATAA CTCCTTGGTG AGTGATTTTA TTGTTTACAT CCTGAGACTG TTCTACAGTT 1560 |
| | TCTTTGACTC CTGGCATTGG CCTTAAGGAC CTATAGCAAG CTGTTTCTAG GATCAGAAAC 1620 |
| | TCAGAGAGG CAATTTCTCTG CTTTTCCTCT AAAGGTCACT TGTTTTAATT TGAACCTGA 1680 |
| | AATGCCTCT TAGCAAGGCC TGTGGTATGG GGTAAAGCCA TGTAAGAAGA GAATAGTCTC 1740 |
| 30 | AGTCACATAT GAAGAGGAAA ATTTGCAGCT GCCAGTGCTT TCCTTGTTGC CCTGCCAAC 1800 |
| | AGCTCTTCCA GGACGAAGCT AGTCCAGCAT GGTTTTGATG TAACCATCCA TGCTTTTATT 1860 |
| | TTTGTTAAGT CTTTGTGAC TGGGACAGTT AATTTTAGTA GCTGAAGAAC GTCTAGTTGT 1920 |
| | TTGCTTGATA TTTGTGAACA TTACTGCAT GGATCAGAAA ACAATATACC CTGTATTCTT 1980 |
| | TACAGCCAC TTATATGCGA CAGGAGTAA ATGTGTACT AGATTCCGGT AGTGCAATTT 2040 |
| 35 | GTCACTGAAT CTGACCTTGA GAATGTACAT TAATCTTAT ATTTTACATA ATGTATGTGT 2100 |
| | TGTTTAAGAA ATGTATATAA AACCTGAAA AAATGAGTAA GAACCTGGCAG AAGTTAAAC 2160 |
| | CCTTTGTATC AAAAGATCTT TATGTGTA GAACCTGTTA TCTTCTGGAT ACTAAAAAT 2220 |
| | TGTATTACAA AGCCAAACAC TTGCATTAC AACTTTAAAA AAAGATCCAA GGAATATT 2280 |
| | ATAATGATGA AATTTCAACT ACATACAAGG AGGAGAAAAT AAGAACCAG TCATAACAGA 2340 |
| 40 | GGAAATCTAT AGGAGTCTGC ATCAATTCAT TCTTAAGGTT GCCTACTCTC TGTTATGTGA 2400 |
| | ATTAGCGTCT GTGTTTCACC CATGTCTGT GTTTAGTCTT TGTTCAACAC TAAGGCAAGG 2460 |
| | AATCTTAAC TAGGCTCTCG TTACCAACT TCTCTTCTC CTCTTCTCC TCTTATTCT 2520 |
| | CCTTCTCTC TTCTTCTTA TATAATGCTA GTATATTCTC AAAATTGCAA AGCTGTGAGA 2580 |
| | ATATTAATAA AATCATGGCT AATGTTCCA TAATGAGGTC TTTGTGCAT TAGTTCGCCA 2640 |
| 45 | TATGATGGTT TTTTTTTAC ATTAAGAGT ATATGTGCT TAATGCAGTC AGATTGTAAA 2700 |
| | AAACAAAC AAAGAACTA AGAATCTTAC TAAAAATCGA TAATGTCAGT TATCTGTTT 2760 |
| | GTCCAATAT GGTAGTACTT TTTTGCCTCT TATGATTCT CTAGCAGATA AATAAAGAA 2820 |
| | ACTTTTGCCA TCC |
| 50 | Protein sequence 8 |
| | Gene name: exostoses (multiple)-like 2 |
| | Unigene number: Hs.61152 |
| | Protein Accession #: NP_001430 |
| | Signal sequence: 1-38 |
| 55 | Transmembrane domains: none found |
| | Cellular Localization: plasma membrane |
| | 1 11 21 31 41 51 |
| | MRCCHICKLP GRVMGIRVLR LSLVVLVLL LVAGALTALL PSVKEDKMLM LRREIKSQGK 60 |
| 60 | STMDSFLLIM QTYNRTDLLL KLNHYQAVP NLHKVIVVMN NIGEKAPDEL WNSLGPPIPI 120 |
| | VIFKQQTANR MRNRLQVFPE LETNAVLMD DDTLISTPDL VFAPSVWQF PDQIVGFVPR 180 |
| | KHVSTSSGIY SYGSFEMQAP GSGNGDQYSM VLIGASFFNS KYLELFQRFQ AAVHALIDDT 240 |
| | QNCDDIAMNF IIAKHIGKTS GIFVKPVNMO NLEKETNSGY SGMWHERAHA LQSYCINKL 300 |
| | VNIYDSMPLR YSNIMISQFG FPYANYKRKI |
| 65 | DNA SEQUENCE 9 |
| | Gene name: Homo sapiens growth differentiation factor 1 (GDF1) |
| | Unigene number: Hs.92614 |
| | Probeset Accession #: AL120193 |
| 70 | Nucleic Acid Accession #: NM_021267 |
| | Coding sequence: 73-1125 |
| | 1 11 21 31 41 51 |
| | ACGCGGGGCG CGCGGCTCCG TCGGCTACCG CGGCGGGGCG CAGGCGACGG GCACGGCGGG 60 |
| 75 | CGAGCGGGCG GTATGGCGGC GCGGGGCCCC GCGCGGGGCG CGACGGGGCC CGAGCCCATG 120 |
| | CGAGGCTAGC CGCAGCTAGT GCAGGCGGCG TGGGGCAGCG CGCTGGCGGC GCGCGGGGCG 180 |
| | TGCACGGACT GCGGCTGGGG GCTGGCGCGT CGCGGCTGGG CTGAGCACGC GCACCTGGCG 240 |
| | CGCGCCGAGC TGCTGCTGCT GCGGCTCGCG CGGCTGGGCT GGACCGCGCT CGCTCCGCG 300 |
| | GCCACTGCGC GCGCTTTTCG GCGGCTGGCG AAGCGGTGCT GCCTCCAGCC CAGAGATGCC 360 |
| 80 | GCCAAGATGC CCGAGAGCGC TTGGAAGTTT CTCTTCTACC TGGGCGAGTG GAGCTACAGT 420 |
| | GCCTACTGCG TGTTTGGCAC CGACTACCCC TTCTTCCATG ACCCACCATC TGCTTCTTAC 480 |
| | GACTGGACGC CGGCGATGGC AGTGCCACGG GACATTGCAG CGGCTACCTT GCTCCAGGGA 540 |
| | AGCTTCTATG GCCACTCCAT CTACGCTACG CTATACATGG ACACCTGGCG CAAGGACTCG 600 |
| | GTGGTCAATG TGCTCCACGA CGTGGTCACT CTCATCTCTA TCGTCTCTCT CTACGCTTCT 660 |
| | CGGTACCACA ATGTGGGCAT CCTTGTGCTC TTCTGCAAG ATATCAGTGA CGTGCAGCTT 720 |

5 GAGTTCACCA AGCTCAACAT TTAATTCAAG TCCCGCGGCG GCTCCTACCA TCGGCTGCAT 780
 GCCTTGGCAG CAGACTTGGG CTGCTCAGC TTGGCTTCA GCTGGTTCTG GTTCCGCTC 840
 TACTGGTTCC CGCTCAAGGT CCTGTATGCC ACCAGTCACT GCAGTCTGCG CACGGTGCCT 900
 GACATCCCCT TCTACTTCTT CTTCATATCG CTCTGTCTGC TGCTCAACCT TATGAACCTC 960
 TACTGGTTCC TGTACATCGT GCGTTTGA GCGAAGGTGT TGACAGGCCA GGTGACAGAG 1020
 CTGAAGGACC TCGGGAGTA TGACACAGCC GAGGCCAGA GCCTGAAGCC CAGCAAAGCC 1080
 GAGAAGCCAC TGAGGAACGG CCTGGTGAAG GACAAGCGCT TCTGAACCCC TCGGCCCCGC 1140
 CCCCCGTGAC CCGGCCCCAC CCCGAATACC CCGGCCACGC TCCCGTCTCT TGGCCGCCCC 1200
 10 TCCACCCCCC CCAACTCTGC TCCTCTAGGG CCGCGGCCAC CTCCCTGGG ACCCCGCCCC 1260
 CTCACTCTGC CTGCAATTTCC CGGCCACGCC CCCAGGACC CCTGCCCTCT CGGGGACACC 1320
 GGCCCGCCCC TCAGCCCACT GGTCCCGGGC CGCCGCGGAC CCTGCGCACT CTCTGGTCAT 1380
 CGCTGGGAG GAAGATGCCA CCGCGCAGC AAGTCCCTG CGGCCACCAC CTCCTCTCTC 1440
 TCCTGGCGCT GCTGCTGCCC TCGCTGCCCC TGACCCGCGC CCCGTGCCC CCAGGCCCAG 1500
 15 CGCGCGCCCT GCTCCAGGCT CTAGGACTGC GCGATGAGCC CCAGGGTGCC CCCAGGCTCC 1560
 GGCCGGTCTG TGGCGCTGTG TGGCGCTGTG TTGACGCGG GAGACCCAG GAGACCAAGT 1620
 CTGGCTCGCG CGGAGCTGCC CCAGGGTCA CCCTGCAACC GTGCCAAGTG GAGGAGCTGG 1680
 GGGTCCCGG AAACATCGTG CGCCACATCC CGGACCGCG TGCGCCACC CGGGCTCTGG 1740
 AGCTGTGCTC GCGCGCGGGG CATGCCCCG AGTGGACAGT CGTCTTGGAC CTGTGCGCTG 1800
 20 TGGAACCCGC TGAGCGCCCG AGCCGGGCC GCCTGGAGCT GCGTTTCCG CGCGCGCGCG 1860
 CGGACGCCCC GAGGGCGCGG TGGGAGCTGA GCGTGGCGCA AGCGGGCCAG GCGCGGGCG 1920
 CGGACCCCGG CGCGGTGCTG CTCGCGCAGT TGGTCCCGC CCTGGGCGCG CCAGTGCGCG 1980
 CGGAGCTGCT GGGCGCGCTG TGGGCTCGCA ACGCCTCATG CGCGCGCAGC CTCGCGCTGG 2040
 CGCTGGCGCT ACGCCCGCGG GCGCCTGCGG CCTGCGCGCG CTGGCGGAG GCTCTGCTGC 2100
 25 TGCTGTGAC CCTGACCCCG CGCCTGTGCC ACCCCTGGC CGCGCGCGCG CGCGAGCGCG 2160
 AACCCGTGTT GCGCGCGCGC CCGGGGGCG CTTGTGCGC GCGCGGCTG TACGTGAGCT 2220
 TCCGCGAGGT GGGCTGGCAC CGCTGGGTCA TCGCGCGCG CGGCTTCTCT GCCAACTACT 2280
 GCGAGGGTCA GTGCGCGCTG CCCGTGCGC TGTGCGGGTC CGGGGGCGCG CCGCGCTCA 2340
 ACCAGCTGTG GCTGCGCGCG CTGATGCAAG CGCGCGCCCC GGGAGCGGCC GACCTGCGCT 2400
 30 GCTGCGTCC CGCGCGCTG TCGCCATCT CCGTGTCTT CTTTGACAAC AGCGACAACG 2460
 TGTGTCTGCG CAGTATGAG GACATGGTGG TGGACGAGTG CGGCTGCCCG TAACCCGGGG

Protein sequence 9

Gene name: Homo sapiens growth differentiation factor 1 (GDF1)

Unigene number: Hs.92614

Protein Accession #: NP_067090

Signal sequence: none found

Transmembrane domains: 106-128, 148-169, 184-206, 244-266, 285-307

Cellular Localization: plasma membrane

40 1 11 21 31 41 51
 | | | | |
 MAAAGPAAGP TGPEPMPSYA QLVQRGWGSA LAAARGCTDC GWGLARRGLA EHAHLAPPEL 60
 LLALGALGW TALRSAATAR LFRPLAKRCC LQPRDAAKMP ESANKFLFYL GSWSYSAFL 120
 FGTDYFFFD PPSVFDWTP GMVPRDIAA AYLLQGSFYG HSIYATLYMD TWRKDSVVML 180
 45 LHHVTLILI VSSYAFRYHN VGILVLFLED ISDVQLEFTK LNIYFKSRGG SYHRLHALAA 240
 DLGLSFGFS WFWRLYWFPL LKVLATSHC SLRTVPDIPF YFFFNALLLL LTLMLNLYWFL 300
 YIVAFPAKVL TQGVHELKDL REYDTAEAS LKPSKAEKPL RNLVVKDKRF

DNA SEQUENCE 10

Gene name: epidermal growth factor receptor (avian erythroblastic leukemia

Unigene number: Hs.77432

Nucleic Acid Accession #: NM_005228

Coding sequence: 187-3819

55 1 11 21 31 41 51
 | | | | |
 GCGCGCTGC GCGGAGTCC CGAGCTAGCC CCGCGCGCGC CGCCGCCAG ACCGACGAC 60
 AGGCCACCTC GTCGGCTGCC GCGCGAGTCC CCGCTCGCC GCCAACGCCA CAACCACCGC 120
 GCACGCGCCC CTGACTCCGT CCAGTATTGA TCGGGAGAGC CGGAGCGAGC TCTTCGGGGA 180
 GCAGCGATCG GACCTCCCG GACGCGCGG GCAGCGCTCC TGGCGCTGCT GGCTGCGCTC 240
 60 TGCCCGCGCA GTCGGGCTCT GGAGGAAAAG AAGTTTGCC AAGGCACGAG TAACAAGCTC 300
 AGGCACTGG GCACCTTTGA AGATCATTTT CTCAGCCTCC AGAGGATGTT CAATAACTGT 360
 GAGGTGGTCC TTGGGAATTT GGAAATTACC TATGTGCAGA GGAATTATGA TCTTTCCTTC 420
 TTAAGACCA TCCAGGAGGT GGCTGGTTAT GTCTCATTTG CCCTCAACAC AGTGGAGCGA 480
 ATTCTTTGG AAAACCTGCA GATCATCAGA GGAAATATGT ACTACGAAAA TTCTATGCC 540
 65 TTAGCAGTCT TATCTAACTA TGATGCAAT AAAACCGGAC TGAAGGAGCT GCCCATGAGA 600
 AATTTACAGG AAATCTGCA TGGCGCGGTG CGGTTACGCA ACAACCTGCG CCTGTGCAAC 660
 GTGGAGAGCA TCCAGTGGCG GGACATAGTC AGCAGTGACT TTCTCAGCAA CATGTCGATG 720
 GACTTCCAGA ACCACTGGG CAGCTGCCAA AAGTGTGATC CAAGCTGTCC CAATGGGAGC 780
 TGCTGGGGTG CAGGAGAGGA GAACTGCCAG AAATGACCA AAATCATCTG TGCCGAGCAG 840
 70 TGCTCGGGCG GCTGCGGTGG CAAGTCCCC AGTGACTGCT GCCACAACCA GTGTGCTGCA 900
 GGCTGCACAG GCCCGCGGGA GAGCGACTGC CTGGTCTGCC GCAATTTCCG AGACGAAGCC 960
 ACGTGAAGG ACACCTGCCC CCCACTCATG CTCTACAACC CCACACAGTA CCAGATGGAT 1020
 GTGAACCCCG AGGGCAAAAT CAGCTTTGGT GCCACCTGCG TGAAGAAAGT TCCCGTAAT 1080
 TATGTGTGA CAGATCACGG CTCGTGCGTC CGAGCCTGTG GGGCCGACAG CTATGAGATG 1140
 GAGGAAGAG GCGTCCGCAA GTGTAAAGAG TGGGAAGGGC CTGCGCGCAA AGTGTGTAA 1200
 75 GGAATAGGTA TTGGTGAATT TAAAGACTCA CTCTCCATAA ATGTACGAA TATTAAACAC 1260
 TTCAAAAACG GCACCTCGAT CAGTGGCGAT CTCACATCCC TGCCGGTGGC ATTTAGGGGT 1320
 GACTCCTTCA CACATACTCC TCCTCTGGAT CCACAGGAAC TGGATATTCT GAAAACCGTA 1380
 AAGGAATCA CAGGGTTTTT GCTGATTGAG GCTTGGCCTG AAAACAGGAG GGAACCTCAT 1440
 80 GCCTTTGAGA ACCTAGAAAT CATACGCGGC AGGACCAAGC AATATGGTCA GTTTTCTCTT 1500
 CGAGTOGTCA GCCTGAACAT AACATCCTTG GGATTACGCT CCCTCAAGGA GATAAGTGAT 1560
 GGAGATGTGA TAATTTACAG AACAAAAAT TTGTGCTATG CAAATACAA TAACTGGAAA 1620
 AAAGTGTGTT GGACCTCCCG TCAGAAAAAC AAAATTATTA GCAACAGAGG TGAACACAGC 1680
 TGCAAGGCCA CAGGCCAGGT CTGCCATGCC TTGTGCTCCC CGGAGGGCTG CTGGGGCCCG 1740
 GAGCCACAGG ACTGCTCTC TTGCGGGAAT GTCAGCGGAG GCAGGGAATG CGTGGACAG 1800

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ALGIGLFMR RHIVRKRTLRLQLERELVE PLTPSGEAPN QALLRLKET EFKKIKVLGS 720
GAFGTVYKGL WIPEGEKVKI PVAIKELREA TSPKANKEIL DEAYVMASVD NPHVCRLLGI 780
CLTSTVQLIT QIMPFGLLD YVREHKDNIG SQYLLNWCQ IAKGMNYLED RRLVHRDLAA 840
RNVLVKTPQH VKITDFGLAK LLGAEEKEYH AEGGKVPKX MALESILHRI YTHQSDVWSY 900
GVTWELMTF GSKPYDGIPI SEISSILEKG ERLPQPPICT IDVYIMVVC WMIDADSRPK 960
FRELIIFFSK MARDPQRYLV IQGDERMHLF SPTDSNFYRA LMDEEDMDV VDAEYLIPO 1020
QGFFSSPSTS RTPLLSSLSA TSNNSTVACI DRNLQSCPI KEDSFLQRYV SDPTGALTED 1080
SDDTFLFVP EYINQSVFKR PAGSVQNFVY HNQPLNPAPS RDPHYQDPHS TAVGNPEYLN 1140
TVQPTCVNST FDSAPHWAQK GSHQISLDNP DYQDFFPKK AKPNGIFKGS TAENAEYLRV 1200
APQSSEFIGA

DNA sequence 11

Gene name: claudin 5 (transmembrane protein deleted in velocardiiofacial syndrome)

Unigene number: Hs.110903

Probeset Accession #: AW245805

Nucleic Acid Accession #: NM_003277

Coding sequence: 121-777

1 11 21 31 41 51
AGGGGACTGG GGCCAAGAGC CGGAGAGCGG GGCSCAAAGS CACCAAGGCC GCGCCAGGGC 60
GCCGCGCAGC ACGGCCTTGG GGGTCTGCGC GGCCTTCGGG TGCGGCTCTC GCCTCTAGCC 120
ATGGGGTCCG CAGCGTTGGA GATCCTGGGC CTGGTCTGT GCCTGTGGG CTGGGGGGGT 180
CTGATCTCGG CGTGGCGGCT GCCCATGTGG CAGGTGACCG CCTTCTCTGA CCACAACATC 240
GTGACGCGCC AGACCACTG GAAGGGCCTG TGGATGTCT GCGTGGTGCA GAGCACCGGG 300
CACATGCAGT GCAAGTGTGA CGACTCGGTG CTGGCTCTGA GCACCGAGGT GCAGGCGGCG 360
CGGGGCTCA CGGTAGAGCG CGTGTGCTG GCGTCTGTG CGCTCTCTGT GACCCCTGGG 420
GGCGGCGAGT GCACCACTG CGTGGGCGCG GCGCGGCGCA AGGCGGCTGT GGCCTCAGC 480
GGAGGCGTGC TCTACCTGTT TTGCGGGCTG CTGGCGCTCG TGCCACTCTG CTGGTTCGCC 540
AACATTGTCT TCGCGAGT TTACGACCGG TCTGTGCGCG TGTGCGAGAA GTACGAGCTG 600
GGCGCAGCGC TGTACATCGG CTGGGCGGCG ACCGCGCTGC TCATGCTAGG CGGCTGCCTC 660
TTGTGCTCGG GCGCCTGGGT CTGACCGCGC GTCGCGGACC TCAGCTTCCC GTGAAGTAC 720
TCAGCGCGCG GCGGCGGCGC GCGCACCGGC GACTACGACA AGAAGAACTA CGTCTGAGGG 780
CGCTGGGCGC GCGGCGGCGC CTCTGCGCAG CCACGCTGCG GAGGCGTTGG ATAAGCCTGG 840
GGAGCCCGCG ATGAGCCGCG GCTTCGCGCG GGTAGCGCGG CGCGCAGGCT CCGGGAAGG 900
TCGGGCTCTG GCGCCGAGCG CGGCTCTCTG ATCGGCTCCT GCCTGCGCCC GCAGCTGACC 960
TTCTCTCTGC ACTAGCCCGG CCCTGCGCCT AACAGACGGA ATGAAGTTTC CTTTCTCTGT 1020
CGCGGCGCTG TTTCCATAGG CAGAGCGGGT GTCAGACTGA GGATTTCGCT TCCCTCCAA 1080
GACGCTGGGG GTCTTGGCTG CTGCTTACT TCCAGAGGCG TCCTGTCTGAC TTCGAGGGGG 1140
CGGATGCAGA GCGCGGGGCG CCCACCGGAA GATGTGTACA GCTGCTCTT ACTCCATCG 1200
CAGGCGCGAG CCCAGGGGAC AGTGACTTGG CCTGGACCTC CCGGTCTCAC TCCAGCATCT 1260
CCCCAGGCAA GGCTTGTGGG CACCGGAGCT TGAGAGAGGG CGGAGTGGG AAGGCTAAGA 1320
ATCTGCTTAG

Protein sequence 11

Gene name: claudin 5 (transmembrane protein deleted in velocardiiofacial syndrome)

Unigene number: Hs.110903

Protein Accession #: NP_003268

Signal sequence: none found

Pfam domain: PMP22 Claudin [4-181]

Transmembrane domains: 5-27, 74-96, 123-145, 164-186

Cellular Localization: plasma membrane

1 11 21 31 41 51
MGSAALEILG LVLCLVGGG LILACGLPMW QVTAFLDHNI VTAQTWVGL WMSCVVQSTG 60
HMQCKVYDSV LALSTEVQAA RALTVSAVL AFVALFVTLA GAQCTTCVAP GPAKARVALT 120
GGVLYLFCGL LALVPLCWFA NIVVREFYDF SVPVSQKYEL GAALYIGWAA TALIMVGGCL 180
LCCGANVCTG RPLDSFPVKY SAPRRPTATG DYDKKNYV

DNA sequence 12

Gene name: vascular endothelial junction-associated molecule

Unigene number: Hs.54650

Probeset Accession #: AA410345

Nucleic Acid Accession #: AF255910

Coding sequence: 241-1137

1 11 21 31 41 51
TTACCATGT GTTGGGCTGC GAGAAGACGA CAGAAGGGGG ACCCGCCTCT TGGCAGCCAG 60
CTGAGAAGGC GCCCGGGGA GGGGAAACT GACATCCCAT CTAGAGCCGT CCTCCTCTT 120
CCTCCCTCC CGACTCTCTG CTCTTTCCC GCCCAGAAAG TTCAAGGGCC CCGGCTCTCC 180
TGCGCTCTCG CGGCGGGAC CCGGACCTC CTCAGAGCAG CCGGCTGCGG CCGCGGGAAG 240
ATGGCGAGGA GAGGCGGCA CCGCTCCTC CTGCTGCTGC TGGCTACCT GGTGGTGGC 300
CTGGGCTATC ATAAGGCTA TGGGTTTCT GCCCAAAAG ACCAACAGGT AGTCACAGCA 360
GTAGAGTACC AAGAGGCTAT TTTAGCTGCG AAAACCCCA AGAAGACTGT TTCCTCCAGA 420
TTAGAGTGA AAGAACTGGG TCGGAGTGTC TCCTTTGTCT ACTATCAACA GACTCTTCAA 480
GGTGATTTA AAAATCGAGC TGAGATGATA GATTTCATA TCCGGATCAA AAATGTGACA 540
AGAAGTGATG CGGGGAAATA TCGTTGTGAA GTTAGTGCCC CATCTGAGCA AGGCCAAAC 600
CTGGAAGAGG ATACAGTAC TCTGGAAGTA TTAGTGGCTC CAGCAGTTCC ATCATGTGAA 660
GTACCTCTT CTGCTCTGAG TGGAACTGTG GTAGAGCTAC GATGTCAAGA CAAAGAAGGG 720
AATCCAGCT CTGAATACAC ATGGTTTAA GATGGCATCC GTTGTCTAGA AAATCCCAA 780
CTGGCTCCC AAAGCACCAC CAGCTCATAC ACAATGAATA CAAAACTGG AACTCTGCAA 840
TTTAATACTG TTTCCAACT GGCACTGGA GAATATCTCT GTGAAGCCCG CAATCTGTT 900
GGATATCCGA GGTGTCTCGG GAAACGAATG CAAGTAGATG ATCTCAACAT AAGTGGCATC 960
ATAGCAGCGC TAGTAGTTGT GGCCTTAGTG ATTTCCGTTT GTGGCTTGG TGTATGCTAT 1020

5 GCTCAGAGGA AAGGCTACTT TTCAAAAGAA ACCTCCITCC AGAAGAGTAA TTCTTCATCT 1080
 AAAGCCACGA CAATGAGTGA AAATGATTTC AAGCACACAA AATCCTTTAT AATTAAAGA 1140
 CTCCACTTTA GAGATACACC AAAGCCACCG TTGTTACACA AGTTATTAAA CTATTATAAA 1200
 ACTCTGCTTT GTCCGACATT TGCAAAGAGG TACACGAGGA AATGGAATTG GTATTTCATT 1260
 TTAATTTTCA TGAATACTAA CTCACCTGAA CTGCTATTAT TAAAMAATA GTTCTGTGCA 1320
 CACCTAAAAT ATAATCTGGC TTCTGTGTC TGGACTAAGT TAAAGAATT AAAATACTTT 1380
 GTAATGTCAA AAAAAA

Protein sequence 12

Gene name: vascular endothelial junction-associated molecule

Unigene number: Hs.54650

Protein Accession #: AAF81223

Signal sequence: 1-22

Igc2 domain: 41-116, 146-221

Transmembrane domains: 239-261

Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 20 MARRSRHRL LLLRLYLVA LGYHKAYGFS APKDQVVTA VEYQAILAC KTPKKTVSSR 60
 LEWKKLGRSV SFVYYQQTLL GDFKNRAEMI DFNIRIKNVT RSDAGKYRCE VSAPSEQQGN 120
 LEEDVTTLLE LVAPAVPSC VPSSALSGTV VELRCQDKEG NPAPEYTWFK DGIRLLENPR 180
 LGSQSTNSY TMNTKTGTLQ FNTVSKLDTG EYSCEARNVS GYRRCPGKRM QVDDLNLISGI 240
 IAAVVVVALV ISVCGLGVCY AQRKGYSFKE TSFQKSNSSS KATTMSENDF KHTKSFII

DNA sequence 13

Gene name: solute carrier family 11 (proton-coupled divalent metal ion

Unigene number: Hs.182611

Probeset Accession #: D50402

Nucleic Acid Accession #: NM_000578

Coding sequence: 1-1653

1 11 21 31 41 51
 | | | | |
 35 ATGACAGGTG ACAAGGGTCC CAAAAGGCTA AGCGGGTCCA GCTATGGTTC CATCTCCAGC 60
 CCGACCAGCC CGACCAGCCC AGGGCCACAG CAAGCACCTC CCAGAGAGAC CTACCTGAGT 120
 GAGAAGATCC CCATCCCAGA CACAAAACCG GGCACCTTCA GGTCTCGGAA GCTATGGGCC 180
 TTCACGGGGC CTGGCTTCCT CATGAGCAIT GCTTTCCTGG ACCCAGGAAA CATCGAGTCA 240
 GATCTTCAGC TNGNCCNGT GCGGGGATTC AAACCTTCTCT GGGTGTCTGT CTGGGCCACC 300
 GTGTTGGGCT TGCTCTGCA GCGACTGGCT GCACGTCTGG GCGTGGTGAC AGGCAAGGAC 360
 TTGGGCGAGG TCTGCCATCT CTACTACCTT AAGGTGCCCC GCACCGTCTT CTGGCTGACC 420
 40 ATCGAGCTAG CCATTGTGGG CTCGACATG CAGGAAGTCA TCGGCACGCG CATTCGATTTC 480
 AATCTGCTCT CAGCTGGAGC AATCCCACTC TGGGGTGGCG TCCTCATCAC CATCGTGGAC 540
 ACCTTCTTCT TCCTCTTCTT CGATAACTAC GGGCTGCGGA AGCTGGGAAGC TTTTITTTGA 600
 CTCCTTATAA CCATTATGCG CTTGACCTTT GGCTATGAGT ATGTGGTGCG GCGTCTTGAG 660
 45 CAGGGAGCGC TTCTTCGGGG CCTGTTCCTG CCTCGTGCC GGGGCTGCGG CCACCCGAG 720
 CTGCTGCAGG CGGTGGGCAT TGTGTGGCGC ATCATCATGC CCCACACAT CTACCTGCAC 780
 TCGGCCCTGG TCAAGTCTCG AGAGATAGAC CGGCCCGGCC GAGTCGACAT CAGAGAAGCC 840
 AACATGTACT TCCTGATTGA GGCCACCATC GCCTGTCCG TCTCCTTTAT CATCAACCTC 900
 TTTGTATGG CTGCTATTGG GCAGSCCTTC TACCAGAAAA CCAAGCAGGC TCGTTCAC 960
 50 ATCTGTGCCA ACAGCAGCCT CCACGACTAC GCTAAGATCT TCCCCATGAA CAAGCCACC 1020
 GTGGCCGTGG ACATTATACCA GGGGGCGGTG ATCCTGGGCT GCTGTTCGG CCCCGCGGCC 1080
 CTCATCATCT GGGCCATAGG TCTCCTGGCG GCTGGGCGA GCTCCACCAT GACGGGACCC 1140
 TACCGGGGAC AGTTCGTGAT GGAGGGCTTC CTGAGGCTGC GGTGGTCAAG CTTCCGCGCT 1200
 GTCCCTCTCA CCGCTCTCTG CGCCATCCTG CCCACCGTGC TCGTGGCTGT CTTCCGGGAC 1260
 55 GTGAGGACT TGTCCGGGCT CAATGATCTG CTCAACGTGC TGCAGAGCCT GCTGCTCCCG 1320
 GTTGGCGTGC TGCCCATCTT CACGTTTACC AGCATGCCCA CCTCATGCA GGAGTTTGCC 1380
 AATGGCGTGC TGAACAAGGT CGTCACCTCT TCCATCATGG TGTAGTCTG CACCATCAAC 1440
 CTCTACTTCG TGGTCAGCTA TCTGCCGAGC CTGCCCCACC CTGCTACTT CGGCCTTGCA 1500
 GCCTTGCTGG CCGCAGCCTA CTTGGGCTTC AGCACCTACC TGGTCTGAGC CTGTTGCCTT 1560
 60 GCCACGAGG CCACTTTCTT GGGCCACAGC TCCACCACC ACTTCTCTGA TGGGCTCCTT 1620
 GAAGAGGACC ACAAAGGGGA GACCTCTGGC TAG

Protein sequence 13

Gene name: solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1

Unigene number: Hs.182611

Protein Accession #: NP_000569

Signal sequence: none found

Pfam domain: Nramp [78-463]

Transmembrane domains: 58-80, 88-110, 159-181, 195-217, 284-306, 349-379, 394-416, 432-454, 468-490, 501-523

Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 70 MTGDKGPQRL SGSSYGSISS PTSPTSPGPQ QAPPRETYLS EKIPIDTPK GTFRLRLKLA 60
 FTGPGFLMSI AFLDPGNIES DLQLGPVAGF KLLVLLWAT VLGLLCQRLA ARLGVVTGKD 120
 75 LGEVCHLYYP KVPRTVLWLT IELAIVGSDM QEVIGTAIAF NLLSAGRIPL WGVLTITVD 180
 TFFFLFDNY GLRLLEAFPG LLITIMALT GYEVVVARPE QGALLRGLFL PSCPGCGHPE 240
 LLQAVGIVGA IIMPHNIYLH SALVKSREID RARRVDIREA NMYFLIEATI ALSVSFIINL 300
 FVMAAFQAF YQRTKQAAFN ICANSSSLHDY AKIFPMNAT VAVDIYQGGV ILGCLFGPAA 360
 LYIWAIGLLA AGQSSMTGT YAGQFVMEGF LRLRWSSPAR VLLTRSCAIL PTVLVAVFRD 420
 80 LRDLGLNLDL LNLVQLLLP VAVLPILTFT SMPILMQEFA NGLLNKVVTS SIMVLVCTIN 480
 LYFVSYLPS LPHPAYFGLA ALLAAAYLGL STYLVMTCC LAGATFLAHS SHHFLYGLL 540
 EEDHKGETSG

DNA sequence 14

Gene name: solute carrier family 7 (cationic amino acid transporter, y+

Unigene number: Hs.184601
 Probeset Accession #: AF104032
 Nucleic Acid Accession #: NM_003486
 Coding sequence: 53-1576

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      GCTCGCTGGG CCGCTGCTCC CGGCTGTCCC AGGCCCGGCC GGTGCGCAGA GCATGGCGGG 60
      TGCGGGCCCG AAGCGGCGCG CGCTAGCGGC GCCGCGCGCC GAGGAGAAGG AAGAGGCGCG 120
      GGAGAAGATG CTGGCCGCCA AGAGCGCGGA CGGCTCGGCG CCGGACGGCG AGGGCGAGGG 180
10     CGTGACCCCTG CAGCGGAACA TCACGCTGCT CAACGGCGTG GCCATCATCG TGGGGACCAT 240
      TATCGGCTCG GGCATCTTCG TGACGCCCAC GGGCGTGCTC AAGGAGGCAG GCTCGCGCGG 300
      GCTGGCGCTG GTGGTGTGGG CCGCGTGCGG CGTCTTCTCC ATCGTGCGCG CGCTCTGCTA 360
      CGCGGAGCTC GGCACCAACA TCTCCAAATC GGGCGGCGAC TACGCTTACA TGCTGGAGGT 420
      CTACGGCTCG CTGCCCGCCT TCCTCAAGCT CTGGATCGAG CTGCTCATCA TCCGGCCCTT 480
15     ATCGCAGTAC ATCGTGGCCC TGGTCTTCGC CACCTACCTG CTCAAGCCGC TCTTCCCAC 540
      TGCCCGGCTG CCGGAGGAGG CAGCCAAAGT CGTGGCCTGC CTGTGCGTGC TGCTGCTCAC 600
      GGCGGTGAAC TGCTACAGCG TGAAGGCCGC CACCCGGGTC CAGGATGCCT TTGCGCGCGC 660
      CAAGCTCCTG GCCTTGGCCC TGATCATCTC GCTGGGCTTC GTCCAGATCG GAAAGGGTGA 720
      TGTGTCCAAT CTAGATCCCA AGTTCTCATT TGAAGGCACC AAATGGATG TGGGGAACAT 780
20     TGTGTGGCA TTATACAGCG GCCTCTTTGC CTATGGAGGA TGAATTACT TGAATTTCT 840
      CACAGAGGAA ATGATCAACC CCTACAGAAA CCTGCCCTG GCCATCATCA TCTCCCTGCC 900
      CATCGTGACG CTGGTGTAGC TGCTGACCAA CTGGGCTTAC TTCAACACC TGTCACCGA 960
      GCAGATGCTG TCGTCCGAGG CCGTGGCGGT GGACTTCGGG AACTATCACC TGGGCGTCAT 1020
25     GTCTTGGATC ATCCCGCTCT TCGTGGCGCT GTCTGCTTTT GGCTCCGTCA ATGGGTCCCT 1080
      GTTCACATCC TCCAGGCTCT TCTTGTGGG GTCCCGGGAA GGCCACCTGC CCTCCATCCT 1140
      CTCATGATC CACCCACAGC TCCTCACCCC CGTGCCGCTC CTGTGTTTCA CGTGTGTGAT 1200
      GACGCTGCTC TACGCTTCTT CCAAGGACAT CTCTCCGTC ATCAACTTCT TCAGCTTCTT 1260
      CAACTGGCTC TCGTGGGCCC TGGCCATCAT CGGCATGATC TGGCTGCGCC ACAGAAAGCC 1320
30     TGAGCTTGAG CGGCCATCA AGGTGAACCT GGCCTGCCT GTGTTCTTCA TCCTGGCCTG 1380
      CCTCTTCTG ATCGCGCTCT CTTCTGGAA GACACCCGTG GAGTGTGGCA TCGGCTTCAC 1440
      CATCATCTC AGCGGCTGCG CCGTCTACTT CTTGGGGTTC TGGTGGAAAA ACAAGCCCAA 1500
      TGGGCTCTC CAGGGCATCT TCTCCACGAC GTCTCTGTGT CAGAACTCA TGCAGGTGGT 1560
      CCCCAGGAG ACATAGCCAG GAGGCCGAGT GGCTGCCGGA GGAGCATGC
  
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35     Protein sequence 14
      Gene name: solute carrier family 7 (cationic amino acid transporter, y+
      Unigene number: Hs.184601
      Protein Accession #: NP_003477
      Pfam domain: aa permeases [46-481]
40     Transmembrane domains: 52-74, 82-104, 120-142, 145-167, 169-191, 200-222, 237-259, 275-297, 323-345, 371-393,
      398-419, 430-452, 455-476
      Cellular Localization: plasma membrane
      1      11      21      31      41      51
      |      |      |      |      |      |
45     MAGAGPKRRA LAAPAAEKE EAREKMLAAK SADGSAPAGE GEGVTLQRNI TLLNGVAIIV 60
      GTIIGSGIFV TPTGVLKEAG SPGLALVVWA ACGVFSIVGA LCYAEIGTTI SKSGGDYAYM 120
      LEVYGSLEPAF LKLWIELLII RPSSQYIVAL VFATYLLKPL FFTCPVPEEA AKLVACLCLV 180
      LLTAVNCSYV KAATRVQDAF AAALLLALAL IILLGFVQIG KGDVSNLDPK FSEFGTKLDV 240
50     GNIVLALYSY LPAYGGWNYL NFVTEEMINP YRNLPLAIII SLPIVTLVYV LTNLAYFTTL 300
      STEQMLSEEA VAVDFGNVHL GVMWSIIPVF VGLSCFGSVN GSLFTSSRLF FVGSREGHLP 360
      SILSMIHPLQ LTFVPSLVFT CVMTLIYAFS KDIFSVINFF SFFNWLCLVAL AIIIGMIWLR 420
      RKPELERPIK VNLALPVFFI LACLFLIAVS FWKTPVECGI GFTIILSGLP VYFFGVWVKN 480
      KPKMLLQGI STTVLCQKLM QVVPQET
  
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55     DNA sequence 15
      Gene name: Glutamate receptor subunit
      Unigene number: Hs.249141
      Nucleic Acid Accession #: S40369
      Coding sequence: 1-2943
60     1.      11      21      31      41      51
      |      |      |      |      |      |
      ATGCGGCTG AGCTGCTGCT GCTGCTGATT GTTGCCTTCG CCAGCCCCAG CTGCCAGGTG 60
      CTCTCATCAC TGCGCATGGC TGCAATCCTG GATGATCAGA CAGTGTGTGG CCGCGGTGAG 120
65     CGTCTGGCCT TGCCTTTGGC CCGGGAGCAG ATCAACGGGA TCATCGAGGT CCCAGCCAAG 180
      GCCCGAGTGG AAGTAGACAT CTTGAGCTG CAGCGGGACA GCCAGTACGA GACCAAGGAC 240
      ACCATGTGTC AGATCTTACC CAAAGGGGTT GTGCTGTGCC TTGGGCCCTC CTCTAGCCCA 300
      GCATCTGCCT CCACCGTGAG CCATATCTGT GGAGAGAAGG AGATCCCCCA CATCAAGGTG 360
      GGTCCCGAGG AGACACCCCG CCTTCAGTAC CTTGCTTCG CGTCTGTGAG CCGTATCCCC 420
70     AGTAACGAGG ACGTCAGCTT GCGGTCTCC CGAATCCTCA AGTCCTTCAA CTACCCCTCG 480
      GCCAGCCTCA TCTGCGCCAA GGCTGAGTGC CTGCTGCGAT TGGAGGAAGT GGTGCGTGGC 540
      TTCTCATCT CCAAGGAGAC GCTGTCACTG AGGATGTTGG ACGACAGCCG GGACCCCA 600
      CCACTGTCTA AGGAGATCCG TGATGACAAG GTGTCCACCA TCATCATCGA CGCCAACGCC 660
      TCCATCTCCC ACCTCATCTT CCGTAAGGCC TCGGAAGTGG GAATGACCTC AGCGTTTAC 720
75     AAGTACATCC TCACCAACAT GGAATCCCC ATCCTGCATC TGGACGGTAT TGTGGAGGAC 780
      TCTCCAAACA TCTTGGGCTT CTCCATGTTT AACACGTCCC ACCCTTCTA CCTGAGTTT 840
      GTCCGAGGCC TCAACATGTC CTGAGGGGAG AACTGTGAAG CCAGCACCTA CCTGGGCCCT 900
      GCGCTGTGAG CCGCCCTGAT GTTTGACGCC GTGCACGTGG TGGTAGCGCG TGTCCGAGAG 960
80     CTGAACCGCA GCCACGAGAT CGGTGTGAAG CCTTGGCCT GTACATCGGC CAACATTGAG 1020
      CCCCACGGGA CCAGCCTCAT GAACTACCTG CGCATGGTAG AGTATGATGG GCTGACCGGG 1080
      CGGTCGAGT TCAACAGCAA AGGGCAGAGA ACCAACTACA CCTGCGCAT CTTAGAAAG 1140
      TCCCGGCAGG GCCACCGTGA GATTGGGGTG TGGTACTCTA ACCGACCCCT GGCCATGAAT 1200
      GCCACACCCC TGGACATCAA CTGTGCGCAG ACATGGGCCA ACAAGACCTT GGTGGTCACA 1260
      ACCATCTTGG AGAACCCATA CGTCATGCGC CGGCCCAACT TCCAGGGCTT TCGGGGGAAC 1320
      GAACGCTTCG AGGGCTTCTG CTGGGACATG CTGCGGGAGC TGGCCGAGCT GCTGCGCTTC 1380
  
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5 CCGTACCGCC TCGGGTTGGT GGAGGATGGG CTGTACGGGG CGCCCGAGCC CAACGGCTCC 1440
 TGGACGGGCA TGGTTGGCGA GCTCATCAAC CGGAAGGCAG ACCTGGCTGT GGCCGCTTC 1500
 ACCATCACAG CTGAGCGGGA GAAGGTCACT GACTTTTCCA AGCCCTTTAT GACCTGGGG 1560
 ATCAGCATCC TCTACGAGT GCACATGGGC CGCAAGCCTG GCTACTTCTC CTTCCTGGAC 1620
 CCCTTCTCCC CTGCTGTGTG GCTCTTCATG CTCTTTGCTT ACCTGGCTGT CAGCTGCGTC 1680
 CTGTTTCTGG CTGCCAGGCT GAGCCCTTAT GAGTGGTATA ACCACACCC ATGCTTGGCG 1740
 GCACGCCCCC ACATCTGGA GAACCACTAC ACGCTGGGCA ACAGCTGTG GTTCCCGTG 1800
 GGGGGCTTCA TGCAGCAGGG CTGGAGATC ATGCCCGGG CGCTGTCCAC GCGCTGTGTC 1860
 AGCGGAGTCT GGTGGGCTT CACCTTGATC ATCATCTCCT CCTACACGGC CAACCTGGCC 1920
 10 GCCTTCTCTA CCGTGCAGCG CATGGAGGTG CCTGTGGAGT CGGCCGATGA CCTGGCAGAT 1980
 CAGACCAACA TCGAGTATGG CACCATCCAC GCGGCTCCA CCATGACCTT CTTCAGAAAT 2040
 TCACGGTACC AAACGTACCA GCGCATGTGG AACTACATGC AGTCGAAGCA GCCCAGCGTG 2100
 TTGCTCAAGA GCACAGAAGA GGGCATTGCC GCGCTCTCA ACTCCCGCTA GCGCTTCTCT 2160
 CTCGAGTCCA CCATGAACGA ATACCACCG CGCCTCAACT GCAACCTCAC CCAGATCGGG 2220
 15 GGACTCTCTG ACACCAAGGG CTACGGCATT GGCATGCGGC TGGGCTCCCC GTTCGGGAT 2280
 GAGATCACAC TGGCCATCCT GCAGCTTCAG GAGAACAAAC GGCTGGAGAT CCTGAAGCGC 2340
 AAGTGTCTGG AGGGGGGCGG GTGCCCAAG GAGGAGGACC ATCGAGCTAA AGGTTTGGCG 2400
 ATGAGGAACA TTGGTGGCAT TTTTATCGTG CTCTCTCTGT GCGCTCATAT TGCTGTCTTC 2460
 20 GTGGCGGTCA TGAATTCTAT ATGGTCCACA CGGAGGTGAG CTGAGTCCGA GGAGGTGTGG 2520
 GTGTGCCAGG AGATGCTGCA GGAGCTGCGC CACGCGGTTT CTTCGCGCAA GACGTGCGGT 2580
 TCCCGCGCGG GCGGAGCGCC GCGCGGCGCG AGCGGGGCGG TGCTGTCACT GCGCGCGGTC 2640
 CGCGAGATGC GCGTCAGCAA CGGCAAGCTC TACTCGGCGG GCGCGGCGCG GATGCGGCG 2700
 AGCGGCGCAG GGGGGCGGCA GCGCTCTCTG GACGACCGCG GCGCGCGCGG CCGAGCGCGA 2760
 25 CCGCGCGCGC CACCCCGCTG CACCCACGTG CCGCTCTGCG AGGAGTGGCG GCGCATCCAG 2820
 GCGTGGCGGG CCTCGGGGGG CCGCGCGCCT CCGCGTGGCG TGGGCGTCCC CGCCGAAGCC 2880
 ACCAGCCCGC CCGGCGCGG GCGTGGCGCC GCGCGCGCCC GGGAGCTGGC GGAGCACGAG 2940
 TGA

30 **Protein sequence 15**
 Gene name: Glutamate receptor subunit
 Unigene number: Hs.249141
 Protein Accession #: AAB22591
 Signal sequence: 1-27
 Pfam domain: ANF receptor [343-400]; PBPe domain [416-785, 799-838]
 35 Transmembrane domains: 297-319, 544-566, 624-646, 803-825
 Cellular Localization: plasma membrane
 1 11 21 31 41 51
 40 MPAELLLLLL VAFASPSQCV LSSLRMAAIL DDQTVCGRGE RLALALAREQ INGIIEVPAK 60
 ARVEVDIFEL QRDSQYETTD TMCQILPKGV VSVLGPSSSP ASASTVSHIC GEKEIPHIKV 120
 GPEETPRQLQ LRFASVSLYP SNEDVSLAVS RILKSPNYPS ASLICKAKAEC LLRLLEELVRG 180
 FLISKETLSV RMLDDSRDPT PLLKEIRDDK VSTIIIDANA SISHLILRKA SELGMTSAFY 240
 KYLLTTMDFP ILHLDGIVED SSNILGFSMF NTSHPFYPEF VRSLNMSWRE NCEASTYLGP 300
 45 ALSAALMFDA VHVVSVAVRE LNRSGEIGVK PLACTSANIW PHGTSMLNLY RMVEYDGLTG 360
 RVEFNSKQGR TNYTLRILEK SRQGHREIGV WYSNRTLAMN ATTLDINLSQ TLANKTLVVT 420
 TILNPYVMR RPNFQGLSGN ERFEGFCVDM LRELAELLFP PYRLRLVEDG LYGAPEFNGS 480
 WIGMVGELIN RKADLAVAAF TITAEREKVI DPKFPMTLG ISILYRVHMG RKPGYFSPFD 540
 PFSPAVLWFM LLAYLAVSCV LFLAARLSPY EWNYPHPCLR ARPHILENQY TLGNLSLFPV 600
 50 GGFMMQGSSEI MPRLASTRCV SGVWNAFTLI IISSTANLA AFLTVQRMEV PVESADDLAD 660
 QTNIEYGTIH AGSTMTTFQW SRYQTYQRMW NYMQSKQPSV FVKSTEEGIA AVILNSRYAFL 720
 LESTMNEYHR RLNCNLTIQIG GLLDTKGYGI GMLPGSPFRD EITLAILLQ ENNRLEILKR 780
 KHWEGGRCPK BEDHRAKGLG MENIGGIFIV LICGLIIAVF VAVMEFIWST RRSASEEVS 840
 VCQEMQLQLR HAVSCRKTSR SRRRRRPGGP SRALLSLRAV REMRLSNGKI YSAGAGGDAG 900
 55 SAHGGPQRLD DDPGPSPGAR PAAPTPTCTHV RVCQECRIQ ALRASGAGAP PRGLGVPAEA 960
 TSPPRPRPGP AGPRELAEHE

DNA sequence 16
 Gene name: adenosine A3 receptor
 60 Unigene number: Hs.258
 ProbeSet Accession #: NM_000677
 Nucleic Acid Accession #: NM_000677
 Coding sequence: 768-1724
 1 11 21 31 41 51
 65 ATCTTTGCTG CAAAGGCTGG GTATCGGCTG TGCTCAGCAA AGCGTCAACT CGTGCAAGAA 60
 CITAGCAGGA ATAGTTCTGG CTAAGGTTAG GAGGCTGCCA CCAAAGTCTC TTTTGTGTTT 120
 CTCTGCTTCT CCCGTTTGCC TCCTTATCAT GAGATCTTTT TGCTAAGCTG GCAGAAAGAT 180
 TGCAATAGTCA GTGCTTCCAG CTCTGCTCCC ACCTGATCCT GCACTGTCTC CTGGTCCCTG 240
 70 AATGAATGAA CTCTGATACC CAATCTTGTC TCGAGCCTTC TCTATGCCAC TCATGGCTCC 300
 TCTTCTGCTC TTTCATCTT TTTGCTGAGA GTTCTGAGCT CTGTACTTCC TCTTGGCCCA 360
 TCTCACTTCC TGAACACACC CTGAAGAGGG TTGCTTATCT TGATGGAAC CAAAAGGCCA 420
 AAAAGCTGCA GGCAGAGGCG TTGAGGACAT CTGTTTGGGG AACTAAGAGC AGCAGCACTT 480
 TCAGATTGAG TCCATATAGA GCTGTCTAC AGCATTCTGG AACTTGGAG ATGTGCGGTG 540
 75 CATAAAGGGG CTGGAAGTGA CCCACCTGTG ATGAGCCCTT TCTAAGGAGA AGGTTTCCA 600
 AGAGATCACC CCACCAGAAA AGGGTAGGAA TGAGCAAGTT GGGAAATTTA GACTGTCACT 660
 GCACATGGAC CTCTGGGAAG ACGTCTGGCG AGAGCTAGGC CCACTGGCCC TACAGACGGA 720
 TCTTGTCTGC TCACCTGTCC CTGTGGAGGT TCCCTGGGA AGGCAAGATG CCCAACAAAC 780
 GCACTGTCTC GTCAATGGCC AATGTTACCT ACATCACCAT GGAATTTTCT ATTGGACTCT 840
 80 GCGCATGATG GGGCAAGCTG CTGGTCACTC GCGTGGTCAA GCTGAACCCC AGCCTGCAGA 900
 CCACACCTT CTATTTCACT GTCTCTCTAG CCCTGGCTGA CATGTCTGTT GGGGTGCTGG 960
 TCATGCTTTT GGCCATTTGT GTCAGCCTGG GCATCACAAT CCCTTCTAC AGCTGCTTTT 1020
 TTATGACTTG CCTACTGCTT ATCTTTACCC ACGCTTCCAT CATGTCTTGG CTGGCCATCG 1080
 CTGTGACCGC ATACTTGGCG GTCAAGCTTA CCGTCAGATA CAAGAGGGTC ACCACTCACA 1140
 GAAGAATATG GCTGGCCTG GGCCTTTGCT GGTGGTGTGC ATTCTGGTG GATTGACCC 1200

TCTGAGATGA TGCATGATGC CCTCCCTCA GCGCAGGCTG CAGAGCCCGG CCCACCTCC 2460
 CTGCGCCCTT GAGGGGCCCC AGCGTCTGCA GGGTGACGCC TGAGACAGCA CCACTGCTGA 2520
 GGAGTCTGAG GACTGTCTCT CCACAGACCC TGCACTGAGG GGCCTCCAT GCGCAGATGA 2580
 GGGGCCACTG ACCACCTGC GCTTCTGCTG GAGGAGGGGA AGCTGGGCCC AAAGGCCAG 2640
 5 GGAGGCAGCG TGGGCTCTGC CAATGTGGGC TGCCCTCGC ACACAGGGCT CACAGGGCAG 2700
 GCCTTGTCTG GGTCCAGGGC TGTGTGAGGA CCCCGAGGGC TGAGGAGCAG CAGGACCCG 2760
 CCTGCTCCCA TCCTCACCCA GATCAGGAAC CAGGGCCTCC CTGTTACGG TGACACAGGT 2820
 CAGGGCTCAG AGTGACCCTC GGCTGTACCG TGCTCACAGG GATGCTGGTG GCTGGTGAGA 2880
 CCCCCTACTG CACACGGGAA TGCTTAGGTC CCTTCCCGAC CCAGCCAGCT GCACTGCAGG 2940
 10 GCACGGGGAC CTGGATAGTT AAGGGCTTTT CCAAAATGTC ATCCATTAC TGACACTTCC 3000
 TGTCTTGTGT CATGAGAGGC TGTTCGCTCC TCCCATAGTG CTTCGAGGC CCGCAGGGCC 3060
 CACCTTGGAC CCTGGTGACC TCCTGTCACT CACTGAGGCC ATCAGGGCCC TGCCCGAGGC 3120
 CTGAGCGGGC CCTCTTCCCT TCCTGTGCCC CAGCTGCCAG GTGGCCCTGG GAGGGGGTGG 3180
 TGTGGTGTGG GGAAGGGGTC CTGCGGGGGG AGGAGGACTT GGAGGGTCTG GGGGCAGCTG 3240
 15 TCCTGAACCG ACTGACCTGT AGGAGGCCGC TTAGTGTGTC TTTGCTTTTC ATCACGCTCC 3300
 CGCACAGTGG ACGGAGGTCC CCGGTTGCTG GTCAGGTCCC CATGGCTTGT TCTCTGGAAC 3360
 CTGACTTTAG ATGTTTGGG ATCAGGAGCC CCCAACACAG GCAAGTCCAC CCCATAATAA 3420
 CCTGTCCAGT GCCACGGTGG GCTGGGGACT CTGGCAGT GATGCCGGGC GCCAGGACAG 3480
 CAGCACTCCC GCTGCACACA GACGGCCTAG GGGTGGCGCT CAGACCCAC CCTACGCTCA 3540
 20 TCTCTGGAAG GGGCAGCCCT GAGTGGTCTC TGGTCAGGGC AGTGGCCAAG CCGTCTGTGT 3600
 CCTTCTCTCA CAAGGTCCCC CCACCGCTCA GTGTACGGC GTGACGTGTG TTCTTTTGAG 3660
 TCCTTGTATG AATAAAGGC TGGAAACCTA AA

25 Protein sequence 17
 Gene name: glypican 1
 Unigene number: Hs.2699
 Protein Accession #: NP_002072
 Signal sequence: none found
 Pfam domain: Glypican protein [2-490]
 30 Transmembrane domains: none found
 Cellular Localization: plasma membrane
 1 11 21 31 41 51
 | | | | |
 MELRARGWVL LCAAAALVAC ARGDPASKSR SCGEVRQIYG AKGFSLSDVP QAEISGEHLR 60
 35 ICPQSYTCCT SEMEENLANR SHAELETALR DSSRLVQAML ATQLRSFDDH FQHLLANDSER 120
 TLQATPPGAF GELYTQNARA FRDLYSELRL YYRGAHLLE ETLAEFWARL LERLKFQLHP 180
 QLQLLPDDYL CLGKQAEALR PFGEAPREL RLRATRAVAA RSFVQLGLVA SDVVRKVAQV 240
 PLGPECSRVA MKLVYCAHCL GVPGARPCPD YCRNVLKGL ANQADLDAEW RNLLDSMVL 300
 40 TDKFWGTSGV ESIVGSVHTW LAEAINALQD NRDTLTAKVI QSCGNPKVNP QGPGPEEKRR 360
 RGLAPRERP PPSGTLEKLV EAKAQLRDVQ DFWSLPGTL CSEKMALSTA SDDRWNMGMA 420
 RGRYLPVEMG DGLANQINNP EVEVDITKPD MTIRQIMQL KIMTNRLRSA YNGNDVDFQD 480
 ASDGSGSGS

45 DNA sequence 18
 Gene name: NY-REN-24 antigen
 Unigene number: Hs.128425
 Nucleic Acid Accession #: AF155102
 Coding sequence: 27-908
 1 11 21 31 41 51
 | | | | |
 GCGAGGGCGA GGGCGAGGGC GTGCTCATGG AGGAGGACCT GATCCAGCAG AGCCTGGACG 60
 ACTACGACGC CGGCAGGTAC AGCCCGCGGC TGCTCACGGC GCAAGAGCTG CCACTGGAGC 120
 CGCACGTGCT GGAACCGGAT GAGGACCTGC AGCGCTGCA GCTCTCGCCG CAGCAGCTCC 180
 AGGTACGGGG AGACGCCAGC GAGAGCGCCG AGGACATCTT CTTCGGCGCG GCCAAGGAGG 240
 55 GCATGGGCCA GGACGAGGCG CAGTTCAGCG TGGAGATGCC ACTCACCGGC AAGGCCTACC 300
 TGTGGGCCGA CAAGTACCGG CCACGCAAGC CGCGTCTCTT CAACCGCGTG CACACGGGCT 360
 TCGAGTGGAA CAAGTACAA CAGACGCACT ACGACTTTGA CAACCCACCG CCAAGATGCT 420
 TGACGGGATA CAAGTTCAAC ATCTTCTACC CCGACCTCAT CGACAGCGC TCCAGCCCG 480
 AGTACTTCTT GGAGGCCTGC GCGACAAACA AGGATTTCGC CATCTTGCCT TTCAGCGCGG 540
 60 GCGGCTACG AGGACATCGC TTCAAGATC GTCAACCGCG AGTGGGAATA CTGACACGCG 600
 CACGGCTTCC GCTGCCAGTT TGCCAACGGC ATCTTCCAGC TGTGCTTTCA CTTCAGCGC 660
 TACCGCTATC GCGGTGACG GCCCTGGGGA ACGGCGAGCC AGGAGGGCCG AGGGCCACAC 720
 GGTGCCCCA GCCCAGGTGC GAGTGGCCCA GCGGCGAGGC TTGTTCTTCA GCATCCGACG 780
 GGAACATCTC CAACAGAAGC AAAACGGAAA GTGCTTCCCG GACCCCGAGA GGGCCACCCA 840
 65 ACCTACCAAG TCACAGCCCC CAGACACCCC ACAGCCCTTC CCAGACACCC CGCCTCATCT 900
 GGAATAAGTT CCGTTTGTCT CTCTAAAAAG ACTTGTAGGT GGGAAAAAAA ATCTTTTGT 960
 CTCATGGAAT TGGCCTATTG GCAAGATCGC ATGTTTTTTT AATAAACGTT GTATTTTAGA 1020
 AATAAA

70 Protein sequence 18
 Gene name: NY-REN-24 antigen
 Unigene number: Hs.128425
 Protein Accession #: AAD42868
 Signal sequence: none found
 75 Transmembrane domains: none found
 Cellular Localization: plasma membrane
 1 11 21 31 41 51
 | | | | |
 80 GEGEAVLME EDLIQQLDD YDAGRYSPRL LTAHELPLDA HVLEPDEDLQ RLQLSRQQLQ 60
 TGDASESAE DIFERRAKG MQQDEAQFSV EMPLTKAYL WADKYRERKP RFFNRVHTGF 120
 WNKYNQTHY DFDNPPPKIV QGYKFNIFYP DLIDKRSTPE YFLEACADNK DFAILRFTRG 180
 LRHGRFQDR QPRVGTILAPP RLPLPVQQRH LPAVLSLQAL PLSAVTALGN GRPGGPRATR 240
 PQPRSEWPS RQACSSASDG NISNRSKTES ASRTPRGPPN LTSHQPQTTH SPSTPRLTW 300

DNA sequence 19

Gene name: tumor necrosis factor receptor superfamily, member 1A
 Unigene number: Hs.159

Probeset Accession #: BE295782

Nucleic Acid Accession #: NM_001065

Coding sequence: 256-1623

1 11 21 31 41 51
 10 OGGCCAGTG ATCTTGAACC CCAAAGGCCA GAACTGGAGC CTCAGTCCAG AGAATTCTGA 60
 GAAAAATTTAA GCAGAGAGGA GGGGAGAGAT CACTGGGACC AGGCGGTGAT CTCTATGCCC 120
 GAGTCTCAAC CCTCAACTGT CACCCCAAGG CACTTGGGAC GTCTGGACA GACCGAGTCC 180
 OGGGAAGCCC CAGCACTGCC GCTGCCACAC TGCCCTGAGC CCAATGGGG GAGTGAGAGG 240
 CCATAGCTGT CTGGCATGGG CCTCTCCACC GTGCTGACC TGCTGCTGCC GCTGGTGCTC 300
 CTGGAGCTGT TGGTGGGAAT ATACCCCTCA GGGGTATTG GACTGGTCCC TCACCTAGGG 360
 15 GACAGGGAGA AGAGAGATAG TGTGTGTCCC CAAGGAAAT ATATCCACCC TCAAAATAAT 420
 TCGATTGTCT GTACCAAGTG CCACAAAGGA ACCTACTTGT ACAATGACTG TCCAGGCCCC 480
 GGGCAGGATA CGGACTGCAG GGAGTGTGAG AGCGGCTCCT TCACCGCTTC AGAAAACCCAC 540
 CTCAGACACT GCCTCAGCTG CTCCAAATGC CGAAAGGAAA TGGGTGAGGT GGAGATCTCT 600
 TCTTGACAGT TGGACCGGGA CACCGTGTGT GGCTGCAGGA AGAACCAGTA CCGGCATTAT 660
 20 TGGAGTGAAA ACCTTTTCCA GTGCTTCAAT TGCAGCCTCT GCCTCAATGG GACCGTGCAC 720
 CTCTCTCGCC AGGAGAAACA GAACACCGTG TGCACCTGCC ATGCAGGTTT CTTTCTAAGA 780
 GAAAAAGGAT GTGTCTCCTG TAGTAACGT AAGAAAAGCC TGGAGTGCAC GAAGTTGTGC 840
 CTACCCAGA TTGAGATGT TAAGGGCACT GAGGACTCAG GCACACAGT GCTGTTGCC 900
 CTGGTCAATT TCTTTGGTCT TTGCTTTTA TCCCTCTCTCT TCATTGGTTT AATGTATGCG 960
 25 TACCAACGCT GGAAGTCCAA GCTCTACTCC ATTGTTTGTG GGAATCGAC ACCTGAAAAA 1020
 GAGGGGAGC TTGAAGGAAC TACTACTAAG CCCCCTGGCC CAAACCCAG CTTCACTCCC 1080
 ACTCCAGGCT TCACCCCAAC CCGGGCTTC AGTCCCGTGC CAGTTCACG CTTCACTCCC 1140
 AGCTCCACCT ATACCCCGG TGACTGTCCC AACTTTGCGG CTCCCGCAG AGAGGTGGCA 1200
 CCACCCATAT AGGGGGCTGA CCCCATCCTT GCGACAGCCC TCGCCTCGA CCCCATCCCC 1260
 30 AACCCCTTTC AGAAGTGGGA GGACAGCGCC CACAAGCCAC AGAGCCTAGA CACTGATGAC 1320
 CCGCGACGCC TGTACGCCCT GGTGGAGAAC GTGCCCCGTG TGGCTGGAA GGAATTCGTG 1380
 CGGCGCCTAG GGCTGAGCGA CCACGAGATC GATCGGCTGG AGCTGCAGAA CGGCGCTGCG 1440
 CTGCGCGAGG CGCAATACAG CATGCTGGCG ACCTGGAGGC GCGCACGCC CCGCGCGAG 1500
 35 GCCACGCTGG AGCTGCTGGG ACGGCTGCTC CGCGACATGG ACCTGCTGGG CTGCGTGGAG 1560
 GACATCAGAG AGGCGCTTTG CGGCCCGGCC GCCCTCCCGC CCGCGCCAG TCTTCTCAGA 1620
 TGAAGCTGCG CCCCCTGCGG CAGCTCTAAG GACCGTCTG CGAGATCGCC TTCCAAACCC 1680
 ACTTTTCTT GGAAGGAGG GGTCTGCGAG GGGCAAGCAG GAGCTAGCAG CGCCTACTT 1740
 GGTGCTAACC CCTCGATGTA CATAGCTTTT CTCAGCTGCC TGGCGCGCG CGACAGTCTG 1800
 40 CGCTGTGCGC GCGGAGAGAG GTGCGCCGTG GGCTCAAGAG CCTGAGTGGG TGGTTTTCGA 1860
 GGATGAGGGA CGCTATGCTT CATGCCGCTT TTGGGTGTCC TCACCAGCAA GGCTGCTCGG 1920
 GGGCCCTGCG TTGCTCCCTG AGCCTTTTTC ACAGTGCTA AGCAGTTTTC TTTGTTTTTG 1980
 TTTTGTTTG TTTGTTTTT AAATCAATCA TGTACACTA ATAGAAACTT GGCACCTCTG 2040
 TGCCCTCTGC CTGGACAAGC ACATAGCAAG CTGAAGTCTC CTAAGGCAGG GCGAGACCTG 2100
 45 GAACAATGGG GCCTTCAGCT GGAGCTGTGG ACTTTGTAC ATACACTAAA ATTCTGAAGT 2160
 T

Protein sequence 19

Gene name: tumor necrosis factor receptor superfamily, member 1A
 Unigene number: Hs.159

Protein Accession #: NP_001056

Signal sequence: 1-29

TNFR domain: 44-81, 84-125, 127-166, 169-195

Transmembrane domains: 211-234

Cellular Localization: plasma membrane

1 11 21 31 41 51
 55 MGLSTVPDLL LPLVLELLV GIYPSGVIGL VPHLGDEKR DSVCPQGYI HPQNNISICT 60
 KCHKGTLYLN DCPGPGQDID CRECESGSFT ASENHLRHCL SCSKCRKEMG QVEISSCTVD 120
 60 RDTVCGCRKN QYRHYNSNL PQCFNCSLCL NGTVHLSQCE KQNTVCTCHA GFFLRENECV 180
 SCSNCKSLE CTRLCLPQIE NVKGTEDSGT TVLLPLVIFV GLCLLSLLFI GLMYRYQRWK 240
 SKLYSIVCGK STPEKEGELE GTTTKPLAPN PSPSPTPGPT PTLGFSVPVS STFTSSSTYT 300
 PGDCPNFAAP RREVAFFYQG ADPILATALA SDPIPPLQK WEDSAHKPQS LDTDDPATLY 360
 AVVENVPPLR WKEFVRRLGL SDHEIDRLLE QNGRCLREAO YSMLATWRRR TPRREATLEL 420
 65 LGRVLRLMDL LGCLIEDIEA LOGPAALPPA PSLLR

DNA sequence 20

Gene name: prominin (mouse)-like 1

Unigene number: Hs.112360

Probeset Accession #: R40057

Nucleic Acid Accession #: NM_006017

Coding sequence: 38-2635

1 11 21 31 41 51
 75 CCAAGTTCTA CCTCATGTTT GGAGGATCTT GCTAGCTATG GCCCTCGTAC TCGGCTCCCT 60
 GTTGCTGCTG GGGCTGTGCG GGAATCTCTT TTCAGGAGGG CAGCCTTCAT CCACAGATGC 120
 TCCTAAGGCT TGAATATTAT AATTGCCTGC AACAAATTAT GAGACCCAAG ACTCCATAA 180
 AGCTGACCC ATTGGCATT CTTTGAAC AGTGCAATC TTTCTCTATG TGGTACAGCC 240
 CGGTGATTTT CCAGAGATA CTTTGAGAAA ATTCTTACAG AAGGCATATG AATCCAAAT 300
 80 TGATTATGAC AAGCCAGAAA CTGTAATCTT AGGTCTAAG ATTGTCTACT ATGAAGCAGG 360
 GATTATTCTA TGTCTGTGTC TGGGGCTGCT GTTTATTATT CTGATGCCTC TGGTGGGGTA 420
 TTTCTTTTGT ATGTGTCTGT GCTGTAACAA ATGTGGTGA GAAATGCACC AGCGACAGAA 480
 GGAAAATGGG CCCCCTCTGA GGAATGCTT TGCAATCTCC CTGTTGGTGA TTTGTATAAT 540
 AATAAGCATT GGCACTCTCT ATGGTTTGT GGCAATCAC CAGGTAAGAA CCGGATCAA 600
 AAGGAGTCGG AAATGGCAG ATAGCAATTT CAAGGACTTG GAACTCTCT TGAATGAAAC 660

| | | | | | | | |
|----|--|-------------|-------------|--------------|-------------|-------------|------|
| | TCCAGAGCAA | ATCAAAATATA | TATTGGCCCCA | GTACAACACT | ACCAAGGACA | AGGCGTTCAC | 720 |
| | AGATCTGAAC | AGTATCAATT | CAGTGTAGG | AGGCGGAATT | CTTGACCGAC | TGAGACCCAA | 780 |
| | CATCATCCCT | GTCTCTGATG | AGATTAAAGTC | CATGGCAACA | GCGATCAAGG | AGACCAAAGA | 840 |
| 5 | GGCGTTGGAG | AACATGAACA | GCACCTTGAA | GAGCTTGAC | CAACAAAGTA | CACAGCTTAG | 900 |
| | CAGCAGTCTG | ACCAGCGTGA | AAACTAGCCT | GCGGTCTATC | CTCAATGACC | CTCTGTGCTT | 960 |
| | GGTGCATCCA | TCAAGTGAAA | CCTGCAACAG | CATCAGATTG | TCTCTAAGCC | AGCTGAATAG | 1020 |
| | CAACCCCTGAA | CTGAGGCAGC | TTCCACCCGT | GGATGCAGAA | CTTGACAACG | TTAATAACGT | 1080 |
| | TCTTAGGACA | GATTITGGATG | GCCTGGTCCA | ACAGGGCTAT | CAATCCCTTA | ATGATATACC | 1140 |
| 10 | TGACAGAGTA | CAACGCCAAA | CCACGACTGT | CGTAGCAGGT | ATCAAAAGGG | TCTTGAATTC | 1200 |
| | CATTGGTTCA | GATATCGACA | ATGTAACCTA | GCGTCTTCCT | ATTCAGGATA | TACTCTCAGC | 1260 |
| | ATTCTCTGTT | TATGTTAATA | ACACTGAAAG | TTACATCCAC | AGAAATTAC | CTACATTGGA | 1320 |
| | AGAGTATGAT | TCATACTGGT | GGCTGGGTGG | CCTGGTCACT | TGCTCTCTGC | TGACCCCTCAT | 1380 |
| | CGTGATTTT | TACTACCTGG | GCTTACTGTG | TGGCGTGTGC | GGCTATGACA | GGCATGCCAC | 1440 |
| 15 | CCCGACCACC | CGAGCTGTG | TCTCCAACAC | CGAGGCGCTC | TTCCTCATGG | TTGGAGTTGG | 1500 |
| | ATTAAGTTTC | CTCTTTTGCT | GGATATTGAT | GATCAITGTG | GTCTTACCT | TGTCTTTGG | 1560 |
| | TGCAAAATGTG | GAAAAACCTA | TCTGTGAACC | TTACACGAGC | AAGGAATTAT | TCGGGGTTTT | 1620 |
| | GGATACACCC | TCTTACTATA | ATGAAGACTG | GGAATACTAT | CTCTCTGGGA | AGCTATTATA | 1680 |
| | TAAATCAAAA | ATGAAGCTCA | CTTTGAACA | AGTTTACAGT | GACTGCAAAA | AAAATAGAGG | 1740 |
| 20 | CACTTACGGC | CACTTTCACC | TGCAGAACAG | CTTCAATATC | AGTGAACATC | TCAACATTAA | 1800 |
| | TGAGCATACT | GGAAGCATAA | GCAGTGAATT | GGAAAGTCTG | AAGGTAAATC | TTAATATCTT | 1860 |
| | TCTGTGGGT | GCACGAGGAA | GAAAAAACCT | TACGATTTT | GCTGCTGTG | GAATAGACAG | 1920 |
| | AATGAATTAT | GACAGCTACT | TGGCTCAGAC | TGGTAAATCC | CCCCCAGGAG | TGAATCTTTT | 1980 |
| | ATCATTTGCA | TATGATCTAG | AAGCAAAAGC | AAACAGTTTG | CCCCCAGGAA | ATTGAGGAA | 2040 |
| 25 | CTCCCTGAAA | AGAGATGCAC | AAACTATTAA | AACAATTCAC | CAGCAACGAG | TCCTTCCTAT | 2100 |
| | AGAACAATCA | CTGAGCCTCT | TATACCAAAG | CGTCAAGATA | CTTCAACGCA | CAGGGAATGG | 2160 |
| | ATTGTTGGAG | AGAGTAACCTA | GGATTCTAGC | TTCTCTGGAT | TTTGCTCAGA | ACTTCTATCAG | 2220 |
| | AAAACAATGAT | TCTCTCTGTTA | TTATTGAGGA | AACTAAGAAG | TATGGGAGAA | CAATAATAGG | 2280 |
| | ATATTTTGAA | CAITATCTGC | AGTGGATCGA | GTTCTCTATC | AGTGAGAAAG | TGGCATCGTG | 2340 |
| 30 | CAAACCTGTG | GCCACCGCTC | TAGATACTGC | TGTTGATGTC | TTTCTGTGTA | GCTACATTAT | 2400 |
| | CGAACCCCTG | AATTTGTTTT | GGTTTGGCAT | AGGAAAAGCT | ACTGTATTTT | TACTTCCGGC | 2460 |
| | TCTAATTTTT | GCGGTAAAAC | TGGCTAAGTA | CTATCGTCGA | ATGATTCCGG | AGGACGTGTA | 2520 |
| | CGATGATGTT | GAACTATATC | CCATGAAAAA | TATGGAAAAA | GGAATAATG | GTTATCATAA | 2580 |
| | AGATCATGTA | TATGGTATTC | ACAATCCTGT | TATGACAAGC | CCATCACAAAC | ATTGATAGCT | 2640 |
| 35 | GATGTTGAAA | CTGCTTGAGC | ATCAGGATAC | TCAAAGTGGA | AAGGATCACA | GATTTTGTGT | 2700 |
| | AGTTTCTGGG | TCTACAAGGA | CTTTCCAAAT | CCAGGAGCAA | CGCCAGTGGC | AACGTAGTGA | 2760 |
| | CTCAGGCGGG | CACCAAGGCA | ACGGCACCAT | TGGTCTCTGG | GTAGTGCTTT | AAGAATGAAC | 2820 |
| | ACAATCACT | TATAGTCCAT | GGTCCATCAC | TATTCAAGGA | TGACTCCCTC | CCTTCTGTGC | 2880 |
| | TATTTTGT | TTTTACTTTT | TTACACTGAG | TTTCTATTTA | GACACTACAA | CATATGGGGT | 2940 |
| 40 | GTTTGTCC | ATTGGATGCA | TTTCTATCAA | AACTCTATCA | AATGTGATGG | CTAGATTCTA | 3000 |
| | ACATATTGCC | ATGTGTGGAG | TGTGCTGAAC | ACACACCAGT | TTACAGGAAA | GATGCATTTT | 3060 |
| | GTGTACAGTA | AACGGTGTAT | ATACCTTTTG | TTACCAAGGA | GTTTCTTAAA | CAAAATGAGTA | 3120 |
| | TTATAGAGCT | TTCTTCTAAA | TGAGCTAAAT | AAGTCACCAT | TGACTCTCTG | GTGCTGTGTA | 3180 |
| | AAATAATCCA | TTTTCTACTAA | AAGTGTGTA | AACCTACAGC | ATATTCTTCA | CGCAGAGATT | 3240 |
| 45 | TTTCTCTATT | ATACCTTATC | AAAGATTGGC | CATGTTCCAC | TTGGAAATGG | CATGCAAAAG | 3300 |
| | CCATCATAGA | GAAACCTGCG | TAACTCCATC | TGACAAATTC | AAAAGAGAGA | GAGAGATCTT | 3360 |
| | GAGAGAGAAA | TGCTGTTTCT | TCAAAAGTGG | AGTTGTTTTA | ACAGGTGCCA | ATTACGGTGT | 3420 |
| | ACAGTTTAAC | AGAGTTTCT | GTTGCATTAG | GATAAACATT | AATTGGAGTG | CAGCTAACAT | 3480 |
| | GAGTATCATC | AGACTAGTAT | CAAGTGTCT | AAAATGAAAT | ATGAGAAGAT | CCTGTACAAA | 3540 |
| 50 | TTCTTAGATC | TGGTGTCCAG | CATGGATGAA | ACCTTTGAGT | TGGTCCCTCA | AAATTTGCATG | 3600 |
| | AAAGCACAG | GTAATATTC | ATTGCTTCA | GGAGTTTCAT | GTTGGATCTG | TCATTATCAA | 3660 |
| | AAGTGATCAG | CAATGAAGAA | CTGGTCGGAC | AAAATTTAAC | GTTGATGTAA | TGGAATTCCA | 3720 |
| | GATGTAGGCA | TTCCCCCAG | GTCTTTTCAT | GTGCAGATTG | CAGTTCTGAT | TCATTTGAAT | 3780 |
| | AAAAAGGAAC | TTGGC | | | | | |
| 55 | <u>Protein sequence 20</u> | | | | | | |
| | Gene name: prominin (mouse)-like 1 | | | | | | |
| | Unigene number: Hs.112360 | | | | | | |
| | Protein Accession #: NP_006008 | | | | | | |
| | Signal sequence: 1-21 | | | | | | |
| 60 | Transmembrane domains: 105-127, 157-179, 438-460, 482-504, 784-806 | | | | | | |
| | Cellular Localization: plasma membrane | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| 65 | MALVLGSLLL | LGLCQNSFSFG | GQPSSTDAPK | AWNYELPATN | YETQDSHKAG | PIGILFELVH | 60 |
| | IFLVVQPRD | FPEDTLRKFL | QKAYESKIDY | DKPETVILGL | KIVYIEAGII | LCCVLGLLFI | 120 |
| | ILMPLVGYYF | CMCRCCNKG | GEMHQKQEN | GPFLRKCFAI | SLLVICIIIS | IGIFYGFVAN | 180 |
| | HQVTRIKRS | RKLADSNFKD | LRTLNETPE | QIKYILAQYN | TTKDKAFTDL | NSINSVLGGG | 240 |
| | ILDLRLPNII | PVLDEIKSMA | TAIKETKEAL | ENMNSTLKS | HQQSTQLSSS | LTSVKTSLS | 300 |
| 70 | SLNDPLCLVH | PSSETCNSTR | LSLSQLNSNP | ELRQLPPVDA | ELDNVNVNLR | TDLDGLVQGG | 360 |
| | YQSLNDIPDR | VQRQTITVVA | GIKRVLNSIG | SDIDNVTQRL | PIQDILSAFS | VYVNNTESYI | 420 |
| | HRNLPTLEBY | DSYWWLGLLV | ICSLTLIVI | FYYLGLLCGV | CGYDRHATPT | TRGCVSNTGG | 480 |
| | VFLMVGVLGS | FLFCWILMII | VVLTFVFGAN | VEKLICEPYT | SKELFRVLD | PYLLNEDWEY | 540 |
| | YLSGLKFNKS | KMKLTFEQVY | SDCKKNRGTY | GTLLHQNFSN | ISEHLNINEH | TGSISSSELES | 600 |
| 75 | LKVNLIIFLL | GAAGRNLQD | FAACGIDRMN | YDSYLAQTKG | SPAGVNLFS | AYDLEAKANS | 660 |
| | LPPGNLRNSL | KRDAQTIKI | HQQRVLPBIEQ | SLSTLYQSVK | ILQRTGNGLL | ERVTRILASL | 720 |
| | DFAQNFITNN | TSSVIIIEETK | KYGRITIGYF | EHYLLQNIIEFS | ISEKVASCCKP | VATALDTAVD | 780 |
| | VFLCSYIIDP | LNLFWFGIGK | ATVFLLPALI | FAVKLAKYYR | RMDSEIDVYD | VETIPMKNE | 840 |
| | NGNNGYHDKH | VYGIHNPVMT | SPSQH | | | | |
| 80 | <u>DNA sequence 21</u> | | | | | | |
| | Gene name: G protein-coupled receptor 39 | | | | | | |
| | Unigene number: Hs.85339 | | | | | | |
| | Nucleic Acid Accession #: NM_001508 | | | | | | |
| | Coding sequence: 1-1362 | | | | | | |

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1      11      21      31      41      51
|      |      |      |      |      |
ATGGCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAA TCATTGATCA CAGTCATGTC 60
CCCCAGTTTG AGGTGGCCAC CTGGATCAAA ATCACCCCTA TTCTGGTGTA CCTGATCATC 120
5 TTCTGTATGG GCCTTCTGGG GAACAGCGCC ACCATTCGGG TCACCCAGGT GCTGCAGAAG 180
AAAGGATACT TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTCGGACATC 240
TTGGTGTTC TCATCGGCAT GCCCATGGAG TTCTACAGCA TCATCTGGAA TCCCTGACC 300
ACGTCCAGCT ACACCTGTCT CTGCAAGCTG CACACTTTCC TCTTCGAGGC CTGCAGCTAC 360
GCTACGCTGC TGCACGTGCT GACACTCAGC TTTGAGCGCT ACATCGCCAT CTGTCACCCC 420
10 TTCAGGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTGCTCTGG 480
GTCACCTCCG CCTCGGTGGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCTCG 540
GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCCG CCACCAAGAG 600
CAGCCCGAGA CCTCCAATAT GTCCATCTGT ACCAACCCTC CCAGCCGCTG GACCGTGTTC 660
CAGTCCAGCA TCTTCGGCGC CTTCGTGGTC TACCTCGTGG TCCCTGCTCTC CGTAGCCTTC 720
15 ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGGCTCGCT GGCCGGGGGC 780
ACGCGGCCCT CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCAG 840
ACCATCATCT TCTCGAGGCT GATTGTGTG ACATTGGCCG TATGCTGGAT GCCCAACAG 900
ATTCCGAGGA TCATGGCTGC GGCCAAACCC AAGCAGGACT GGACGAGGTC CTACTTCGG 960
GCGTACATGA TCCTCTCTCC CTTCCTGGAG ACCTTTTCT ACCTCAGCTC GGTTCATCAAC 1020
20 CCGCTCCTGT ACACGGTGTG CTGCAGCAG TTTCCGCGGG GTTCTGTGCA GGTGCTGTGC 1080
TGCCCGCTGT CGCTGCAGCA CGCCAAACCC GAGAAGCGCC TGCGCGTACA TGCGCACTCC 1140
ACCAACGACA CGCCCGCTTT TGTGAGCGC CCGTGTCTCT TCGCGTCCCG GCGCCAGTCC 1200
TCTGCAAGGA GAACTGAGAA GATTTTCTTA AGCACTTTTC AGACGAGGC CGAGCCCCAG 1260
25 TCTAAGTCCC AGTCATTGAG TCTCGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACCAGCC 1320
AATTCGCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA

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Protein sequence 21

Gene name: G protein-coupled receptor 39

Unigene number: Hs.85339

Protein Accession #: NM_001508, NP_001409

Signal sequence: none found

Pfam domains: 7tm_1 [72-172, 224-344]

Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342

Cellular Localization: plasma membrane

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35      1      11      21      31      41      51
|      |      |      |      |      |
MASPSLPGSD CSQIIDSHSV PEFEVATWIK ITLILVYLII FVMGLLGNSA TIRVTOVLQK 60
KGYLQKEVD HMVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLCKSL HTFLFEACSY 120
40 ATLLHVLTL FERYIAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFAMGTEYPL 180
VNVPSHRLGT CNRSSTRHHE QPETSNSMIC TNLSSRTVTF QSSIFGAFVY YLVVLLSVAF 240
MCWNMMQVLM KSKQGLSLAG TRPFPQLRKSE SEESRTARRQ TIIFLRILIV TLAVCWMFNP 300
IRIRMAAAKP KHDWTRSYFR AYMLLPFSE TFFYLSSVIN PLLYTVSSQQ FRRVFVQVLC 360
CRLSLQHANH EKRLRVHAHS TTDSARFVQR PLLFASRRQS SARTEKIFL STFQSEAEPE 420
45 SKSQSLSLSE LEPNSGAKPA NSAAENGFBQ HEV

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TABLE 8A: ABOUT 1260 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT TISSUES

Table 8A lists about 1260 genes up-regulated in glioblastoma compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" glioblastoma to "average" normal adult tissues was greater than or equal to 2.5. The "average" glioblastoma level was set to the 75th percentile amongst various glioblastoma tumors. The "average" normal adult tissue level was set to the 85th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigenelD: Unigene number

Unigene Title: Unigene gene title

R1: Ratio of 75th percentile tumor to 85th percentile normal body tissue

| Pkey | ExAccn | UnigenelD | Unigene Title | R1 |
|--------|-----------|-----------|--|------|
| 431917 | D16181 | Hs.2868 | peripheral myelin protein 2 | 75.2 |
| 427343 | A1880044 | Hs.176977 | protein kinase C binding protein 2 | 74.6 |
| 455601 | A1368680 | Hs.816 | SRY (sex determining region Y)-box 2 | 74.2 |
| 428321 | A1699994 | Hs.2868 | peripheral myelin protein 2 | 71.6 |
| 412719 | AW016610 | Hs.129911 | ESTs | 70.7 |
| 449494 | AW237014 | Hs.315369 | Homo sapiens cDNA: FLJ23075 fis, clone L | 66.3 |
| 415817 | U88967 | Hs.78867 | protein tyrosine phosphatase, receptor-t | 64.3 |
| 413472 | BE242870 | Hs.75379 | solute carrier family 1 (glial high affi | 60.1 |
| 456759 | BE259150 | Hs.127792 | delta (Drosophila)-like 3 | 52.3 |
| 435147 | AL133731 | Hs.4774 | Homo sapiens mRNA: cDNA DKFp761C1712 (f | 46.7 |
| 425842 | A1587490 | Hs.159623 | NK-2 (Drosophila) homolog B | 40.1 |
| 412733 | AA984472 | Hs.74554 | KIAA0080 protein | 39.0 |
| 418375 | NM_003081 | Hs.84389 | synaptosomal-associated protein, 25kD | 38.7 |
| 453392 | U23752 | Hs.32964 | SRY (sex determining region Y)-box 11 | 37.2 |
| 423849 | AL157425 | Hs.133315 | Homo sapiens mRNA: cDNA DKFp761J1324 (f | 36.8 |
| 413333 | M74028 | Hs.75297 | fibroblast growth factor 1 (acidic) | 32.8 |
| 416829 | AB013805 | Hs.80220 | catenin (cadherin-associated protein), d | 31.8 |
| 431941 | AK000106 | Hs.272227 | Homo sapiens cDNA FLJ20099 fis, clone CO | 31.8 |
| 436878 | BE465204 | Hs.47448 | ESTs | 31.4 |
| 426325 | D28114 | Hs.169309 | myelin-associated oligodendrocyte basic | 30.9 |
| 425057 | AA826434 | Hs.1619 | achaete-scute complex (Drosophila) homol | 30.4 |
| 446711 | AF169692 | Hs.12450 | protocadherin 9 | 30.2 |
| 439415 | F05538 | Hs.12825 | ESTs | 28.3 |
| 430838 | N46664 | Hs.169395 | hypothetical protein FLJ12015 | 26.9 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 429466 | M85835 | Hs.12827 | ESTs | 25.9 |
| | 447004 | AW296968 | Hs.157539 | ESTs | 25.3 |
| | 424581 | M62062 | Hs.150917 | calenin (cadherin-associated protein), a | 24.8 |
| 5 | 452744 | A1267652 | Hs.30504 | Homo sapiens mRNA; cDNA DKFZp434E082 (fr | 24.8 |
| | 441285 | NM_002374 | Hs.167 | microtubule-associated protein 2 | 24.3 |
| | 453642 | A1370936 | Hs.34074 | dipeptidylpeptidase VI | 24.3 |
| | 424140 | Z48051 | Hs.141308 | myelin oligodendrocyte glycoprotein | 24.2 |
| | 450133 | AW969769 | Hs.105201 | ESTs | 24.2 |
| 10 | 408562 | A436323 | Hs.31141 | Homo sapiens mRNA for KIAA1568 protein, | 23.3 |
| | 448672 | A955511 | Hs.225106 | ESTs | 22.7 |
| | 435708 | A1362949 | Hs.75169 | ESTs | 22.0 |
| | 407034 | U84540 | | gb.Human dystrobrevin isoform DTN-3 (DTN | 21.9 |
| | 407168 | R45175 | Hs.117183 | ESTs | 21.7 |
| 15 | 431019 | NM_005249 | Hs.2714 | forkhead box G1B | 21.5 |
| | 409049 | A423132 | Hs.146343 | ESTs | 21.4 |
| | 433896 | AW294729 | Hs.274461 | ESTs | 21.1 |
| | 445041 | T64183 | Hs.282982 | solute carrier | 21.0 |
| | 418738 | AW388633 | Hs.6682 | solute carrier family 7, (cationic amino | 20.4 |
| 20 | 444378 | R41339 | Hs.12569 | ESTs | 20.0 |
| | 411305 | BE241596 | Hs.69547 | myelin basic protein | 19.9 |
| | 437414 | AW894071 | Hs.48448 | hypothetical protein DKFZp547C176 | 19.8 |
| | 441016 | AW138653 | Hs.25845 | ESTs | 19.6 |
| | 440435 | AL042201 | Hs.21273 | transcription factor NYD-sp10 | 18.5 |
| 25 | 438209 | AL120659 | Hs.6111 | aryl-hydrocarbon receptor nuclear transi | 18.4 |
| | 452461 | N78223 | Hs.108106 | transcription factor | 18.1 |
| | 409395 | U46745 | Hs.54435 | dystrobrevin, alpha | 18.1 |
| | 417183 | R52089 | Hs.172717 | ESTs | 18.0 |
| | 409638 | AW450420 | Hs.21335 | ESTs | 18.0 |
| 30 | 428392 | H10233 | Hs.2265 | secretory granule, neuroendocrine protei | 18.0 |
| | 449611 | A1970394 | Hs.197075 | ESTs | 17.0 |
| | 446692 | Z44514 | Hs.156829 | Homo sapiens mRNA for KIAA1763 protein, | 16.9 |
| | 425088 | AA663372 | Hs.169395 | hypothetical protein FLJ12015 | 16.9 |
| | 444471 | AB020684 | Hs.11217 | KIAA0877 protein | 16.8 |
| 35 | 421659 | NM_014459 | Hs.105511 | protocadherin 17 | 16.7 |
| | 431725 | X65724 | Hs.2839 | Norrie disease (pseudoglioma) | 16.6 |
| | 429276 | AF056085 | Hs.198612 | G protein-coupled receptor 51 | 16.6 |
| | 416892 | L24498 | Hs.80409 | growth arrest and DNA-damage-inducible, | 16.5 |
| | 441440 | A1807981 | Hs.30495 | ESTs | 15.7 |
| 40 | 449433 | A1672096 | Hs.9012 | ESTs, Weakly similar to S26650 DNA-bind | 15.7 |
| | 421264 | AL039123 | Hs.103042 | microtubule-associated protein 1B | 15.5 |
| | 415910 | U20350 | Hs.78913 | chemokine (C-X3-C) receptor 1 | 15.3 |
| | 413597 | AW302885 | Hs.117183 | ESTs | 15.1 |
| | 424945 | A1221919 | Hs.173438 | hypothetical protein FLJ10582 | 14.9 |
| 45 | 447414 | D82343 | Hs.18551 | neuroblastoma (nerve tissue) protein | 14.9 |
| | 426269 | H15302 | Hs.168950 | Homo sapiens mRNA; cDNA DKFZp566A1046 (f | 14.8 |
| | 416857 | AA188775 | Hs.292453 | ESTs | 14.7 |
| | 419721 | NM_001650 | Hs.288650 | aquaporin 4 | 14.6 |
| | 411078 | A1222020 | Hs.182364 | CocoaCrisp | 14.4 |
| 50 | 453924 | R49295 | Hs.24886 | ESTs | 14.4 |
| | 409389 | AB007979 | Hs.301281 | Homo sapiens mRNA, chromosome 1 specific | 14.3 |
| | 430130 | AL137311 | Hs.234074 | Homo sapiens mRNA; cDNA DKFZp761G02121 (| 14.1 |
| | 410909 | AW898161 | Hs.53112 | ESTs, Moderately similar to ALU8_HUMAN A | 14.0 |
| | 412266 | N59006 | Hs.26133 | ESTs | 14.0 |
| 55 | 412986 | X81120 | Hs.75110 | cannabinoid receptor 1 (brain) | 14.0 |
| | 424790 | AL119344 | Hs.13326 | ESTs, Weakly similar to 2004399A chromos | 14.0 |
| | 439239 | AJ031540 | Hs.235331 | ESTs | 14.0 |
| | 441497 | R51064 | Hs.23172 | ESTs | 14.0 |
| | 445495 | BE622641 | Hs.38489 | ESTs, Weakly similar to I38022 hypotheti | 14.0 |
| 60 | 414245 | BE148072 | Hs.75850 | WAS protein family, member 1 | 13.7 |
| | 429900 | AA460421 | Hs.30875 | ESTs | 13.6 |
| | 448595 | AB014544 | Hs.21572 | KIAA0644 gene product | 13.6 |
| | 449605 | AW138581 | Hs.198416 | ESTs | 13.6 |
| | 452526 | W38537 | Hs.280740 | hypothetical protein MGC3040 | 13.6 |
| 65 | 420547 | AF155140 | Hs.98738 | gonadotropin-regulated testicular RNA he | 13.3 |
| | 441350 | AB020690 | Hs.7782 | paraneoplastic antigen MA2 | 13.3 |
| | 420077 | AW512260 | Hs.87767 | ESTs | 13.2 |
| | 424120 | T80579 | Hs.290270 | ESTs | 13.2 |
| | 456965 | AW131888 | Hs.172792 | ESTs, Weakly similar to hypothetical pro | 13.2 |
| 70 | 423361 | AW170055 | Hs.47628 | ESTs | 13.1 |
| | 428409 | AW117207 | Hs.98523 | ESTs | 12.9 |
| | 417160 | N76497 | Hs.1787 | proteolipid protein 1 (Pelizaeus-Merzbac | 12.6 |
| | 451621 | A1879148 | Hs.26770 | fatty acid binding protein 7, brain | 12.5 |
| | 411379 | A1816344 | Hs.12554 | ESTs, Weakly similar to NPL4_HUMAN NUCLE | 12.5 |
| 75 | 436954 | AA740151 | Hs.130425 | ESTs | 12.4 |
| | 430691 | C14187 | Hs.103538 | ESTs | 12.4 |
| | 433551 | A1985544 | Hs.12450 | protocadherin 9 | 12.4 |
| | 422544 | AB018259 | Hs.118140 | KIAA0716 gene product | 12.2 |
| | 427540 | R12014 | Hs.20976 | ESTs | 12.1 |
| 80 | 435624 | AF218942 | Hs.24889 | formin 2 | 12.1 |
| | 415849 | R20529 | Hs.6806 | ESTs | 12.1 |
| | 428845 | AL157579 | Hs.153610 | KIAA0751 gene product | 11.9 |
| | 442671 | AJ005668 | Hs.134779 | EST | 11.9 |
| | 444396 | T65213 | Hs.4257 | ESTs | 11.8 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 452752 | AW044058 | Hs.33578 | KIAA0820 protein | 11.8 |
| | 425523 | AB007948 | Hs.158244 | KIAA0479 protein | 11.8 |
| | 416072 | AL110370 | Hs.79000 | growth associated protein 43 | 11.7 |
| 5 | 440184 | AB002297 | Hs.7022 | dedicator of cyto-kinesis 3 | 11.7 |
| | 428976 | AL037824 | Hs.194695 | ras homolog gene family, member I | 11.6 |
| | 444783 | AK001458 | Hs.62180 | anillin (Drosophila Scraps homolog), act | 11.6 |
| | 448299 | AA497044 | Hs.20887 | hypothetical protein FLJ10392 | 11.6 |
| | 414214 | D49958 | Hs.75819 | glycoprotein M6A | 11.5 |
| 10 | 428982 | NM_005097 | Hs.194704 | leucine-rich, glioma inactivated 1 | 11.5 |
| | 405238 | | | | 11.4 |
| | 420362 | U79734 | Hs.97205 | huntingtin interacting protein 1 | 11.4 |
| | 422980 | N45569 | Hs.76722 | CCAAT/enhancer binding protein (C/EBP), | 11.4 |
| | 424918 | R13982 | Hs.169309 | myelin-associated oligodendrocyte basic | 11.4 |
| | 434277 | X77748 | Hs.3786 | glutamate receptor, metabotropic 3 | 11.4 |
| 15 | 451952 | AL120173 | Hs.301663 | ESTs | 11.3 |
| | 408829 | NM_006042 | Hs.48384 | heparan sulfate (glucosamine) 3-O-sulfot | 11.3 |
| | 424278 | AK000723 | Hs.144517 | hypothetical protein FLJ20716 | 11.3 |
| | 429418 | AJ381028 | Hs.118769 | ESTs | 11.3 |
| 20 | 429918 | AW873986 | Hs.119383 | ESTs | 11.3 |
| | 443912 | R37257 | Hs.184780 | ESTs | 11.3 |
| | 448743 | AB032962 | Hs.21896 | KIAA1136 protein | 11.3 |
| | 420092 | AAB14043 | Hs.88045 | ESTs | 11.2 |
| | 408081 | AW451597 | Hs.167409 | ESTs | 11.2 |
| 25 | 411642 | NM_014932 | Hs.71132 | neurotigin 1 | 10.9 |
| | 415170 | R44386 | Hs.164578 | ESTs | 10.9 |
| | 426320 | W47595 | Hs.169300 | transforming growth factor, beta 2 | 10.8 |
| | 450568 | AL050078 | Hs.25159 | Homo sapiens cDNA FLJ10784 fs, clone NT | 10.8 |
| | 425799 | T08133 | Hs.182906 | Homo sapiens mRNA for KIAA1872 protein, | 10.8 |
| 30 | 423853 | AB011537 | Hs.133456 | slit (Drosophila) homolog 1 | 10.7 |
| | 400293 | N51002 | Hs.306480 | Homo sapiens mRNA; cDNA DKFZp761E2112 (f | 10.7 |
| | 447773 | AI423930 | Hs.36790 | ESTs, Weakly similar to putative p150 [H | 10.7 |
| | 448321 | NM_005883 | Hs.20912 | adenomatous polyposis coli like | 10.5 |
| | 448533 | AL119710 | Hs.21365 | nucleosome assembly protein 1-like 3 | 10.5 |
| 35 | 440684 | AI253123 | Hs.127356 | ESTs, Highly similar to S21424 nestin [H | 10.3 |
| | 444017 | U04840 | Hs.214 | neuro-oncological ventral antigen 1 | 10.3 |
| | 438380 | T06430 | Hs.6194 | chondroitin sulfate proteoglycan BEHAB/b | 10.3 |
| | 440471 | AA886146 | Hs.307944 | ESTs | 10.2 |
| | 413063 | AL035737 | Hs.75184 | chitinase 3-like 1 (cartilage glycoprote | 10.1 |
| 40 | 439978 | BE139460 | Hs.124573 | Homo sapiens cDNA FLJ11477 fs, clone HE | 10.1 |
| | 448902 | Z45998 | Hs.22543 | Homo sapiens mRNA; cDNA DKFZp761I1912 (f | 10.1 |
| | 424932 | R14070 | Hs.315369 | Homo sapiens cDNA: FLJ23075 fs, clone L | 9.9 |
| | 431721 | AB032996 | Hs.268044 | KIAA1170 protein | 9.9 |
| | 419088 | AJ538323 | Hs.52620 | integrin, beta 8 | 9.8 |
| 45 | 420602 | AF060877 | Hs.99236 | regulator of G-protein signalling 20 | 9.8 |
| | 436511 | AA721252 | Hs.291502 | ESTs | 9.8 |
| | 414696 | AF002020 | Hs.76918 | Niemann-Pick disease, type C1 | 9.7 |
| | 449539 | W80363 | Hs.58446 | ESTs | 9.7 |
| | 412959 | D87458 | Hs.75090 | KIAA0282 protein | 9.6 |
| 50 | 412811 | H06382 | Hs.21400 | ESTs | 9.6 |
| | 449300 | AI656959 | Hs.222165 | ESTs | 9.6 |
| | 426344 | H41821 | Hs.322469 | transcriptional activator of the c-fos p | 9.5 |
| | 419271 | N34901 | Hs.238532 | ESTs | 9.5 |
| | 419078 | M93119 | Hs.89584 | insulinoma-associated 1 | 9.4 |
| 55 | 451516 | AI800515 | Hs.12024 | ESTs | 9.4 |
| | 422656 | AI870435 | Hs.1569 | LIM homeobox protein 2 | 9.3 |
| | 449318 | AW236021 | Hs.78531 | Homo sapiens, Similar to RIKEN cDNA 5730 | 9.3 |
| | 414175 | AI308876 | Hs.103849 | hypothetical protein DKFZp761D112 | 9.3 |
| | 415279 | F04237 | Hs.1447 | glial fibrillary acidic protein | 9.2 |
| 60 | 428784 | Y12851 | Hs.193470 | purinergic receptor P2X, ligand-gated io | 9.2 |
| | 429903 | AL134197 | Hs.93597 | cyclin-dependent kinase 5, regulatory su | 9.2 |
| | 424641 | AB001106 | Hs.151413 | glia maturation factor, beta | 9.1 |
| | 417435 | NM_005181 | Hs.82129 | carbonic anhydrase III, muscle specific | 9.1 |
| | 449448 | D60730 | Hs.57471 | ESTs | 9.1 |
| 65 | 408508 | AI806109 | Hs.135736 | KIAA1580 protein | 9.0 |
| | 452785 | AL359942 | Hs.298434 | erythroid differentiation and denucleati | 9.0 |
| | 448986 | H42169 | Hs.18653 | hypothetical protein FLJ14627 | 8.9 |
| | 447072 | D61594 | Hs.17279 | tyrosylprotein sulfotransferase 1 | 8.9 |
| | 433800 | AI034361 | Hs.135150 | lung type-I cell membrane-associated gly | 8.9 |
| 70 | 408926 | AF217525 | Hs.49002 | Down syndrome cell adhesion molecule | 8.8 |
| | 449625 | NM_014253 | Hs.23796 | odc (odd Oz/ten-m, Drosophila) homolog 1 | 8.8 |
| | 400292 | AA250737 | Hs.72472 | ESTs | 8.7 |
| | 417404 | NM_007350 | Hs.82101 | pleckstrin homology-like domain, family | 8.7 |
| | 420345 | AW295230 | Hs.25231 | ESTs | 8.7 |
| 75 | 429927 | NM_001115 | Hs.2522 | adenylate cyclase 8 (brain) | 8.7 |
| | 437528 | N59646 | Hs.169745 | crumbs (Drosophila) homolog 1 | 8.7 |
| | 440152 | AB002376 | Hs.7006 | KIAA0378 protein | 8.7 |
| | 451099 | R52795 | Hs.25954 | interleukin 13 receptor, alpha 2 | 8.6 |
| | 400780 | | | | 8.6 |
| 80 | 434891 | AA814309 | Hs.123583 | ESTs | 8.6 |
| | 449277 | AA001064 | Hs.172976 | ESTs | 8.6 |
| | 415709 | AA649850 | Hs.278558 | ESTs | 8.5 |
| | 439947 | AB006627 | Hs.6788 | astrotactin | 8.5 |
| | 447197 | R36075 | | gb:yh88b01.s1 Soares placenta Nb2HP Homo | 8.5 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 433042 | AW193534 | Hs.281895 | Homo sapiens cDNA FLJ11660 fis, clone HE | 8.4 |
| | 416370 | N90470 | Hs.203697 | ESTs, Weakly similar to I38022 hypotheti | 8.4 |
| | 452786 | R61362 | Hs.106642 | ESTs, Weakly similar to T09052 hypotheti | 8.4 |
| | 415796 | R87548 | Hs.78854 | ATPase, Na+/K+ transporting, beta 2 poly | 8.3 |
| 5 | 426271 | AF026547 | Hs.169047 | chondroitin sulfate proteoglycan 3 (neur | 8.3 |
| | 408947 | AL080093 | Hs.49117 | Homo sapiens mRNA; cDNA DKFZp564N1662 (f | 8.3 |
| | 419863 | AW952691 | Hs.93485 | Homo sapiens mRNA; cDNA DKFZp761D191 (fr | 8.3 |
| | 433447 | U29195 | Hs.3281 | neuronal pentraxin II | 8.3 |
| 10 | 431467 | N71831 | Hs.256398 | Homo sapiens mRNA; cDNA DKFZp434E0528 (f | 8.3 |
| | 409327 | L41162 | Hs.53563 | collagen, type IX, alpha 3 | 8.3 |
| | 414300 | AI304870 | Hs.188680 | ESTs | 8.2 |
| | 407728 | AW071502 | Hs.175931 | ESTs | 8.2 |
| | 422798 | R92347 | Hs.34574 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 8.2 |
| | 419704 | AA429104 | Hs.45057 | ESTs | 8.2 |
| 15 | 429007 | D80642 | | gb:HUM092E09B Human fetal brain (TFujiwa | 8.1 |
| | 442710 | AI015631 | Hs.23210 | ESTs | 8.1 |
| | 425048 | H05468 | Hs.164502 | ESTs | 8.1 |
| | 429149 | AW193360 | Hs.197962 | ESTs, Weakly similar to I38022 hypotheti | 8.0 |
| | 445740 | T78281 | Hs.13226 | Homo sapiens clone 25181 mRNA sequence | 8.0 |
| 20 | 418771 | AA807881 | Hs.25329 | ESTs | 7.9 |
| | 422728 | AW937826 | Hs.103262 | ESTs, Weakly similar to ZN91_HUMAN ZINC | 7.9 |
| | 425984 | AW836277 | Hs.165636 | hypothetical protein DKFZp761C07121 | 7.9 |
| | 448408 | AA322866 | Hs.21107 | neurofilin | 7.9 |
| | 455364 | H72176 | Hs.4273 | hypothetical protein FLJ13159 | 7.9 |
| 25 | 446619 | AI076643 | Hs.313 | secreted phosphoprotein 1 (osteopontin, | 7.9 |
| | 435501 | AW051819 | Hs.129908 | KIAA0591 protein | 7.8 |
| | 423600 | AI633559 | Hs.310359 | ESTs | 7.8 |
| | 450625 | AW970107 | | gb:EST382188 MAGE resequences, MAGK Homo | 7.8 |
| 30 | 415314 | N88802 | Hs.5422 | glycoprotein M6B | 7.7 |
| | 420036 | R60336 | Hs.52792 | Homo sapiens mRNA; cDNA DKFZp586I1823 (f | 7.7 |
| | 427687 | AW003867 | Hs.1570 | histamine receptor H1 | 7.7 |
| | 449328 | AI962493 | Hs.197647 | ESTs | 7.7 |
| | 419249 | X14767 | Hs.89768 | gamma-aminobutyric acid (GABA) A recepto | 7.7 |
| 35 | 407896 | D76435 | Hs.41154 | Zic family member 1 (odd-paired Drosophi | 7.7 |
| | 419103 | Z40229 | Hs.96423 | hypothetical protein FLJ23033 | 7.6 |
| | 439779 | NM_003787 | Hs.6414 | nucleolar protein 4 | 7.6 |
| | 433532 | AW975367 | | gb:EST387475 MAGE resequences, MAGN Homo | 7.6 |
| | 448555 | AI536697 | Hs.159863 | ESTs | 7.5 |
| 40 | 439662 | H97552 | Hs.269060 | ESTs | 7.5 |
| | 448543 | AW897741 | Hs.21380 | Homo sapiens mRNA; cDNA DKFZp586P1124 (f | 7.5 |
| | 410099 | AA081630 | Hs.169387 | KIAA0036 gene product | 7.5 |
| | 431592 | R69016 | Hs.213194 | hypothetical protein MGC10895 | 7.4 |
| | 409731 | AA125985 | Hs.56145 | thymosin, beta, identified in neuroblast | 7.4 |
| | 405819 | | | | 7.4 |
| 45 | 407886 | AW969688 | Hs.100826 | ESTs | 7.4 |
| | 437416 | AL359605 | Hs.283851 | Homo sapiens mRNA; cDNA DKFZp547G036 (fr | 7.4 |
| | 437698 | R61837 | Hs.7990 | ESTs, Moderately similar to I84505 calci | 7.4 |
| | 408604 | D51408 | Hs.21925 | ESTs | 7.4 |
| 50 | 418506 | AA084248 | Hs.85339 | G protein-coupled receptor 39 | 7.3 |
| | 447499 | AW262580 | Hs.147674 | protocadherin beta 16 | 7.3 |
| | 454036 | AA374756 | Hs.93560 | Homo sapiens mRNA for KIAA1771 protein, | 7.3 |
| | 409746 | NM_004794 | Hs.56294 | RAB33A, member RAS oncogene family | 7.2 |
| | 410037 | AB020725 | Hs.58009 | KIAA0918 protein | 7.2 |
| 55 | 419318 | AW969742 | Hs.291005 | ESTs | 7.2 |
| | 424051 | AL110203 | Hs.138411 | Homo sapiens mRNA; cDNA DKFZp586J1922 (f | 7.2 |
| | 442026 | AI243749 | Hs.8074 | brain-specific angiogenesis inhibitor 3 | 7.2 |
| | 448243 | AW369771 | Hs.52620 | integrin, beta 8 | 7.2 |
| | 436281 | AW411194 | Hs.85195 | myeloid leukemia factor 1 | 7.2 |
| 60 | 426429 | X73114 | Hs.169849 | myosin-binding protein C, slow-type | 7.2 |
| | 407182 | AA312551 | Hs.230157 | ESTs | 7.1 |
| | 415293 | R49462 | Hs.106541 | ESTs | 7.1 |
| | 422764 | AI767727 | Hs.47522 | ESTs | 7.1 |
| | 451592 | AI805416 | Hs.213897 | ESTs | 7.1 |
| 65 | 429469 | M64590 | Hs.27 | glycine dehydrogenase (decarboxylating; | 7.0 |
| | 415734 | NM_014747 | Hs.78748 | KIAA0237 gene product | 7.0 |
| | 434149 | Z43829 | Hs.19574 | hypothetical protein MGC5469 | 7.0 |
| | 436726 | AA324975 | Hs.128993 | ESTs, Weakly similar to T00079 hypotheti | 7.0 |
| | 417632 | R20855 | Hs.5422 | glycoprotein M6B | 7.0 |
| 70 | 422421 | AA325138 | Hs.235873 | hypothetical protein FLJ22672 | 6.9 |
| | 435267 | N23797 | Hs.110114 | ESTs | 6.9 |
| | 437117 | AL049256 | Hs.122593 | ESTs | 6.9 |
| | 445523 | Z30118 | Hs.293788 | ESTs, Moderately similar to unnamed prot | 6.9 |
| | 445900 | AF070526 | Hs.13429 | Homo sapiens clone 24787 mRNA sequence | 6.9 |
| 75 | 445745 | AB007924 | Hs.13245 | KIAA0455 gene product | 6.9 |
| | 424085 | NM_002914 | Hs.139226 | replication factor C (activator 1) 2 (40 | 6.9 |
| | 428588 | F12101 | Hs.185701 | Homo sapiens mRNA full length insert cDN | 6.8 |
| | 421723 | AA620400 | Hs.300717 | sodium channel, voltage-gated, type III, | 6.8 |
| | 447342 | AI199268 | Hs.19322 | Homo sapiens, Similar to RIKEN cDNA 2010 | 6.7 |
| 80 | 443297 | AI049864 | Hs.133029 | ESTs | 6.7 |
| | 443992 | AW022228 | Hs.322922 | ESTs | 6.7 |
| | 453096 | AW294631 | Hs.11325 | ESTs | 6.7 |
| | 453857 | AL080235 | Hs.35861 | DKFZP586E1621 protein | 6.7 |
| | 443761 | AI525743 | Hs.160603 | ESTs | 6.6 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 429609 | AF002246 | Hs.210863 | cell adhesion molecule with homology to | 6.6 |
| | 435056 | AW023337 | Hs.5422 | glycoprotein M6B | 6.5 |
| | 453431 | AF094754 | Hs.32973 | glycine receptor, beta | 6.5 |
| 5 | 444190 | AI878918 | Hs.10526 | cysteine and glycine-rich protein 2 | 6.5 |
| | 418110 | R43523 | Hs.217754 | hypothetical protein FLJ22202 | 6.5 |
| | 413988 | MB1883 | Hs.324784 | glutamate decarboxylase 1 (brain, 67kD) | 6.5 |
| | 420805 | L10333 | Hs.99947 | reticulon 1 | 6.4 |
| | 429125 | AA446854 | Hs.271004 | ESTs, Weakly similar to 138022 hypothe | 6.4 |
| 10 | 435256 | AF193766 | Hs.13872 | cytokine-like protein C17 | 6.4 |
| | 407866 | AW088232 | Hs.89506 | paired box gene 6 (aniridia, keratitis) | 6.3 |
| | 440700 | AW952281 | Hs.296184 | guanine nucleotide binding protein (G pr | 6.3 |
| | 427701 | AA411101 | Hs.243886 | nuclear autoantigenic sperm protein (his | 6.3 |
| | 422949 | AA319435 | | gb:EST21657 Adrenal gland tumor Homo sap | 6.2 |
| 15 | 445102 | AW204610 | Hs.22270 | ESTs | 6.2 |
| | 452401 | NM_007115 | Hs.29352 | tumor necrosis factor, alpha-induced pro | 6.2 |
| | 435538 | AB011540 | Hs.4930 | low density lipoprotein receptor-related | 6.2 |
| | 410102 | AW248508 | Hs.279727 | Homo sapiens cDNA FLJ14035 fis, clone HE | 6.2 |
| | 416871 | H98716 | | gb:yx13d08.s1 Soares melanocyte 2NbHM Ho | 6.1 |
| 20 | 416702 | AA186428 | Hs.85591 | ESTs | 6.1 |
| | 419347 | C15944 | Hs.90005 | superiorcervical ganglia, neural specifi | 6.1 |
| | 424997 | AL138167 | Hs.96920 | ESTs | 6.1 |
| | 438660 | U95740 | Hs.6349 | Homo sapiens, clone IMAGE:3010666, mRNA, | 6.1 |
| | 453649 | Y07494 | Hs.34114 | ATPase, Na+/K+ transporting, alpha 2 (+) | 6.1 |
| 25 | 449444 | AW818436 | Hs.23590 | solute carrier family 16 (monocarboxylic | 6.1 |
| | 414117 | W88559 | Hs.1787 | proteolipid protein 1 (Pelizaeus-Merzbac | 6.0 |
| | 425517 | AF121179 | | gb:AF121179 Homo sapiens liver (Chang L- | 6.0 |
| | 427457 | AW779105 | Hs.164682 | ESTs | 6.0 |
| | 437034 | AA742643 | | gb:ny91c01.s1 NCI_CGAP_GCB1 Homo sapiens | 6.0 |
| 30 | 444170 | AW613879 | Hs.102408 | ESTs | 6.0 |
| | 457183 | H91882 | Hs.118569 | Dvl-binding protein IDAX (inhibition of | 6.0 |
| | 448999 | AF179274 | Hs.22791 | transmembrane protein with EGF-like and | 6.0 |
| | 454048 | H05626 | Hs.6921 | ESTs | 6.0 |
| | 439772 | AL365406 | Hs.10268 | Homo sapiens mRNA full length insert cDN | 5.9 |
| 35 | 448944 | AB014605 | Hs.22599 | atrophin-1 interacting protein 1; activi | 5.9 |
| | 410011 | AB020641 | Hs.57856 | PFTAIIE protein kinase 1 | 5.9 |
| | 415486 | H12214 | Hs.13284 | ESTs, Weakly similar to 2109260A B cell | 5.9 |
| | 438993 | AA828995 | | gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens | 5.9 |
| | 447350 | AI375572 | Hs.172634 | ESTs | 5.9 |
| 40 | 451783 | R42554 | Hs.210862 | T-box, brain, 1 | 5.9 |
| | 447101 | N72185 | Hs.44189 | ESTs | 5.9 |
| | 440492 | R39127 | Hs.21433 | hypothetical protein DKFZp547J036 | 5.9 |
| | 440274 | R24595 | Hs.7122 | scrapie responsive protein 1 | 5.9 |
| | 438451 | AW075485 | Hs.286049 | phosphoserine aminotransferase | 5.9 |
| 45 | 418064 | BE387287 | Hs.83384 | S100 calcium-binding protein, beta (neur | 5.8 |
| | 437036 | AI571514 | Hs.133022 | ESTs | 5.7 |
| | 412225 | AW902042 | | gb:QV0-NN1022-170400-193-c02 NN1022 Homo | 5.7 |
| | 426342 | AF093419 | Hs.169378 | multiple PDZ domain protein | 5.7 |
| | 444218 | AF070641 | Hs.10684 | Homo sapiens clone 24421 mRNA sequence | 5.7 |
| 50 | 445828 | F05802 | Hs.81907 | ESTs | 5.7 |
| | 447198 | D61523 | Hs.283435 | ESTs | 5.7 |
| | 427897 | NM_017413 | Hs.303084 | apelin; peptide ligand for APJ receptor | 5.7 |
| | 448499 | BE613280 | Hs.77550 | hypothetical protein MGC1780 | 5.7 |
| | 443672 | AA323362 | Hs.9567 | butyrobetaine (gamma), 2-oxoglutarate di | 5.6 |
| 55 | 412155 | R38167 | Hs.12449 | Homo sapiens transmembrane protein HTMP1 | 5.6 |
| | 435718 | R06569 | Hs.269534 | ESTs | 5.6 |
| | 449340 | AW235786 | Hs.195359 | hypothetical protein MGC10954 | 5.6 |
| | 424481 | R19453 | Hs.1787 | proteolipid protein 1 (Pelizaeus-Merzbac | 5.6 |
| | 451996 | AW514021 | Hs.245510 | ESTs | 5.6 |
| | 422411 | AW749443 | Hs.22511 | ESTs | 5.6 |
| 60 | 438328 | AI492261 | Hs.32450 | ESTs | 5.6 |
| | 433244 | AB040943 | Hs.271285 | KIAA1510 protein | 5.6 |
| | 435191 | R15912 | Hs.4817 | Homo sapiens clone 24461 mRNA sequence | 5.5 |
| | 418677 | S83308 | Hs.87224 | SRY (sex determining region Y)-box 5 | 5.5 |
| 65 | 400859 | | | | 5.5 |
| | 413625 | AW451103 | Hs.71371 | ESTs | 5.5 |
| | 421863 | AI952677 | Hs.108972 | Homo sapiens mRNA; cDNA DKFZp434P228 (tr | 5.5 |
| | 434933 | R91095 | Hs.4276 | KIAA1701 protein | 5.5 |
| | 438702 | AI879064 | Hs.54618 | ESTs | 5.5 |
| 70 | 452055 | AI377431 | Hs.141693 | hypothetical protein MGC10858 | 5.5 |
| | 430979 | AI479755 | Hs.129010 | ESTs | 5.5 |
| | 412709 | AL022327 | Hs.74518 | KIAA0027 protein | 5.5 |
| | 439920 | H05430 | Hs.288433 | neurotrimin | 5.5 |
| | 424343 | AW956360 | Hs.4748 | adenylate cyclase activating polypeptide | 5.4 |
| 75 | 407846 | AA426202 | Hs.40403 | Cbp/p300-interacting transactivator, wit | 5.4 |
| | 419235 | AW470411 | Hs.288433 | neurotrimin | 5.4 |
| | 418030 | BE207573 | Hs.83321 | neuromedin B | 5.4 |
| | 410330 | AW023630 | Hs.46786 | ESTs | 5.4 |
| | 410781 | AI375672 | Hs.165028 | ESTs | 5.4 |
| 80 | 420658 | AW965215 | Hs.336656 | ESTs | 5.4 |
| | 421308 | AA687322 | Hs.192843 | leucine zipper protein FKSG14 | 5.4 |
| | 443740 | R56434 | Hs.21062 | ESTs | 5.4 |
| | 426457 | AW894667 | Hs.169965 | chimerin (chimaerin) 1 | 5.4 |
| | 450375 | AA009647 | Hs.8850 | a disintegrin and metalloproteinase doma | 5.4 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| 5 | 412494 | AL133900 | Hs.792 | ADP-ribosylation factor domain protein 1 | 5.4 |
| | 426600 | NM_003378 | Hs.171014 | VGF nerve growth factor inducible | 5.4 |
| | 424432 | AB037821 | Hs.146858 | protocadherin 10 | 5.4 |
| | 429250 | H56585 | Hs.198308 | tryptophan rich basic protein | 5.4 |
| | 443785 | AW449952 | Hs.190125 | basic-helix-loop-helix-PAS protein | 5.4 |
| 10 | 436282 | R91913 | Hs.272104 | ESTs, Moderately similar to ALU1_HUMAN A | 5.4 |
| | 404584 | | | | 5.3 |
| | 430091 | AB032958 | Hs.233023 | KIAA1132 protein | 5.3 |
| | 439845 | AL355743 | Hs.55663 | Homo sapiens EST from clone 41214, full | 5.3 |
| | 424001 | W67883 | Hs.137476 | paternally expressed 10 | 5.3 |
| 15 | 425073 | W39609 | Hs.22003 | solute carrier family 6 (neurotransmitter) | 5.3 |
| | 426625 | T78300 | Hs.300642 | serologically defined colon cancer antigen | 5.3 |
| | 428137 | AA421792 | Hs.170999 | ESTs | 5.3 |
| | 428679 | AA431765 | | gbzw80c03.s1 Soares_testis_NHT Homo sap | 5.3 |
| | 438176 | AW138970 | Hs.122113 | ESTs | 5.3 |
| 20 | 440138 | AB033023 | Hs.318127 | hypothetical protein FLJ10201 | 5.3 |
| | 451018 | AW965599 | Hs.247324 | mitochondrial ribosomal protein S14 | 5.3 |
| | 416340 | N31772 | Hs.79226 | fasciculation and elongation protein zeta | 5.3 |
| | 435244 | N77221 | Hs.187824 | ESTs | 5.3 |
| | 446035 | NM_006558 | Hs.13565 | Sam68-like phosphotyrosine protein, T-ST | 5.3 |
| 25 | 424624 | AB032947 | Hs.151301 | Ca2+-dependent activator protein for secretion | 5.3 |
| | 407748 | AL079409 | Hs.38176 | KIAA0606 protein; SCN Circadian Oscillator | 5.3 |
| | 430437 | AI768801 | Hs.169943 | Homo sapiens cDNA FLJ13569 fis, clone PL | 5.3 |
| | 414825 | X06370 | Hs.77432 | epidermal growth factor receptor (avian) | 5.2 |
| | 453941 | U39817 | Hs.36820 | Bloom syndrome | 5.2 |
| 30 | 424998 | U58515 | Hs.154138 | chitinase 3-like 2 | 5.2 |
| | 423419 | R55336 | Hs.23539 | ESTs | 5.2 |
| | 424922 | BE386547 | Hs.217112 | hypothetical protein MGC10825 | 5.2 |
| | 447359 | NM_012093 | Hs.18268 | adenylate kinase 5 | 5.2 |
| | 408206 | AF041853 | Hs.43670 | kinesin family member 3A | 5.2 |
| 35 | 421013 | M62397 | Hs.1345 | mutated in colorectal cancers | 5.2 |
| | 429443 | AB028967 | Hs.202687 | potassium voltage-gated channel, Shal-related | 5.2 |
| | 434367 | AB020700 | Hs.3830 | KIAA0893 protein | 5.2 |
| | 444861 | R46789 | Hs.76118 | ubiquitin carboxyl-terminal esterase L1 | 5.2 |
| | 446142 | AI754693 | Hs.145968 | ESTs | 5.2 |
| 40 | 448816 | AB033052 | Hs.22151 | KIAA1226 protein | 5.2 |
| | 451050 | AW937420 | Hs.69662 | ESTs | 5.2 |
| | 451106 | BE382701 | Hs.25960 | v-myc avian myelocytomatosis viral related | 5.2 |
| | 439285 | AL133916 | Hs.172572 | hypothetical protein FLJ20093 | 5.2 |
| | 416737 | AF154335 | Hs.79691 | LIM domain protein | 5.2 |
| 45 | 424800 | AL035588 | Hs.153203 | MyoD family inhibitor | 5.2 |
| | 443695 | AW204099 | Hs.337720 | ESTs, Weakly similar to AF126780 1 retin | 5.2 |
| | 415257 | F03016 | Hs.27513 | ESTs | 5.2 |
| | 433929 | AI375499 | Hs.27379 | ESTs | 5.1 |
| | 415651 | AI207162 | Hs.3815 | stathmin-like-protein RB3 | 5.1 |
| 50 | 451027 | AW519204 | Hs.40808 | ESTs | 5.1 |
| | 409172 | Z99399 | Hs.118145 | ESTs | 5.1 |
| | 423343 | AA324643 | Hs.246106 | ESTs | 5.1 |
| | 429172 | AA447417 | Hs.285491 | ESTs | 5.1 |
| | 437268 | AI754847 | Hs.227571 | regulator of G-protein signaling 4 | 5.1 |
| 55 | 451270 | AW341392 | Hs.235795 | ESTs | 5.1 |
| | 452904 | AL157581 | Hs.30957 | Homo sapiens mRNA; cDNA DKFZp434E0626 (f | 5.1 |
| | 420560 | AW207748 | Hs.59115 | ESTs | 5.1 |
| | 418097 | R45137 | Hs.21868 | ESTs | 5.1 |
| | 442910 | AI365130 | Hs.11307 | ESTs, Weakly similar to T19326 hypothetical | 5.1 |
| 60 | 434849 | AW292765 | Hs.8053 | ESTs | 5.1 |
| | 413554 | AA319146 | Hs.75426 | secretogranin II (chromogranin C) | 5.1 |
| | 414217 | AI309298 | Hs.279898 | Homo sapiens cDNA: FLJ23165 fis, clone L | 5.1 |
| | 412068 | S72043 | Hs.73133 | metallothionein 3 (growth inhibitory factor) | 5.0 |
| | 413627 | BE182082 | Hs.246973 | ESTs | 5.0 |
| 65 | 418661 | NM_001949 | Hs.1189 | E2F transcription factor 3 | 5.0 |
| | 422438 | AA445925 | Hs.270896 | ESTs, Moderately similar to Z195_HUMAN Z | 5.0 |
| | 423728 | AW891294 | Hs.132136 | solute carrier family 4, sodium bicarbonate | 5.0 |
| | 431431 | AL096711 | Hs.252953 | Human DNA sequence from clone RP3-403A15 | 5.0 |
| | 435087 | AW975241 | Hs.23567 | ESTs | 5.0 |
| 70 | 452097 | AB002364 | Hs.27916 | a disintegrin-like and metalloprotease (| 5.0 |
| | 410434 | AF051152 | Hs.63568 | toll-like receptor 2 | 4.9 |
| | 408692 | AL040127 | Hs.34074 | dipeptidylpeptidase VI | 4.9 |
| | 407808 | AA663559 | Hs.279789 | histone deacetylase 3 | 4.9 |
| | 418940 | H17739 | Hs.288513 | Human DNA sequence from clone RP5-899C14 | 4.9 |
| 75 | 425977 | R15138 | Hs.165570 | Homo sapiens clone Z5052 mRNA sequence | 4.9 |
| | 426814 | AF036943 | Hs.172619 | myelin transcription factor 1-like | 4.9 |
| | 447112 | H17800 | Hs.7154 | ESTs | 4.9 |
| | 449574 | F05048 | Hs.175373 | ESTs | 4.9 |
| | 453652 | AW009640 | Hs.28368 | ESTs, Moderately similar to S65657 alpha | 4.9 |
| 80 | 423869 | BE409301 | Hs.134012 | C1q-related factor | 4.9 |
| | 413248 | T64858 | Hs.21433 | hypothetical protein DKFZp547J036 | 4.9 |
| | 449176 | AI633545 | Hs.198072 | ESTs | 4.9 |
| | 448451 | AW015994 | | gb:U1-H-B10p-abh-g-09-0-U1.s1 NCI_CGAP_S | 4.8 |
| | 402604 | | | | 4.8 |
| | 436039 | AW023323 | Hs.121070 | ESTs | 4.8 |
| | 448769 | N66037 | Hs.38173 | ESTs | 4.8 |
| | 423578 | AW963357 | Hs.7847 | ESTs | 4.8 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 439451 | AF086270 | Hs.278554 | heterochromatin-like protein 1 | 4.8 |
| | 425870 | R13406 | Hs.56782 | ESTs | 4.8 |
| | 408777 | U71204 | Hs.47626 | Ric (Drosophila)-like, expressed in neur | 4.8 |
| 5 | 413409 | AI638418 | Hs.78580 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypep | 4.8 |
| | 413623 | AA825721 | Hs.246973 | ESTs | 4.8 |
| | 417246 | AI760098 | Hs.21411 | ESTs | 4.8 |
| | 420900 | AL045633 | Hs.44269 | ESTs | 4.8 |
| | 424153 | AA451737 | Hs.141496 | MAGE-like 2 | 4.8 |
| 10 | 443539 | AI076182 | Hs.134074 | ESTs, Moderately similar to ALU6_HUMAN A | 4.8 |
| | 448750 | U95020 | Hs.21903 | calcium channel, voltage-dependent, beta | 4.8 |
| | 454030 | AW021429 | Hs.231980 | ESTs | 4.8 |
| | 424458 | M29273 | Hs.1780 | myelin associated glycoprotein | 4.8 |
| | 444119 | R41231 | Hs.184261 | ESTs, Weakly similar to T26686 hypotheti | 4.8 |
| | 407792 | AI077715 | Hs.39384 | putative secreted ligand homologous to f | 4.8 |
| 15 | 431462 | AW583672 | Hs.256311 | granin-like neuroendocrine peptide precu | 4.7 |
| | 431103 | M57359 | Hs.44 | pleiotrophin (heparin binding growth fac | 4.7 |
| | 429956 | AI374651 | Hs.22542 | ESTs | 4.7 |
| | 435060 | AI422719 | Hs.233349 | ESTs, Weakly similar to fork head like p | 4.7 |
| 20 | 436203 | BE384982 | Hs.5076 | Homo sapiens cDNA: FLJ22128 fis, clone H | 4.7 |
| | 448475 | BE613134 | Hs.247474 | hypothetical protein FLJ21032 | 4.7 |
| | 422222 | AI699372 | Hs.193247 | hypothetical protein DKFZp434A171 | 4.7 |
| | 431733 | AW298410 | Hs.21475 | ESTs | 4.7 |
| | 449353 | AA001220 | Hs.271369 | ESTs | 4.7 |
| 25 | 452022 | AW072330 | Hs.293875 | ESTs | 4.7 |
| | 454269 | AI951060 | Hs.129908 | KIAA0591 protein | 4.7 |
| | 404541 | | | | 4.7 |
| | 428189 | AA424030 | Hs.46627 | ESTs | 4.7 |
| | 409125 | R17268 | Hs.259873 | axonal transport of synaptic vesicles | 4.7 |
| 30 | 458435 | AI418718 | Hs.144121 | ESTs, Weakly similar to T46916 hypotheti | 4.6 |
| | 425745 | U44060 | Hs.14427 | Homo sapiens cDNA: FLJ21800 fis, clone H | 4.6 |
| | 413492 | D87470 | Hs.75400 | KIAA0280 protein | 4.6 |
| | 419629 | AB020695 | Hs.91662 | KIAA0888 protein | 4.6 |
| | 407638 | AJ404672 | Hs.334483 | hypothetical protein FLJ23571 | 4.6 |
| 35 | 436140 | W87355 | Hs.269587 | ESTs | 4.6 |
| | 439169 | AI912122 | Hs.41095 | ESTs | 4.6 |
| | 443150 | AI034467 | Hs.34650 | ESTs | 4.6 |
| | 451073 | AI758905 | Hs.208063 | ESTs | 4.6 |
| | 451659 | BE379761 | Hs.14248 | ESTs | 4.6 |
| 40 | 452106 | AI141031 | Hs.21342 | ESTs | 4.6 |
| | 451407 | AA131376 | Hs.326401 | fibroblast growth factor 12B | 4.6 |
| | 448765 | R15337 | Hs.21958 | Homo sapiens mRNA; cDNA DKFZp547D086 (fr | 4.6 |
| | 430147 | R60704 | Hs.234434 | hairly/enhancer-of-split related with YRP | 4.6 |
| | 437204 | AL110216 | Hs.12285 | ESTs, Weakly similar to I55214 salivary | 4.6 |
| 45 | 431117 | AF003522 | Hs.250500 | delta (Drosophila)-like 1 | 4.5 |
| | 422175 | N79885 | Hs.6382 | ESTs, Highly similar to T00391 hypotheti | 4.5 |
| | 407889 | R34556 | Hs.30800 | ESTs, Weakly similar to S65657 alpha-1C- | 4.5 |
| | 419343 | AA456245 | Hs.85603 | down-regulated by Ctnnb1, a | 4.5 |
| | 421790 | AW896201 | Hs.22654 | sodium channel, voltage-gated, type I, a | 4.5 |
| 50 | 429399 | AA452244 | Hs.16727 | ESTs | 4.5 |
| | 450149 | AW969781 | Hs.132863 | Zic family member 2 (odd-paired Drosophi | 4.5 |
| | 453118 | AW195849 | Hs.252757 | ESTs | 4.5 |
| | 443455 | AB001025 | Hs.9349 | ryanodine receptor 3 | 4.4 |
| | 442613 | AI004002 | Hs.130522 | Kv channel-interacting protein 1 | 4.4 |
| 55 | 429643 | AA455889 | Hs.167279 | FYVE-finger-containing Rab5 effector pro | 4.4 |
| | 416209 | AA236776 | Hs.79078 | MAD2 (mitotic arrest deficient, yeast, h | 4.4 |
| | 418845 | AA852985 | Hs.89232 | chromobox homolog 5 (Drosophila HP1 alph | 4.4 |
| | 435202 | AI971313 | Hs.170204 | KIAA0551 protein | 4.4 |
| | 437496 | AA452378 | Hs.170144 | Homo sapiens mRNA; cDNA DKFZp547J125 (fr | 4.4 |
| 60 | 451254 | AI571016 | Hs.172967 | ESTs | 4.4 |
| | 439039 | AI656707 | Hs.48713 | ESTs | 4.4 |
| | 439979 | AW600291 | Hs.6823 | hypothetical protein FLJ10430 | 4.4 |
| | 441607 | NM_005010 | Hs.7912 | neuronal cell adhesion molecule | 4.4 |
| | 424983 | AI742434 | Hs.169911 | ESTs | 4.4 |
| 65 | 410611 | AW954134 | Hs.20924 | KIAA1628 protein | 4.4 |
| | 402605 | | | | 4.4 |
| | 409248 | AB033035 | Hs.51965 | KIAA1209 protein | 4.4 |
| | 442222 | AI061301 | Hs.164773 | ESTs | 4.4 |
| | 454027 | R40192 | Hs.21527 | Human DNA sequence from clone GS1-115M3 | 4.4 |
| 70 | 454293 | H49739 | Hs.134013 | ESTs, Moderately similar to HK61_HUMAN H | 4.4 |
| | 442832 | AW206560 | Hs.253569 | ESTs | 4.4 |
| | 407304 | AA565832 | | gb:nj32b03.s1 NCI_CGAP_AA1 Homo sapiens | 4.4 |
| | 423279 | AW959861 | Hs.290943 | ESTs | 4.3 |
| | 427194 | AA399018 | Hs.250835 | ESTs | 4.3 |
| 75 | 419723 | AL120193 | Hs.92614 | longevity assurance (LAG1, S. cerevisiae | 4.3 |
| | 445810 | AW265700 | Hs.155660 | ESTs | 4.3 |
| | 409734 | BE161664 | Hs.56155 | hypothetical protein | 4.3 |
| | 410389 | AW954049 | Hs.8177 | ESTs, Weakly similar to PIHUB6 salivary | 4.3 |
| | 411571 | AA122393 | Hs.70811 | hypothetical protein FLJ20516 | 4.3 |
| 80 | 433024 | AA573847 | Hs.26549 | KIAA1708 protein | 4.3 |
| | 453202 | AW085781 | Hs.26270 | hypothetical protein FLJ11588 | 4.3 |
| | 425264 | AA353953 | Hs.20369 | ESTs, Weakly similar to gonadotropin ind | 4.3 |
| | 416427 | BE244050 | Hs.79307 | Rac/Cdc42 guanine exchange factor (GEF) | 4.3 |
| | 431789 | H19500 | Hs.269222 | mitogen-activated protein kinase 4 | 4.3 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 444600 | R41398 | Hs.6996 | ESTs | 4.3 |
| | 454042 | H22570 | Hs.172572 | hypothetical protein FLJ20093 | 4.3 |
| | 441899 | AJ372588 | Hs.8022 | TU3A protein | 4.3 |
| 5 | 425256 | BE297611 | Hs.155392 | collapsin response mediator protein 1 | 4.3 |
| | 410358 | AW975168 | Hs.13337 | ESTs, Weakly similar to unnamed protein | 4.2 |
| | 430291 | AV660345 | Hs.238126 | CGI-49 protein | 4.2 |
| | 433597 | AA708205 | Hs.100343 | ESTs | 4.2 |
| | 444127 | N63620 | Hs.13281 | ESTs | 4.2 |
| 10 | 448507 | AL133109 | Hs.21333 | Homo sapiens mRNA; cDNA DKFZp566N1047 (f | 4.2 |
| | 413589 | AW452631 | Hs.313803 | ESTs, Highly similar to AF157833 1 noncl | 4.2 |
| | 408577 | H50572 | Hs.19515 | ESTs, Highly similar to NRG3_HUMAN PRO-N | 4.2 |
| | 409719 | AI769160 | Hs.108681 | Homo sapiens brain tumor associated prot | 4.2 |
| | 428536 | AI143139 | Hs.2288 | visinin-like 1 | 4.2 |
| 15 | 429118 | H20669 | Hs.35406 | ESTs, Highly similar to unnamed protein | 4.2 |
| | 432865 | AI753709 | Hs.152484 | ESTs, Weakly similar to I38022 hypotheti | 4.2 |
| | 447138 | AJ439112 | Hs.93828 | ESTs, Weakly similar to Z109260A B cell | 4.2 |
| | 450648 | AI703366 | Hs.26766 | ESTs | 4.2 |
| | 451459 | AI797515 | Hs.270560 | ESTs, Moderately similar to ALU7_HUMAN A | 4.2 |
| 20 | 421686 | AB011156 | Hs.106794 | KIAA0584 protein | 4.2 |
| | 452776 | AA194540 | Hs.13522 | ESTs, Weakly similar to I38022 hypotheti | 4.2 |
| | 436421 | AI678031 | Hs.122813 | ESTs, Weakly similar to ZN22_HUMAN ZINC | 4.2 |
| | 423858 | AL137326 | Hs.133483 | Homo sapiens mRNA; cDNA DKFZp434B0650 (f | 4.2 |
| | 434001 | AW950905 | Hs.3697 | serine (or cysteine) proteinase inhibitor | 4.2 |
| 25 | 437380 | AL359577 | Hs.112198 | Homo sapiens mRNA; cDNA DKFZp547M073 (fr | 4.2 |
| | 432328 | AI572739 | Hs.195471 | 6-phosphofructo-2-kinase/fructose-2,6-bi | 4.1 |
| | 439607 | BE540565 | Hs.159460 | ESTs | 4.1 |
| | 424028 | AF055084 | Hs.153592 | Homo sapiens cDNA FLJ14354 fis, clone Y7 | 4.1 |
| | 446936 | H10207 | Hs.47314 | ESTs | 4.1 |
| 30 | 424240 | AB023185 | Hs.143535 | calcium/calmodulin-dependent protein kin | 4.1 |
| | 412446 | AI768015 | Hs.92127 | ESTs | 4.1 |
| | 409953 | AA332277 | Hs.57691 | cadherin 18, type 2 | 4.1 |
| | 416220 | N49776 | Hs.170994 | hypothetical protein MGC10946 | 4.1 |
| | 419683 | AA248897 | Hs.48784 | ESTs | 4.1 |
| | 426071 | AW138057 | Hs.163835 | ESTs | 4.1 |
| 35 | 428743 | AL080060 | Hs.301549 | Homo sapiens mRNA; cDNA DKFZp564H172 (fr | 4.1 |
| | 432809 | AA565509 | Hs.131703 | ESTs | 4.1 |
| | 440105 | AA694010 | Hs.6932 | Homo sapiens clone Z3809 mRNA sequence | 4.1 |
| | 452039 | AI922988 | Hs.172510 | ESTs | 4.1 |
| 40 | 425905 | AB032959 | Hs.318584 | novel C3HC4 type Zinc finger (ring finger | 4.1 |
| | 457561 | AA331517 | Hs.286055 | chimerin (chimaerin) 2 | 4.1 |
| | 429038 | AL023513 | Hs.194766 | seizure related gene 6 (mouse)-like | 4.1 |
| | 433932 | AW954599 | Hs.169330 | neuronal protein | 4.1 |
| | 436637 | AI783629 | Hs.26766 | ESTs | 4.1 |
| 45 | 439231 | AW581935 | Hs.141480 | Homo sapiens mRNA; cDNA DKFZp434N079 (fr | 4.1 |
| | 450530 | NM_006668 | Hs.25121 | cytochrome P450, subfamily 46 (cholester | 4.1 |
| | 407721 | Y12735 | Hs.38018 | dual-specificity tyrosine-(Y)-phosphoryl | 4.1 |
| | 407881 | AW072003 | Hs.40968 | heparan sulfate (glucosamine) 3-O-sulfot | 4.1 |
| | 410486 | AW235094 | Hs.69233 | zinc finger protein | 4.0 |
| 50 | 413916 | N49813 | Hs.75615 | apolipoprotein C-II | 4.0 |
| | 438703 | AI803373 | Hs.31599 | ESTs | 4.0 |
| | 424726 | AK001007 | Hs.138760 | Homo sapiens cDNA FLJ10145 fis, clone HE | 4.0 |
| | 405771 | | | | 4.0 |
| | 418841 | NM_002332 | Hs.89137 | low density lipoprotein-related protein | 4.0 |
| 55 | 421764 | AI681535 | Hs.148135 | serine/threonine kinase 33 | 4.0 |
| | 424176 | AL137273 | Hs.142307 | hypothetical protein | 4.0 |
| | 425773 | N21279 | Hs.237749 | ESTs | 4.0 |
| | 427304 | AA761526 | Hs.163853 | ESTs | 4.0 |
| | 428882 | AA436915 | Hs.131748 | ESTs, Moderately similar to ALU7_HUMAN A | 4.0 |
| 60 | 452834 | AI538627 | Hs.105685 | KIAA1688 protein | 4.0 |
| | 453745 | AA952989 | Hs.63908 | hypothetical protein MGC14726 | 4.0 |
| | 405239 | U89281 | Hs.11958 | oxidative 3 alpha hydroxysteroid dehydro | 4.0 |
| | 413801 | M62246 | Hs.35406 | ESTs, Highly similar to unnamed protein | 4.0 |
| | 429698 | AI685086 | Hs.26339 | ESTs, Weakly similar to S21348 probable | 4.0 |
| 65 | 435854 | AJ278120 | Hs.4996 | putative ankyrin-repeat containing prote | 4.0 |
| | 439199 | R40373 | Hs.26299 | ESTs | 4.0 |
| | 439450 | R51613 | Hs.125304 | ESTs | 4.0 |
| | 446782 | AI653048 | Hs.144006 | ESTs | 4.0 |
| | 419687 | AI638859 | Hs.227699 | ESTs, Weakly similar to T203_HUMAN TRANS | 3.9 |
| 70 | 402408 | | | | 3.9 |
| | 453362 | H14988 | Hs.107375 | ESTs | 3.9 |
| | 414219 | W20010 | Hs.75823 | ALL1-fused gene from chromosome 1q | 3.9 |
| | 420578 | AA813546 | Hs.99034 | GTP-binding protein Rho7 | 3.9 |
| | 425010 | T16837 | Hs.4241 | ESTs | 3.9 |
| 75 | 444230 | H95537 | Hs.146067 | ESTs | 3.9 |
| | 441736 | AW292779 | Hs.169799 | ESTs | 3.9 |
| | 418951 | F07809 | Hs.89506 | paired box gene 6 (aniridia, keratitis) | 3.9 |
| | 406311 | | | | 3.9 |
| | 408460 | AA054726 | Hs.285574 | ESTs | 3.9 |
| 80 | 410658 | AW105231 | Hs.192035 | ESTs | 3.9 |
| | 414699 | AI815523 | Hs.76930 | synuclein, alpha (non A4 component of am | 3.9 |
| | 418849 | AW474547 | Hs.53565 | Homo sapiens PIG-M mRNA for mannosyltran | 3.9 |
| | 429477 | AI275514 | Hs.6658 | ESTs | 3.9 |
| | 433766 | AA609234 | Hs.112669 | ESTs | 3.9 |

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|----|--------|-----------|-----------|--|-----|
| | 436190 | AK001059 | | gb:Homo sapiens cDNA FLJ10197 fis, clone | 3.9 |
| | 447891 | R41754 | Hs.6496 | ESTs | 3.9 |
| | 450221 | AA328102 | Hs.24641 | cytoskeleton associated protein 2 | 3.9 |
| | 404283 | | | | 3.9 |
| 5 | 453919 | AW959912 | Hs.7076 | KIAA1705 protein | 3.9 |
| | 429656 | X05608 | Hs.211584 | neurofilament, light polypeptide (68kD) | 3.9 |
| | 412754 | AW160375 | Hs.74565 | amyloid beta (A4) precursor-like protein | 3.9 |
| | 445314 | AI689948 | Hs.55489 | Homo sapiens cDNA: FLJ21517 fis, clone C | 3.9 |
| | 435652 | N32388 | Hs.334370 | uncharacterized hypothalamus protein HBE | 3.9 |
| 10 | 407378 | AA299264 | Hs.57776 | ESTs, Moderately similar to I38022 hypot | 3.9 |
| | 438054 | AA776526 | Hs.62183 | ESTs | 3.9 |
| | 436420 | AA443966 | Hs.31595 | ESTs | 3.9 |
| | 445133 | AW157646 | Hs.153506 | ESTs | 3.9 |
| | 432590 | AI609273 | Hs.110783 | ESTs | 3.9 |
| 15 | 453331 | AI240665 | Hs.8895 | ESTs | 3.9 |
| | 410227 | AB009284 | Hs.61152 | exostoses (multiple)-like 2 | 3.8 |
| | 424635 | AA420687 | Hs.115455 | Homo sapiens cDNA FLJ14259 fis, clone PL | 3.8 |
| | 451489 | NM_005503 | Hs.26468 | amyloid beta (A4) precursor protein-bind | 3.8 |
| | 447247 | AW369351 | Hs.287955 | Homo sapiens cDNA FLJ13090 fis, clone NT | 3.8 |
| 20 | 448302 | AI480208 | Hs.182906 | Homo sapiens mRNA for KIAA1872 protein, | 3.8 |
| | 415669 | NM_005025 | Hs.78589 | serine (or cysteine) proteinase inhibito | 3.8 |
| | 417355 | D13168 | Hs.82002 | endothelin receptor type B | 3.8 |
| | 446727 | AB011095 | Hs.16032 | KIAA0523 protein | 3.8 |
| | 424340 | AA339036 | Hs.7033 | ESTs | 3.8 |
| 25 | 423346 | AI267677 | Hs.127416 | synaptojanin 1 | 3.8 |
| | 412788 | AA120960 | Hs.198416 | ESTs | 3.8 |
| | 404593 | | | | 3.8 |
| | 416856 | N27833 | Hs.269028 | ESTs, Weakly similar to I38022 hypotheti | 3.8 |
| 30 | 429896 | AA460367 | Hs.224223 | ESTs, Moderately similar to I38022 hypot | 3.8 |
| | 439619 | AW975998 | Hs.58595 | ESTs, Weakly similar to I38022 hypotheti | 3.8 |
| | 439634 | W79377 | Hs.167 | microtubule-associated protein 2 | 3.8 |
| | 440322 | AA879430 | | gb:oj91d08.s1 Soares_NFL_T_GBC_S1 Homo s | 3.8 |
| | 447761 | AF061573 | Hs.19492 | protocadherin 8 | 3.8 |
| | 452453 | AI902519 | | gb:QV-BT009-101198-051 BT009 Homo sapien | 3.8 |
| 35 | 439671 | AW162840 | Hs.6641 | kinesin family member 5C | 3.8 |
| | 447937 | AL109716 | Hs.20034 | Homo sapiens mRNA full length insert cDN | 3.8 |
| | 459278 | AW294659 | Hs.34054 | Homo sapiens cDNA: FLJ22488 fis, clone H | 3.8 |
| | 447028 | AI973128 | Hs.167257 | brain link protein-1 | 3.8 |
| 40 | 449458 | AI805078 | Hs.208261 | ESTs | 3.8 |
| | 445888 | AF070564 | Hs.13415 | Homo sapiens clone 24571 mRNA sequence | 3.8 |
| | 407385 | AA610150 | Hs.272072 | ESTs, Weakly similar to I38022 hypotheti | 3.8 |
| | 428841 | AI418430 | Hs.104935 | ESTs | 3.8 |
| | 430643 | AW970065 | Hs.287425 | MEGF10 protein | 3.8 |
| 45 | 422263 | AA307639 | Hs.129908 | KIAA0591 protein | 3.8 |
| | 451625 | RS6793 | Hs.106576 | alanine-glyoxylate aminotransferase 2-li | 3.8 |
| | 439236 | BE160952 | Hs.247117 | ESTs, Moderately similar to ALUF_HUMAN I | 3.8 |
| | 441928 | AI370188 | Hs.211454 | ESTs | 3.8 |
| | 441797 | AI936933 | Hs.214635 | ESTs | 3.7 |
| 50 | 414922 | D00723 | Hs.77631 | glycine cleavage system protein H (amino | 3.7 |
| | 425588 | F07396 | Hs.46751 | ESTs | 3.7 |
| | 437007 | AA741300 | Hs.202599 | ESTs, Weakly similar to I38022 hypotheti | 3.7 |
| | 435793 | AB037734 | Hs.4993 | KIAA1313 protein | 3.7 |
| | 443682 | AI383061 | Hs.47248 | ESTs, Highly similar to similar to Cdc14 | 3.7 |
| 55 | 425741 | AF052152 | Hs.159412 | Homo sapiens clone 24628 mRNA sequence | 3.7 |
| | 418211 | BE244746 | Hs.247474 | hypothetical protein FLJ21032 | 3.7 |
| | 440080 | AW051597 | Hs.143707 | ESTs | 3.7 |
| | 452898 | AA814497 | Hs.78792 | ESTs | 3.7 |
| | 435575 | AF213457 | Hs.44234 | triggering receptor expressed on myeloid | 3.7 |
| 60 | 409234 | AI879419 | Hs.27206 | ESTs | 3.7 |
| | 420489 | AA815089 | Hs.193513 | ESTs | 3.7 |
| | 426890 | AA393167 | Hs.41294 | ESTs | 3.7 |
| | 438849 | W28948 | Hs.10762 | ESTs | 3.7 |
| | 441869 | NM_003947 | Hs.8004 | huntingtin-associated protein interactin | 3.7 |
| 65 | 448796 | AA147829 | Hs.301431 | endothelial zinc finger protein induced | 3.7 |
| | 459318 | NM_000038 | | gb:Homo sapiens adenomatosis polyposis c | 3.7 |
| | 459518 | AI937419 | Hs.294069 | Homo sapiens cDNA FLJ13384 fis, clone PL | 3.7 |
| | 434444 | AI765276 | Hs.101257 | hypothetical protein MGC3295 | 3.7 |
| | 421183 | AL135740 | Hs.102447 | TSC-22-like | 3.7 |
| | 410555 | U92649 | Hs.64311 | a disintegrin and metalloproteinase doma | 3.7 |
| 70 | 421637 | AF035290 | Hs.106300 | Homo sapiens clone Z3556 mRNA sequence | 3.7 |
| | 418522 | AA605038 | Hs.7149 | Homo sapiens cDNA: FLJ21950 fis, clone H | 3.7 |
| | 420807 | AA280627 | Hs.57846 | ESTs | 3.7 |
| | 449961 | AW265634 | Hs.133100 | ESTs | 3.7 |
| 75 | 422634 | NM_016010 | Hs.118821 | CGI-62 protein | 3.7 |
| | 421030 | AW161357 | Hs.101174 | microtubule-associated protein tau | 3.7 |
| | 427099 | AB032953 | Hs.173560 | odd Oz/ten-m homolog 2 (Drosophila, mous | 3.7 |
| | 452355 | N54926 | Hs.29202 | G protein-coupled receptor 34 | 3.7 |
| | 440483 | AI200836 | Hs.150386 | ESTs | 3.7 |
| 80 | 429597 | NM_003816 | Hs.2442 | a disintegrin and metalloproteinase doma | 3.7 |
| | 423756 | AA828125 | | gb:od71a09.s1 NCL_CGAP_Ov2 Homo sapiens | 3.6 |
| | 425187 | AW014486 | Hs.22509 | ESTs | 3.6 |
| | 434859 | BE255080 | Hs.299315 | collapsin response mediator protein-5; C | 3.6 |
| | 413199 | M62843 | Hs.75236 | ELAV (embryonic lethal, abnormal vision, | 3.6 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 445729 | H21066 | Hs.13223 | Homo sapiens mRNA full length insert cDN | 3.6 |
| | 416120 | H45739 | | gbyo14h02.s1 Soares adult brain N2b5H85 | 3.6 |
| | 429239 | AA448419 | Hs.45209 | ESTs | 3.6 |
| 5 | 419086 | NM_000216 | Hs.89591 | Kalman syndrome 1 sequence | 3.6 |
| | 446659 | AJ335361 | Hs.226376 | ESTs | 3.6 |
| | 426757 | AW205640 | Hs.158206 | ESTs | 3.6 |
| | 418819 | AA228776 | Hs.191721 | ESTs | 3.6 |
| | 458332 | AI000341 | Hs.220491 | ESTs | 3.6 |
| 10 | 408826 | AF216077 | Hs.48376 | Homo sapiens clone HB-2 mRNA sequence | 3.6 |
| | 410343 | AA084273 | Hs.76561 | ESTs, Weakly similar to S47072 finger pr | 3.6 |
| | 410507 | AA355288 | Hs.40834 | transitional epithelia response protein | 3.6 |
| | 422977 | AA631498 | | gb:np83h04.s1 NCL_CGAP_Thy1 Homo sapiens | 3.6 |
| | 425305 | AA363025 | Hs.155572 | Human clone 23801 mRNA sequence | 3.6 |
| 15 | 428002 | AA418703 | | gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi | 3.6 |
| | 428505 | AL035461 | Hs.2281 | chromogranin B (secretogranin 1) | 3.6 |
| | 430530 | AA480870 | Hs.47660 | ESTs | 3.6 |
| | 436425 | AJ913146 | Hs.318725 | CGI-72 protein | 3.6 |
| | 438078 | AJ016377 | Hs.131693 | ESTs | 3.6 |
| 20 | 442927 | AJ024347 | Hs.131519 | ESTs | 3.6 |
| | 446242 | N66336 | Hs.7360 | ESTs | 3.6 |
| | 448831 | AL080123 | Hs.22182 | zinc finger protein 23 (KOX 16) | 3.6 |
| | 450474 | AW872844 | Hs.201919 | ESTs | 3.6 |
| | 452198 | AJ097550 | Hs.61210 | ESTs, Weakly similar to I38022 hypothesi | 3.6 |
| 25 | 455800 | R22479 | Hs.167073 | Homo sapiens cDNA FLJ13047 fis, clone NT | 3.6 |
| | 436443 | AW138211 | Hs.128746 | ESTs | 3.6 |
| | 426514 | BE616633 | Hs.170195 | bone morphogenetic protein 7 (osteogenic | 3.6 |
| | 456038 | AA203285 | Hs.294141 | ESTs, Weakly similar to alternatively sp | 3.6 |
| | 408902 | AW014869 | Hs.5510 | ESTs | 3.6 |
| 30 | 442950 | AJ500417 | Hs.46764 | ESTs | 3.6 |
| | 442905 | AW579960 | Hs.135150 | lung type-I cell membrane-associated gly | 3.6 |
| | 425478 | AB007953 | Hs.268840 | ESTs | 3.6 |
| | 453884 | AA355925 | Hs.36232 | KIAA0186 gene product | 3.6 |
| | 404721 | | | | 3.6 |
| 35 | 408453 | AJ369838 | Hs.45127 | chondroitin sulfate proteoglycan 5 (neur | 3.6 |
| | 440553 | AA889416 | Hs.295362 | Homo sapiens cDNA FLJ14459 fis, clone HE | 3.5 |
| | 446372 | AB020644 | Hs.14945 | long fatty acyl-CoA synthetase 2 gene | 3.5 |
| | 413999 | N46124 | Hs.34460 | ESTs | 3.5 |
| 40 | 421458 | NM_003654 | Hs.104576 | carbohydrate (keratan sulfate Gal-6) sul | 3.5 |
| | 425017 | AL119305 | Hs.288405 | ESTs | 3.5 |
| | 435958 | H98180 | Hs.117975 | ESTs | 3.5 |
| | 415101 | R45531 | Hs.144534 | ESTs | 3.5 |
| | 451320 | AW118072 | Hs.89981 | diacylglycerol kinase, zeta (104kD) | 3.5 |
| 45 | 430290 | AJ734110 | Hs.136355 | ESTs | 3.5 |
| | 416836 | D54745 | Hs.80247 | cholecystokinin | 3.5 |
| | 414821 | M63835 | Hs.77424 | Fc fragment of IgG, high affinity Ia, re | 3.5 |
| | 419412 | AW161058 | Hs.90297 | synuclein, beta | 3.5 |
| | 437860 | AA333063 | Hs.279898 | Homo sapiens cDNA: FLJ23165 fis, clone L | 3.5 |
| | 452689 | F33868 | Hs.284176 | transferrin | 3.5 |
| 50 | 416661 | AA634543 | Hs.79440 | IGF-II mRNA-binding protein 3 | 3.5 |
| | 427491 | R43279 | Hs.22574 | ESTs, Weakly similar to I38022 hypothesi | 3.5 |
| | 428037 | N47474 | Hs.89230 | potassium intermediate/small conductance | 3.5 |
| | 444584 | AJ168422 | | gb:ok30e11.x1 Soares_NSF_FB_9W_OT_PA_P_S | 3.5 |
| | 408296 | AL117452 | Hs.44155 | DKFZP586G1517 protein | 3.5 |
| 55 | 453775 | NM_002916 | Hs.35120 | replication factor C (activator 1) 4 (37 | 3.5 |
| | 412659 | AW753865 | Hs.74376 | olactomedin related ER localized protei | 3.5 |
| | 429077 | AB028983 | Hs.2352 | adenylate cyclase 2 (brain) | 3.5 |
| | 436887 | AW953157 | Hs.193235 | hypothetical protein DKFZp547D155 | 3.5 |
| | 450784 | AW246803 | Hs.47289 | ESTs | 3.5 |
| 60 | 446827 | AW451243 | Hs.157069 | ESTs | 3.5 |
| | 436434 | N50465 | Hs.92927 | putative 47 kDa protein | 3.5 |
| | 412777 | AJ335773 | Hs.270123 | ESTs | 3.5 |
| | 436476 | AA325108 | Hs.33829 | bHLH protein DEC2 | 3.5 |
| | 408601 | U47928 | Hs.86122 | protein A | 3.4 |
| 65 | 429401 | AW296102 | Hs.99272 | ESTs, Weakly similar to S32567 A4 protei | 3.4 |
| | 448425 | AJ500359 | Hs.233401 | ESTs | 3.4 |
| | 418727 | AA227609 | Hs.94834 | ESTs | 3.4 |
| | 451729 | AW160725 | Hs.312469 | ESTs | 3.4 |
| | 435910 | AJ084152 | Hs.21782 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 3.4 |
| 70 | 434577 | R37316 | Hs.179769 | Homo sapiens cDNA: FLJ22487 fis, clone H | 3.4 |
| | 414598 | AJ094221 | Hs.135150 | lung type-I cell membrane-associated gly | 3.4 |
| | 439627 | BE621702 | Hs.29076 | hypothetical protein FLJ21841 | 3.4 |
| | 413293 | AL047483 | Hs.302498 | GTP-binding protein homologous to Saccha | 3.4 |
| | 423992 | AW898292 | Hs.137206 | Homo sapiens mRNA; cDNA DKFZp564H1663 (f | 3.4 |
| 75 | 426249 | F05422 | Hs.168352 | nucleoporin-like protein 1 | 3.4 |
| | 426968 | U07616 | Hs.173034 | amphiphysin (Stiff-Mann syndrome with br | 3.4 |
| | 430388 | AA356923 | Hs.240770 | nuclear cap binding protein subunit 2, 2 | 3.4 |
| | 435061 | AJ651474 | Hs.163944 | ESTs | 3.4 |
| | 452291 | AF015592 | Hs.28853 | CDC7 (cell division cycle 7, S. cerevisi | 3.4 |
| 80 | 449714 | AB033015 | Hs.23941 | KIAA1189 protein | 3.4 |
| | 443392 | AJ055821 | Hs.293420 | ESTs | 3.4 |
| | 410082 | AA081594 | Hs.158311 | Musashi (Drosophila) homolog 1 | 3.4 |
| | 445337 | NM_013280 | Hs.12523 | fibronectin leucine rich transmembrane p | 3.4 |
| | 408493 | BE206854 | Hs.46039 | phosphoglycerate mutase 2 (muscle) | 3.4 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| 5 | 432731 | R31178 | Hs.287820 | fibronectin 1 | 3.4 |
| | 448758 | AB018311 | Hs.21917 | KIAA0768 protein | 3.4 |
| | 432613 | AW081698 | Hs.80712 | KIAA0202 protein | 3.4 |
| | 434164 | AW207019 | Hs.148135 | serine/threonine kinase 33 | 3.4 |
| | 425294 | AF033827 | Hs.155553 | HNK-1 sulfotransferase | 3.4 |
| 10 | 410108 | AA081659 | Hs.318775 | OSBP-related protein 6 | 3.4 |
| | 406815 | AA833930 | Hs.288036 | tRNA isopentenylpyrophosphate transferase | 3.4 |
| | 402855 | | | | 3.3 |
| | 422170 | AI791949 | Hs.112432 | anti-Müllerian hormone | 3.3 |
| | 445034 | AW293376 | Hs.143659 | ESTs | 3.3 |
| 15 | 424378 | W28020 | Hs.167988 | neural cell adhesion molecule 1 | 3.3 |
| | 423611 | AB011163 | Hs.129908 | KIAA0591 protein | 3.3 |
| | 435593 | R88872 | Hs.4964 | DKFZP586J1624 protein | 3.3 |
| | 404819 | | | | 3.3 |
| | 436607 | AW661783 | Hs.211061 | ESTs | 3.3 |
| 20 | 427315 | AA179949 | Hs.175563 | Homo sapiens mRNA; cDNA DKFZp564N0763 (f | 3.3 |
| | 452693 | T79153 | Hs.48589 | zinc finger protein 228 | 3.3 |
| | 454996 | AW850180 | | gb:IL3-CT0219-271099-022-C09 CT0219 Homo | 3.3 |
| | 406927 | M26460 | | gb:Homo sapiens (clone 104) retinoblasto | 3.3 |
| | 409045 | AA635062 | Hs.50094 | Homo sapiens mRNA; cDNA DKFZp43400515 (f | 3.3 |
| 25 | 415238 | R37780 | Hs.21422 | ESTs | 3.3 |
| | 417845 | AL117461 | Hs.82719 | Homo sapiens mRNA; cDNA DKFZp586F1822 (f | 3.3 |
| | 421192 | AA833718 | Hs.204529 | KIAA1806 protein | 3.3 |
| | 426695 | AW118191 | Hs.112729 | ESTs | 3.3 |
| | 438885 | AI886558 | Hs.184987 | ESTs | 3.3 |
| 30 | 451762 | AF222980 | Hs.26985 | disrupted in schizophrenia 1 | 3.3 |
| | 452103 | R42764 | Hs.339654 | ESTs, Weakly similar to I38022 hypotheti | 3.3 |
| | 453590 | AF150278 | Hs.33578 | KIAA0820 protein | 3.3 |
| | 453616 | NM_003462 | Hs.33846 | dynein, axonemal, light intermediate pol | 3.3 |
| | 457285 | AI038858 | Hs.130522 | Kv channel-interacting protein 1 | 3.3 |
| 35 | 436045 | AB037723 | Hs.5028 | DKFZP564O0423 protein | 3.3 |
| | 437470 | AL390147 | Hs.134742 | hypothetical protein DKFZp547D065 | 3.3 |
| | 448520 | AB002367 | Hs.21355 | doublecortin and CaM kinase-like 1 | 3.3 |
| | 436480 | AJ271643 | Hs.87469 | putative acid-sensing ion channel | 3.3 |
| | 432656 | NM_000246 | Hs.3076 | MHC class II transactivator | 3.3 |
| 40 | 443898 | AW804296 | Hs.9950 | Sec61 gamma | 3.3 |
| | 423582 | BE000831 | Hs.23837 | Homo sapiens cDNA FLJ11812 fis, clone HE | 3.3 |
| | 445953 | AI612775 | Hs.145710 | ESTs | 3.3 |
| | 427940 | AA417812 | Hs.38775 | ESTs | 3.3 |
| | 414683 | S78296 | Hs.76888 | hypothetical protein MGC12702 | 3.3 |
| 45 | 428484 | AF104032 | Hs.184601 | solute carrier family 7 (cationic amino | 3.3 |
| | 420649 | AI866964 | Hs.124704 | ESTs, Moderately similar to S6557 alpha | 3.3 |
| | 419498 | AL036591 | Hs.20887 | hypothetical protein FLJ10392 | 3.3 |
| | 457579 | AB030816 | Hs.36761 | HRAS-like suppressor | 3.3 |
| | 436556 | AI364997 | Hs.7572 | ESTs | 3.2 |
| 50 | 424369 | R87622 | Hs.26714 | KIAA1831 protein | 3.2 |
| | 457065 | AJ476318 | Hs.192480 | ESTs | 3.2 |
| | 440210 | AW674562 | Hs.125296 | ESTs | 3.2 |
| | 444513 | AL120214 | Hs.7117 | glutamate receptor, ionotropic, AMPA 1 | 3.2 |
| | 434353 | AA630863 | Hs.131375 | ESTs, Moderately similar to ALU8_HUMAN I | 3.2 |
| 55 | 414430 | AI346201 | Hs.76118 | ubiquitin carboxyl-terminal esterase L1 | 3.2 |
| | 439924 | AI985897 | Hs.125293 | ESTs | 3.2 |
| | 411505 | AF155659 | Hs.70565 | molybdenum cofactor synthesis 2 | 3.2 |
| | 423175 | W27595 | Hs.18653 | hypothetical protein FLJ14627 | 3.2 |
| | 415115 | AA214228 | Hs.127751 | hypothetical protein | 3.2 |
| 60 | 407878 | D87468 | Hs.40888 | activity-regulated cytoskeleton-associat | 3.2 |
| | 410274 | AA381807 | Hs.61762 | hypoxia-inducible protein 2 | 3.2 |
| | 437762 | T78028 | Hs.154679 | synaptotagmin I | 3.2 |
| | 438944 | AA302517 | Hs.92732 | KIAA1444 protein | 3.2 |
| | 450313 | AI038989 | Hs.332633 | Bardet-Biedl syndrome 2 | 3.2 |
| 65 | 409459 | D86407 | Hs.54481 | low density lipoprotein receptor-related | 3.2 |
| | 410953 | AW811766 | Hs.334858 | hypothetical protein MGC12250 | 3.2 |
| | 418527 | AA450386 | Hs.7149 | Homo sapiens cDNA: FLJ21950 fis, clone H | 3.2 |
| | 420081 | AW510776 | Hs.94958 | tubulin tyrosine ligase-like 1 | 3.2 |
| | 429496 | AA453800 | Hs.192793 | ESTs | 3.2 |
| 70 | 430099 | AW194988 | Hs.20537 | hypothetical protein FLJ13942 | 3.2 |
| | 434928 | AW015595 | Hs.4267 | Homo sapiens clones 24714 and 24715 mRNA | 3.2 |
| | 435532 | AW291488 | Hs.117305 | Homo sapiens, clone IMAGE:3682908, mRNA | 3.2 |
| | 438306 | AW188266 | Hs.163645 | ESTs | 3.2 |
| | 439274 | AF086092 | Hs.48372 | ESTs | 3.2 |
| 75 | 440847 | AA907511 | Hs.130178 | ESTs | 3.2 |
| | 447750 | AI422234 | Hs.143434 | contactin 1 | 3.2 |
| | 455350 | AW901809 | | gb:QVO-NN1020-170400-195-h02 NN1020 Homo | 3.2 |
| | 430890 | X54232 | Hs.2699 | glypican 1 | 3.2 |
| | 420568 | F09247 | Hs.247735 | protocadherin alpha 10 | 3.2 |
| 80 | 410768 | AF038185 | Hs.66187 | Homo sapiens clone 23700 mRNA sequence | 3.2 |
| | 427450 | AB014526 | Hs.178121 | KIAA0626 gene product | 3.2 |
| | 430456 | AA314998 | Hs.241503 | hypothetical protein | 3.2 |
| | 430181 | AF065314 | Hs.234785 | cyclic nucleotide gated channel alpha 3 | 3.2 |
| | 418512 | AW498974 | Hs.89981 | diacylglycerol kinase, zeta (104kD) | 3.2 |
| | 419912 | AF249745 | Hs.6066 | Rho guanine nucleotide exchange factor (| 3.2 |
| | 450689 | AI369275 | Hs.243010 | Homo sapiens cDNA FLJ14445 fis, clone HE | 3.2 |
| | 424899 | AL119387 | Hs.119062 | ESTs | 3.2 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 436277 | R88520 | Hs.120917 | ESTs | |
| | 451455 | AJ937227 | Hs.8821 | hepcidin antimicrobial peptide | 3.2 |
| | 445078 | AI869975 | Hs.4775 | junctophilin 3 | 3.2 |
| 5 | 447746 | AW015920 | Hs.161359 | ESTs | 3.2 |
| | 435458 | F11872 | Hs.4892 | Homo sapiens clone 24841 mRNA sequence | 3.2 |
| | 427729 | AB033100 | Hs.300646 | KIAA protein (similar to mouse paladin) | 3.2 |
| | 417417 | F05745 | Hs.89512 | ATPase, Ca ⁺⁺ transporting, plasma membra | 3.1 |
| | 438810 | AW897846 | Hs.6421 | hypothetical protein DKFZp761N09121 | 3.1 |
| 10 | 439570 | T79925 | Hs.269165 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.1 |
| | 432527 | AW975028 | Hs.102754 | ESTs | 3.1 |
| | 416801 | X98834 | Hs.79971 | sal (Drosophila)-like 2 | 3.1 |
| | 421988 | AW450481 | Hs.161333 | ESTs | 3.1 |
| | 426509 | M31165 | Hs.2050 | pentactin-related gene, rapidly induced b | 3.1 |
| 15 | 408786 | AA773187 | Hs.294027 | ESTs | 3.1 |
| | 433494 | AB029396 | Hs.3353 | beta-1,3-glucuronyltransferase 1 (glucur | 3.1 |
| | 412723 | AA648459 | Hs.335951 | hypothetical protein AF301222 | 3.1 |
| | 418329 | AW247430 | Hs.84152 | cystathionine-beta-synthase | 3.1 |
| | 439456 | AI752409 | Hs.109314 | hypothetical protein FLJ20980 | 3.1 |
| 20 | 428832 | AA578229 | Hs.324239 | ESTs, Moderately similar to ZN91_HUMAN Z | 3.1 |
| | 452780 | BE171598 | Hs.13522 | ESTs, Weakly similar to I38022 hypothe | 3.1 |
| | 438192 | AI859065 | Hs.337620 | Homo sapiens AFG3L1 isoform 1 mRNA, part | 3.1 |
| | 424939 | AK000059 | Hs.153881 | Homo sapiens NY-REN-82 antigen mRNA, par | 3.1 |
| | 403053 | R58624 | Hs.2186 | eukaryotic translation elongation factor | 3.1 |
| 25 | 404299 | | | | 3.1 |
| | 407864 | AF069291 | Hs.40539 | chromosome 8 open reading frame 1 | 3.1 |
| | 410181 | AJ468210 | Hs.261285 | pleiotropic regulator 1 (PRL1, Arabidops | 3.1 |
| | 418852 | BE537037 | Hs.273294 | hypothetical protein FLJ20069 | 3.1 |
| | 449101 | AA205847 | Hs.23016 | G protein-coupled receptor | 3.1 |
| 30 | 453240 | AI969564 | Hs.166254 | hypothetical protein DKFZp5661133 | 3.1 |
| | 440486 | BE243513 | Hs.7212 | hypothetical protein PP1044 | 3.1 |
| | 408096 | BE250162 | Hs.83765 | dihydrofolate reductase | 3.1 |
| | 439864 | AI720078 | Hs.291997 | ESTs, Weakly similar to A47582 B-cell gr | 3.1 |
| | 414705 | AW340125 | Hs.76989 | KIAA0097 gene product | 3.1 |
| 35 | 436315 | BE390513 | Hs.27935 | hypothetical protein MGC4837 | 3.1 |
| | 426855 | AL117427 | Hs.172778 | Homo sapiens mRNA; cDNA DKFZp566P013 (fr | 3.1 |
| | 425683 | AB037813 | Hs.159200 | hypothetical protein DKFZp762K222 | 3.1 |
| | 410126 | BE169274 | Hs.169387 | KIAA0036 gene product | 3.1 |
| | 435312 | AJ243396 | Hs.4865 | voltage-gated sodium channel beta-3 subu | 3.1 |
| 40 | 425491 | AA883316 | Hs.255221 | ESTs | 3.1 |
| | 456273 | AF154846 | Hs.1148 | zinc finger protein | 3.1 |
| | 412140 | AA219691 | Hs.73625 | RAB6 interacting, kinasin-like (rabkines | 3.1 |
| | 445255 | NM_014841 | Hs.12477 | synaptosomal-associated protein, 91 kDa | 3.1 |
| | 432154 | AI701523 | Hs.112577 | ESTs | 3.1 |
| 45 | 453128 | AW026516 | Hs.31791 | acylphosphatase 2, muscle type | 3.1 |
| | 438458 | AW975186 | | gb:EST387294 MAGE resequences, MAGN Homo | 3.1 |
| | 448616 | AF035621 | Hs.21611 | kinesin family member 3C | 3.0 |
| | 429281 | AA830856 | Hs.29808 | Homo sapiens cDNA: FLJ21122 fis, clone C | 3.0 |
| | 443906 | AA348031 | Hs.7913 | ESTs | 3.0 |
| 50 | 417318 | AW953937 | Hs.12891 | ESTs | 3.0 |
| | 452619 | AW298597 | Hs.61884 | Homo sapiens, clone IMAGE:4298026, mRNA, | 3.0 |
| | 444153 | AK001610 | Hs.10414 | hypothetical protein FLJ10748 | 3.0 |
| | 408790 | AW580227 | Hs.47860 | neurotrophic tyrosine kinase, receptor, | 3.0 |
| | 426327 | W03242 | Hs.44898 | Homo sapiens clone TCCTA00151 mRNA sequ | 3.0 |
| 55 | 451468 | AW503398 | Hs.293663 | ESTs, Moderately similar to I38022 hypot | 3.0 |
| | 422758 | AF152329 | Hs.284180 | protocadherin gamma subfamily C, 3 | 3.0 |
| | 421633 | AF121860 | Hs.106260 | sorting nexin 10 | 3.0 |
| | 428361 | NM_015905 | Hs.183858 | transcriptional intermediary factor 1 | 3.0 |
| | 418932 | L34059 | Hs.89484 | cadherin 4, type 1, R-cadherin (retinal) | 3.0 |
| 60 | 416805 | F13271 | Hs.79981 | Human clone 23560 mRNA sequence | 3.0 |
| | 419518 | U79289 | Hs.90798 | Human clone 23695 mRNA sequence | 3.0 |
| | 422709 | AA315331 | Hs.153485 | ESTs | 3.0 |
| | 423135 | N67655 | Hs.26411 | ESTs | 3.0 |
| | 424901 | Z11933 | Hs.182505 | POU domain, class 3, transcription facto | 3.0 |
| 65 | 426617 | W58006 | Hs.266258 | endonuclease G-like 1 | 3.0 |
| | 427386 | AW836261 | Hs.337717 | ESTs | 3.0 |
| | 429859 | NM_007050 | Hs.225952 | protein tyrosine phosphatase, receptor t | 3.0 |
| | 435071 | D60883 | Hs.35495 | ESTs | 3.0 |
| | 435092 | AL137310 | Hs.4749 | Homo sapiens mRNA; cDNA DKFZp761E13121 (| 3.0 |
| 70 | 436211 | AK001581 | Hs.334828 | hypothetical protein FLJ10719; KIAA1794 | 3.0 |
| | 436936 | AL134451 | Hs.197478 | ESTs | 3.0 |
| | 445855 | BE247129 | Hs.145569 | ESTs | 3.0 |
| | 452294 | AI871925 | Hs.117895 | ESTs, Moderately similar to A47582 B-cel | 3.0 |
| | 433980 | AA137152 | Hs.286049 | phosphoserine aminotransferase | 3.0 |
| 75 | 430228 | AW950939 | Hs.6382 | ESTs, Highly similar to T00391 hypotheti | 3.0 |
| | 451026 | AA013218 | Hs.157492 | cer-d4 (mouse) homolog | 3.0 |
| | 435232 | NM_001262 | Hs.4854 | cyclin-dependent kinase inhibitor 2C (p1 | 3.0 |
| | 439566 | AF086387 | | gb:Homo sapiens full length insert cDNA | 3.0 |
| | 425782 | U66468 | Hs.159525 | cell growth regulatory with EF-hand doma | 3.0 |
| 80 | 416586 | D44643 | Hs.14144 | secreted modular calcium-binding protein | 3.0 |
| | 416874 | H98752 | Hs.42568 | ESTs | 3.0 |
| | 410386 | W26187 | Hs.3327 | Homo sapiens cDNA: FLJ22219 fis, clone H | 3.0 |
| | 411411 | AA345241 | Hs.55950 | ESTs, Weakly similar to KIAA1330 protein | 3.0 |
| | 424066 | Z99348 | Hs.112461 | ESTs, Weakly similar to I38022 hypotheti | 3.0 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 404048 | | | | 3.0 |
| | 429163 | AA884766 | | gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s | 3.0 |
| | 454117 | BE410100 | Hs.40358 | adaptor-related protein complex 1, sigma | 3.0 |
| | 418196 | A1745649 | Hs.26549 | KIAA1708 protein | 3.0 |
| 5 | 434131 | A1858275 | Hs.143659 | ESTs | 3.0 |
| | 441255 | R06350 | Hs.171635 | ESTs | 2.9 |
| | 453900 | AW003582 | Hs.226414 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 2.9 |
| | 453905 | NM_002314 | Hs.36566 | LIM domain kinase 1 | 2.9 |
| | 416602 | NM_006159 | Hs.79389 | nel (chicken)-like 2 | 2.9 |
| 10 | 431173 | AW971198 | Hs.294068 | ESTs | 2.9 |
| | 425599 | AW366745 | Hs.214140 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.9 |
| | 436401 | A1087958 | Hs.29088 | ESTs | 2.9 |
| | 422960 | AW890487 | Hs.63984 | cadherin 13, H-cadherin (heart) | 2.9 |
| | 451558 | NM_001089 | Hs.26630 | ATP-binding cassette, sub-family A (ABC1 | 2.9 |
| 15 | 412490 | AW803564 | Hs.288850 | Homo sapiens cDNA: FLJ22528 fis, clone H | 2.9 |
| | 433149 | BE257672 | Hs.42949 | hypothetical protein HES6 | 2.9 |
| | 434811 | AW971205 | Hs.114280 | ESTs | 2.9 |
| | 425897 | AA935315 | Hs.48965 | Homo sapiens cDNA: FLJ21693 fis, clone C | 2.9 |
| | 452092 | BE245374 | Hs.27842 | hypothetical protein FLJ11210 | 2.9 |
| 20 | 453496 | AA442103 | Hs.33084 | solute carrier family 2 (facilitated glu | 2.9 |
| | 411124 | AW196937 | Hs.53929 | ESTs, Weakly similar to ALUB_HUMAN IIII | 2.9 |
| | 419227 | BE537383 | Hs.89739 | cholinergic receptor, nicotinic, beta po | 2.9 |
| | 427651 | AW405731 | Hs.18498 | Homo sapiens cDNA FLJ12277 fis, clone MA | 2.9 |
| | 441707 | R42637 | Hs.21963 | hypothetical protein DKFZp761B0514 | 2.9 |
| 25 | 435741 | A1240668 | Hs.113099 | ESTs | 2.9 |
| | 437273 | AL137451 | Hs.120873 | ESTs, Highly similar to T46266 hypothei | 2.9 |
| | 422939 | AW394055 | Hs.98427 | ESTs, Weakly similar to I38022 hypothei | 2.9 |
| | 439376 | AA883521 | Hs.222064 | ESTs | 2.9 |
| | 439935 | S75105 | Hs.301676 | glutamate receptor, ionotropic, kainate | 2.9 |
| 30 | 437267 | AW511443 | Hs.258110 | ESTs | 2.9 |
| | 453740 | AL120295 | Hs.311809 | ESTs, Moderately similar to PC4259 fami | 2.9 |
| | 400250 | | | | 2.9 |
| | 400992 | | | | 2.9 |
| 35 | 408814 | N62499 | Hs.176227 | hypothetical protein FLJ11155 | 2.9 |
| | 411849 | AW964970 | Hs.18861 | ESTs, Moderately similar to KIAA1276 pro | 2.9 |
| | 414853 | U31116 | Hs.77501 | sarcoglycan, beta (43kD dystrophin-assoc | 2.9 |
| | 423751 | AW235633 | Hs.46525 | ESTs | 2.9 |
| | 426910 | AA470023 | Hs.190089 | ESTs, Moderately similar to ALU1_HUMAN A | 2.9 |
| 40 | 450203 | AF097994 | Hs.301528 | L-tyrosine/alpha-aminoadipate aminotra | 2.9 |
| | 459311 | R40192 | Hs.21527 | Human DNA sequence from clone GS1-115M3 | 2.9 |
| | 425304 | AA463844 | Hs.31339 | fibroblast growth factor 11 | 2.9 |
| | 428500 | A1815395 | Hs.184641 | fatty acid desaturase 2 | 2.9 |
| | 421641 | A1638184 | Hs.106334 | Homo sapiens clone 23836 mRNA sequence | 2.9 |
| | 421141 | AW117261 | Hs.125914 | ESTs | 2.9 |
| 45 | 407870 | AB032990 | Hs.40719 | hypothetical protein KIAA1164 | 2.9 |
| | 456723 | Z43902 | Hs.4748 | adenylate cyclase activating polypeptide | 2.9 |
| | 436456 | AW292577 | Hs.248122 | G protein-coupled receptor 24 | 2.9 |
| | 421483 | NM_003388 | Hs.104717 | hypothetical protein MGC11333 | 2.9 |
| | 412190 | R16180 | Hs.274461 | ESTs | 2.9 |
| 50 | 446131 | NM_000929 | Hs.290 | phospholipase A2, group V | 2.9 |
| | 441668 | A1611973 | Hs.127525 | ESTs | 2.9 |
| | 437387 | A198874 | Hs.28847 | AD026 protein | 2.9 |
| | 423420 | A1571364 | Hs.128382 | Homo sapiens mRNA; cDNA DKFZp7611224 (f | 2.9 |
| 55 | 427958 | AA418000 | Hs.98280 | potassium intermediate/small conductance | 2.9 |
| | 429084 | AJ001443 | Hs.195614 | splicing factor 3b, subunit 3, 130kD | 2.9 |
| | 447067 | R42098 | Hs.21964 | ESTs | 2.9 |
| | 430887 | N66801 | Hs.260287 | KIAA1841 protein | 2.9 |
| | 441824 | AB007871 | Hs.7977 | KIAA0411 gene product | 2.9 |
| 60 | 424126 | AA335635 | Hs.96917 | ESTs | 2.9 |
| | 408739 | W01556 | Hs.238797 | ESTs, Moderately similar to I38022 hypot | 2.9 |
| | 447422 | BE618703 | Hs.98258 | orthopedia (Drosophila) homolog | 2.9 |
| | 435615 | Y15065 | Hs.4975 | potassium voltage-gated channel, KQT-tik | 2.9 |
| | 446997 | AA383439 | Hs.16758 | Spir-1 protein | 2.9 |
| 65 | 433573 | AF234887 | Hs.57652 | cadherin, EGF LAG seven-pass G-type rece | 2.9 |
| | 408447 | AK002089 | Hs.45080 | Homo sapiens cDNA FLJ11227 fis, clone PL | 2.9 |
| | 419586 | AJ088485 | Hs.144759 | ESTs, Weakly similar to I38022 hypothei | 2.8 |
| | 417022 | NM_014737 | Hs.80905 | Ras association (RalGDS/AF-6) domain fam | 2.8 |
| | 408432 | AW195262 | | gb:xm67b05.x1 NCI_CGAP_CML1 Homo sapiens | 2.8 |
| 70 | 420320 | AB002361 | Hs.96633 | KIAA0363 protein | 2.8 |
| | 425241 | AA324624 | Hs.155247 | aldolase C, fructose-bisphosphate | 2.8 |
| | 428670 | AA431682 | Hs.134832 | ESTs | 2.8 |
| | 424415 | NM_001975 | Hs.146580 | enolase 2, (gamma, neuronal) | 2.8 |
| | 409185 | AW961601 | Hs.252406 | hypothetical protein FLJ12296 similar to | 2.8 |
| | 411555 | AF113537 | Hs.70669 | HMP19 protein | 2.8 |
| 75 | 426847 | S78723 | Hs.298623 | 5-hydroxytryptamine (serotonin) receptor | 2.8 |
| | 458809 | AW972512 | Hs.20985 | sin3-associated polypeptide, 30kD | 2.8 |
| | 420071 | AB028985 | Hs.94806 | ATP-binding cassette, sub-family A (ABC1 | 2.8 |
| | 424572 | M19650 | Hs.150741 | 2',3'-cyclic nucleotide 3' phosphodiester | 2.8 |
| | 444670 | H58373 | Hs.332938 | hypothetical protein MGC5370 | 2.8 |
| 80 | 411089 | AA456454 | Hs.183418 | cell division cycle 2-like 1 (PITSLRE pr | 2.8 |
| | 416111 | AA033813 | Hs.79018 | chromatin assembly factor 1, subunit A (| 2.8 |
| | 440637 | AW900115 | Hs.7309 | Homo sapiens clone 23741 mRNA sequence | 2.8 |
| | 408554 | AA836381 | Hs.315111 | nuclear receptor co-repressor/HDAC3 comp | 2.8 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 403056 | R58624 | Hs.2186 | eukaryotic translation elongation factor | 2.8 |
| | 423449 | AJ497900 | Hs.33067 | ESTs | 2.8 |
| | 424188 | AW954552 | Hs.142634 | zinc finger protein | 2.8 |
| 5 | 429006 | AA443143 | Hs.50929 | hypothetical protein FLJ13842 | 2.8 |
| | 434981 | AW182577 | Hs.293077 | ESTs | 2.8 |
| | 437435 | AA249439 | Hs.27027 | hypothetical protein DKFZp762H1311 | 2.8 |
| | 442748 | AI016713 | Hs.135787 | ESTs | 2.8 |
| | 443312 | N52025 | Hs.46616 | ESTs | 2.8 |
| 10 | 450940 | AI744943 | Hs.143209 | ESTs, Weakly similar to I38022 hypotheti | 2.8 |
| | 452738 | AL133800 | Hs.7086 | hypothetical protein MGC12435 | 2.8 |
| | 409182 | AA064970 | Hs.118145 | ESTs | 2.8 |
| | 439793 | AA018825 | Hs.7934 | Kruppel-like factor 4 (gulf) | 2.8 |
| | 432683 | AW995441 | Hs.10475 | ESTs | 2.8 |
| 15 | 434269 | AK001991 | Hs.3781 | similar to murine leucine-rich repeat pr | 2.8 |
| | 429500 | X78565 | Hs.289114 | hexabrachion (tenascin C, cytolactin) | 2.8 |
| | 433290 | R20077 | Hs.302185 | Homo sapiens clone 23618 mRNA sequence | 2.8 |
| | 434276 | AF123659 | Hs.93605 | leucine zipper, putative tumor suppresso | 2.8 |
| | 435977 | AL138079 | Hs.5012 | brain-specific membrane-anchored protein | 2.8 |
| 20 | 430294 | A1538226 | Hs.32976 | guanine nucleotide binding protein 4 | 2.8 |
| | 425168 | R96366 | | gb:Yq37d04.s1 Soares fetal liver spleen | 2.8 |
| | 428180 | AI129767 | Hs.182874 | guanine nucleotide binding protein (G pr | 2.8 |
| | 409348 | AI401535 | Hs.146090 | ESTs | 2.8 |
| | 409887 | AL137534 | Hs.56876 | Homo sapiens mRNA; cDNA DKFZp434H1419 (f | 2.8 |
| 25 | 457211 | AW972565 | Hs.32399 | ESTs, Weakly similar to S51797 vasodilat | 2.8 |
| | 430039 | BE253012 | Hs.153400 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.8 |
| | 417642 | BE302665 | Hs.105461 | hypothetical protein FLJ20357 | 2.8 |
| | 419169 | AW851980 | Hs.262346 | ESTs, Weakly similar to S72482 hypotheti | 2.8 |
| | 434008 | AA740878 | Hs.112982 | ESTs | 2.8 |
| 30 | 446776 | AW293417 | Hs.156455 | ESTs | 2.8 |
| | 408838 | AI669535 | Hs.40369 | ESTs | 2.8 |
| | 422565 | BE259035 | Hs.118400 | singed (Drosophila)-like (sea urchin fas | 2.8 |
| | 447397 | BE247676 | Hs.18442 | E-1 enzyme | 2.8 |
| | 412530 | AA766268 | Hs.265273 | hypothetical protein FLJ13346 | 2.8 |
| 35 | 424330 | AW073953 | Hs.333396 | Homo sapiens cDNA FLJ13596 fis, clone PL | 2.8 |
| | 446377 | AW014022 | Hs.170953 | ESTs | 2.8 |
| | 458924 | BE242158 | Hs.24427 | DKFZP566O1646 protein | 2.8 |
| | 447710 | AI420523 | Hs.328241 | ESTs | 2.8 |
| | 404049 | | | | 2.8 |
| 40 | 416913 | AW934714 | | gb:RC1-DT0001-031299-011-a11 DT0001 Homo | 2.8 |
| | 426400 | M78361 | Hs.169743 | Homo sapiens clone 25121 neuronal olfact | 2.8 |
| | 413264 | W26456 | Hs.134757 | hypothetical protein FLJ20033 | 2.8 |
| | 458997 | AW937420 | Hs.69662 | ESTs | 2.7 |
| | 422864 | AA318323 | | gb:EST20390 Retina II Homo sapiens cDNA | 2.7 |
| 45 | 430526 | AF181862 | Hs.242407 | G protein-coupled receptor, family C, gr | 2.7 |
| | 452023 | AB032999 | Hs.27566 | KIAA1173 protein | 2.7 |
| | 432022 | AL162042 | Hs.272348 | Homo sapiens mRNA; cDNA DKFZp761L1212 (f | 2.7 |
| | 452438 | BE514230 | Hs.29595 | JM4 protein | 2.7 |
| | 435408 | H07897 | Hs.4302 | ESTs, Weakly similar to T29299 hypotheti | 2.7 |
| 50 | 418791 | AA935633 | Hs.194628 | ESTs | 2.7 |
| | 439821 | AA826425 | Hs.291829 | ESTs | 2.7 |
| | 423464 | NM_016240 | Hs.126856 | CSR1 protein | 2.7 |
| | 442091 | AW770493 | Hs.182874 | guanine nucleotide binding protein (G pr | 2.7 |
| | 442242 | AV647908 | Hs.90424 | Homo sapiens cDNA: FLJ23285 fis, clone H | 2.7 |
| 55 | 412436 | AA665089 | | gb:nu76d01.s1 NCL_CGAP_Alv1 Homo sapiens | 2.7 |
| | 432821 | BE170702 | Hs.279005 | solute carrier family 21 (organic anion | 2.7 |
| | 416404 | AA180138 | Hs.107924 | ESTs | 2.7 |
| | 441364 | AW450466 | Hs.126830 | ESTs, Weakly similar to YD38_YEAST HYPOT | 2.7 |
| | 450202 | AW969756 | Hs.34145 | ESTs, Weakly similar to B49647 GTP-bindi | 2.7 |
| 60 | 426304 | AA374532 | Hs.124673 | Homo sapiens cDNA FLJ11477 fis, clone HE | 2.7 |
| | 428722 | U76456 | Hs.190787 | tissue inhibitor of metalloproteinase 4 | 2.7 |
| | 449701 | AW952323 | Hs.129908 | KIAA0591 protein | 2.7 |
| | 420372 | AW960049 | Hs.293660 | Homo sapiens, clone IMAGE:3535476, mRNA, | 2.7 |
| | 410318 | AA084050 | Hs.269259 | ESTs, Weakly similar to S23650 retroviru | 2.7 |
| 65 | 414603 | R58394 | Hs.25119 | ESTs, Weakly similar to YEX0_YEAST HYPOT | 2.7 |
| | 416096 | H18577 | Hs.88974 | cytochrome b-245, beta polypeptide (chro | 2.7 |
| | 420896 | AW149342 | Hs.24444 | Homo sapiens cDNA: FLJ22165 fis, clone H | 2.7 |
| | 424856 | AA347746 | Hs.9521 | ESTs, Weakly similar to ZN43_HUMAN ZINC | 2.7 |
| | 436304 | AA339622 | Hs.108887 | ESTs | 2.7 |
| 70 | 441027 | AI911412 | Hs.126444 | ESTs | 2.7 |
| | 452545 | N31940 | Hs.14434 | ESTs, Weakly similar to I38022 hypotheti | 2.7 |
| | 454201 | AB023191 | Hs.44131 | KIAA0974 protein | 2.7 |
| | 448560 | BE613183 | Hs.23213 | ESTs | 2.7 |
| | 426807 | AA385315 | Hs.156682 | ESTs | 2.7 |
| 75 | 425825 | AI929508 | Hs.159590 | lymphocyte antigen 6 complex, locus H | 2.7 |
| | 440351 | AF030933 | Hs.7179 | RAD1 (S. pombe) homolog | 2.7 |
| | 425390 | AI092634 | Hs.156114 | protein tyrosine phosphatase, non-recept | 2.7 |
| | 427624 | AA406245 | Hs.24895 | ESTs | 2.7 |
| | 426413 | AA377823 | | gb:EST90805 Synovial sarcoma Homo sapien | 2.7 |
| 80 | 422491 | AA338548 | Hs.117546 | neuronatin | 2.7 |
| | 424560 | AA158727 | Hs.150555 | protein predicted by clone 23733 | 2.7 |
| | 432415 | T16971 | Hs.289014 | ESTs, Weakly similar to A43932 mucin 2 p | 2.7 |
| | 414865 | AA157155 | Hs.274414 | hypothetical protein FLJ14457 | 2.7 |
| | 415827 | H17462 | Hs.23079 | ESTs | 2.7 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 445568 | H00918 | Hs.268744 | KIAA1796 protein | 2.7 |
| | 433315 | R96754 | Hs.239706 | GRB2-associated binding protein 1 | 2.7 |
| | 428862 | NM_000346 | Hs.2316 | SRY (sex determining region Y)-box 9 (ca | 2.7 |
| 5 | 447959 | AI452784 | Hs.270270 | ESTs, Weakly similar to 2109260A B cell | 2.7 |
| | 426420 | BE383808 | Hs.322430 | NDRG family, member 4 | 2.7 |
| | 436899 | AA764852 | Hs.291567 | ESTs | 2.7 |
| | 444100 | AA383343 | Hs.22116 | CDC14 (cell division cycle 14, S. cerevi | 2.7 |
| | 426501 | AW043782 | Hs.293616 | ESTs | 2.7 |
| 10 | 449092 | U91641 | Hs.22985 | alpha2,8-sialyltransferase | 2.7 |
| | 427311 | AB020672 | Hs.175411 | KIAA0865 protein | 2.7 |
| | 453313 | BE005771 | Hs.153746 | hypothetical protein FLJ22490 | 2.7 |
| | 404029 | | | | 2.7 |
| | 416289 | W26333 | Hs.337438 | ESTs | 2.7 |
| 15 | 439108 | AW163034 | Hs.6467 | synaptogyrin 3 | 2.6 |
| | 418746 | AI955289 | Hs.300759 | ribosomal protein L36 | 2.6 |
| | 412046 | Y07847 | Hs.73088 | RAS-related on chromosome 22 | 2.6 |
| | 435040 | AI932350 | Hs.152825 | ESTs | 2.6 |
| | 453083 | U87223 | Hs.31622 | contactin associated protein 1 | 2.6 |
| 20 | 428167 | AA770021 | Hs.16332 | ESTs | 2.6 |
| | 420028 | AB014680 | Hs.8786 | carbohydrate (N-acetylglucosamine-6-O) s | 2.6 |
| | 443715 | AI583187 | Hs.9700 | cydin E1 | 2.6 |
| | 412147 | BE391727 | Hs.102910 | general transcription factor IIH, polype | 2.6 |
| | 424687 | J05070 | Hs.151738 | matrix metalloproteinase 9 (gelatinase B | 2.6 |
| 25 | 415056 | AB004662 | Hs.77867 | adenosine A1 receptor | 2.6 |
| | 451697 | AW449774 | Hs.295380 | POM (POM121 rat homolog) and ZP3 fusion | 2.6 |
| | 433701 | AW445023 | Hs.15155 | ESTs | 2.6 |
| | 457358 | AI479755 | Hs.129010 | ESTs | 2.6 |
| | 430347 | NM_002039 | Hs.239706 | GRB2-associated binding protein 1 | 2.6 |
| 30 | 418027 | AB037807 | Hs.83293 | hypothetical protein | 2.6 |
| | 440491 | R35252 | Hs.24944 | ESTs, Weakly similar to 2109260A B cell | 2.6 |
| | 425171 | AW732240 | Hs.16365 | ESTs | 2.6 |
| | 459335 | AW298545 | Hs.250726 | EST | 2.6 |
| | 425402 | AI215881 | Hs.24970 | ESTs, Weakly similar to B34323 GTP-bindi | 2.6 |
| 35 | 453169 | AB037815 | Hs.32156 | KIAA1394 protein | 2.6 |
| | 433647 | AA603367 | Hs.222294 | ESTs | 2.6 |
| | 450414 | AI907735 | Hs.21446 | KIAA1716 protein | 2.6 |
| | 446233 | AI282028 | Hs.25205 | ESTs | 2.6 |
| | 415446 | F08898 | Hs.66075 | ESTs | 2.6 |
| 40 | 445873 | AA250970 | Hs.251946 | poly(A)-binding protein, cytoplasmic 1-I | 2.6 |
| | 413012 | D83777 | Hs.75137 | KIAA0193 gene product | 2.6 |
| | 428671 | BE297851 | Hs.189482 | zinc finger protein 179 | 2.6 |
| | 427158 | AA935603 | Hs.166231 | ESTs | 2.6 |
| | 408988 | AL119844 | Hs.49476 | Homo sapiens clone TUA8 Cri-du-chat regi | 2.6 |
| 45 | 459516 | AI049662 | Hs.246858 | EST | 2.6 |
| | 402693 | | | | 2.6 |
| | 408039 | AA131424 | Hs.50340 | ESTs | 2.6 |
| | 422896 | AW961489 | Hs.154116 | ESTs | 2.6 |
| | 423130 | AW897586 | Hs.21213 | ESTs | 2.6 |
| 50 | 438796 | W67821 | Hs.109590 | genethonin 1 | 2.6 |
| | 439871 | R88518 | Hs.46736 | hypothetical protein FLJ23476 | 2.6 |
| | 440192 | AA872282 | Hs.190596 | ESTs | 2.6 |
| | 419708 | AK000753 | Hs.92374 | hypothetical protein | 2.6 |
| | 449436 | AA860329 | Hs.279307 | hypothetical protein DKFZp434I2117 | 2.6 |
| 55 | 436870 | AW204219 | Hs.155560 | calnexin | 2.6 |
| | 448424 | AW009892 | Hs.31924 | ESTs | 2.6 |
| | 401324 | | | | 2.6 |
| | 414136 | AA812434 | Hs.119023 | SMC2 (structural maintenance of chromoso | 2.6 |
| | 433943 | AA992805 | Hs.44865 | lymphoid enhancer-binding factor 1 | 2.6 |
| 60 | 428001 | H97428 | Hs.219507 | ESTs, Moderately similar to Transforming | 2.6 |
| | 429139 | F09092 | Hs.66087 | ESTs | 2.6 |
| | 423073 | BE252922 | Hs.123119 | MAD (mothers against decapentaplegic, Dr | 2.6 |
| | 448966 | AW372914 | Hs.86149 | phosphoinositol 3-phosphate-binding prot | 2.6 |
| | 444001 | AI095087 | Hs.152299 | ESTs, Moderately similar to S65657 alpha | 2.6 |
| 65 | 412049 | N53437 | Hs.18268 | adenylate kinase 5 | 2.6 |
| | 441783 | BE313412 | Hs.7961 | Homo sapiens clone 25012 mRNA sequence | 2.6 |
| | 425287 | R88249 | Hs.155524 | peanut (Drosophila)-like 2 | 2.6 |
| | 432149 | AW614326 | Hs.157022 | ESTs, Weakly similar to T34549 probable | 2.6 |
| | 452234 | AW084176 | Hs.223296 | ESTs, Weakly similar to I38022 hypotheti | 2.6 |
| 70 | 453478 | AF083898 | Hs.33021 | neuro-oncological ventral antigen 2 | 2.6 |
| | 418962 | AA714835 | Hs.271863 | ESTs | 2.6 |
| | 418858 | AW961605 | Hs.21145 | hypothetical protein RG083M05.2 | 2.6 |
| | 443257 | AI334040 | Hs.11614 | HSPC065 protein | 2.6 |
| | 428748 | AW593206 | Hs.98785 | Ksp37 protein | 2.6 |
| 75 | 444984 | H15474 | Hs.132898 | fatty acid desaturase 1 | 2.6 |
| | 433404 | T32982 | Hs.102720 | ESTs | 2.6 |
| | 434779 | AF153815 | Hs.50151 | potassium inwardly-rectifying channel, s | 2.6 |
| | 420582 | BE047878 | Hs.99083 | Homo sapiens chromosome 19, cosmid R2837 | 2.6 |
| | 452856 | AF034799 | Hs.30881 | protein tyrosine phosphatase, receptor t | 2.6 |
| 80 | 436440 | AI471862 | Hs.196008 | Homo sapiens cDNA FLJ11723 fis, clone HE | 2.6 |
| | 438527 | AI969251 | Hs.115325 | RAB7, member RAS oncogene family-like 1 | 2.6 |
| | 433216 | AF217412 | Hs.47320 | neuroigin 3 | 2.6 |
| | 435380 | AA679001 | Hs.192221 | ESTs | 2.6 |
| | 428966 | AF059214 | Hs.194687 | cholesterol 25-hydroxylase | 2.6 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 439653 | AW021103 | Hs.6631 | hypothetical protein FLJ20373 | 2.6 |
| | 419304 | AI271326 | Hs.146101 | ESTs, Weakly similar to T45070 protein k | 2.6 |
| | 422991 | H10940 | Hs.48965 | Homo sapiens cDNA: FLJ21693 fis, clone C | 2.6 |
| 5 | 448548 | R13209 | Hs.21413 | solute carrier family 12, (potassium-chl | 2.6 |
| | 435370 | AI964074 | Hs.225838 | ESTs | 2.6 |
| | 408875 | NM_015434 | Hs.48604 | DKFZP434B168 protein | 2.5 |
| | 457005 | AJ007421 | Hs.172597 | sal (Drosophila)-like 3 | 2.5 |
| | 430154 | AW583058 | Hs.234726 | serine (or cysteine) proteinase inhibito | 2.5 |
| 10 | 438549 | BE386801 | Hs.21858 | trinucleotide repeat containing 3 | 2.5 |
| | 427951 | AI826125 | Hs.43546 | ESTs | 2.5 |
| | 411800 | N39342 | Hs.103042 | microtubule-associated protein 1B | 2.5 |
| | 457683 | AI821877 | Hs.140002 | ESTs, Moderately similar to ALU7_HUMAN A | 2.5 |
| | 451422 | AB002336 | Hs.26395 | erythrocyte membrane protein band 4.1-f | 2.5 |
| 15 | 430713 | AA351647 | Hs.2642 | eukaryotic translation elongation factor | 2.5 |
| | 428826 | AL048842 | Hs.194019 | atractin | 2.5 |
| | 428963 | AW382682 | Hs.258208 | Homo sapiens, clone MGC:15606, mRNA, com | 2.5 |
| | 428141 | D50402 | Hs.182611 | solute carrier family 11 (proton-coupled | 2.5 |
| | 429550 | AW293055 | Hs.119357 | ESTs | 2.5 |
| 20 | 438662 | AA223599 | Hs.6351 | cleavage and polyadenylation specific fa | 2.5 |
| | 435760 | AF231922 | Hs.213004 | chromosome 21 open reading frame 62 | 2.5 |
| | 427513 | AI476318 | Hs.192480 | ESTs | 2.5 |
| | 430061 | AB037817 | Hs.230188 | KIAA1396 protein | 2.5 |
| | 435923 | BE301930 | Hs.5010 | Homo sapiens clone 24672 mRNA sequence | 2.5 |
| 25 | 417123 | BE326521 | Hs.159450 | ESTs | 2.5 |
| | 439699 | AF086534 | Hs.187561 | ESTs, Moderately similar to ALU1_HUMAN A | 2.5 |
| | 412980 | AI815750 | Hs.20977 | hypothetical protein MGC3129 similar to | 2.5 |
| | 427209 | H06509 | Hs.92423 | KIAA1566 protein | 2.5 |
| | 424327 | AA431707 | Hs.31209 | ESTs | 2.5 |
| 30 | 436340 | R42246 | Hs.21605 | ESTs | 2.5 |
| | 450650 | T65617 | Hs.101257 | hypothetical protein MGC3295 | 2.5 |
| | 439444 | AI277652 | Hs.54578 | ESTs, Weakly similar to I38022 hypothei | 2.5 |
| | 400777 | | | | 2.5 |
| | 439478 | AF049460 | Hs.6574 | deformed epidermal autoregulatory factor | 2.5 |
| 35 | 450407 | NM_000810 | Hs.24969 | gamma-aminobutyric acid (GABA) A recepto | 2.5 |
| | 450385 | AI631024 | Hs.24948 | synuclein, alpha interacting protein (sy | 2.5 |
| | 432558 | R97268 | Hs.177269 | ESTs | 2.5 |
| | 400860 | | | | 2.5 |
| | 410361 | BE391804 | Hs.62661 | guanylate binding protein 1, interferon- | 2.5 |
| 40 | 416063 | BE047699 | Hs.93454 | ESTs | 2.5 |
| | 414998 | NM_002543 | Hs.77729 | oxidised low density lipoprotein (lectin | 2.5 |
| | 452823 | AB012124 | Hs.30696 | transcription factor-like 5 (basic helix | 2.5 |
| | 417791 | AW965339 | Hs.111471 | ESTs | 2.5 |
| | 418079 | R40058 | Hs.6911 | ESTs | 2.5 |
| 45 | 408495 | W68796 | Hs.237731 | ESTs | 2.5 |
| | 442104 | L20871 | Hs.188 | phosphodiesterase 4B, cAMP-specific (dun | 2.5 |
| | 437370 | AL359567 | Hs.161962 | Homo sapiens mRNA; cDNA DKFZp547D023 (fr | 2.5 |
| | 429803 | W81489 | Hs.223025 | RAB31, member RAS oncogene family | 2.5 |
| | 424959 | NM_005781 | Hs.153937 | activated p21cdc42Hs kinase | 2.5 |
| 50 | 427413 | BE547647 | Hs.177781 | hypothetical protein MGC5618 | 2.5 |
| | 408955 | BE315170 | Hs.8087 | NAG-5 protein | 2.5 |
| | 415261 | T40928 | Hs.8346 | ESTs | 2.5 |
| | 415716 | N59294 | Hs.179662 | nucleosome assembly protein 1-like 1 | 2.5 |
| | 417873 | BE266659 | Hs.293659 | Homo sapiens, Similar to RIKEN cDNA A430 | 2.5 |
| 55 | 418388 | R72332 | Hs.29258 | Homo sapiens cDNA FLJ11364 fis, clone HE | 2.5 |
| | 421002 | AF116030 | Hs.100932 | transcription factor 17 | 2.5 |
| | 423244 | AL039379 | Hs.209602 | ESTs, Weakly similar to ubiquitous TPR m | 2.5 |
| | 423553 | AA405635 | Hs.95854 | ESTs, Weakly similar to DYLL_HUMAN CYTOP | 2.5 |
| | 427961 | AW293165 | Hs.143134 | ESTs | 2.5 |
| 60 | 428301 | AW628666 | Hs.98440 | ESTs, Weakly similar to I38022 hypothei | 2.5 |
| | 428508 | BE252383 | Hs.184668 | SBB131 protein | 2.5 |
| | 428858 | AA436760 | | gbzv67d11.r1 Soares_total_fetus_Nb2HF8_ | 2.5 |
| | 428943 | AW086180 | Hs.37636 | ESTs, Weakly similar to KIAA1392 protein | 2.5 |
| | 432427 | AL037630 | Hs.6638 | Homo sapiens cDNA FLJ11602 fis, clone HE | 2.5 |
| 65 | 435347 | AW014873 | Hs.116963 | ESTs | 2.5 |
| | 437949 | U78519 | Hs.41654 | ESTs, Weakly similar to A46010 X-linked | 2.5 |
| | 438208 | AL041224 | Hs.65379 | ESTs | 2.5 |
| | 440286 | U29589 | Hs.7138 | cholinergic receptor, muscarinic 3 | 2.5 |
| | 441523 | AW514263 | Hs.301771 | ESTs, Weakly similar to ALUF_HUMAN !!!! | 2.5 |
| 70 | 441805 | AA285136 | Hs.301914 | neuronal specific transcription factor D | 2.5 |
| | 442337 | AI371029 | Hs.129257 | ESTs, Weakly similar to TC17_HUMAN TRANS | 2.5 |
| | 442789 | AW904361 | Hs.131191 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 2.5 |
| | 445556 | AI910241 | Hs.12887 | actin-related protein 3-beta | 2.5 |
| | 449086 | AI628357 | Hs.208037 | ESTs | 2.5 |
| 75 | 459583 | AI907673 | | gb:IL-BT152-080399-004 BT152 Homo sapien | 2.5 |

TABLE 8B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

| | | |
|--------|------------|--------------------------|
| Pkey | CAT Number | Accession |
| 408432 | 1058667_1 | AW195262 R27868 AW811262 |
| 412225 | 1284108_1 | AW902042 N77591 |

| | | | |
|----|--------|-----------|---|
| 5 | 412436 | 129439_1 | AA665089 AA135130 AA484059 AA102419 AW877765 |
| | 416120 | 1571266_1 | H46739 H51513 H19779 |
| | 416871 | 1626761_1 | H98716 N90792 N24283 |
| | 416913 | 163001_1 | AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499 |
| | 422864 | 222336_1 | AA318323 H11145 R15289 AA451945 AA476690 AA436954 Z43802 F11753 T65491 D81821 |
| | 422949 | 223184_1 | AA319435 N56456 AA319377 AW961532 T48452 AA894424 |
| | 422977 | 223410_1 | AA631498 AI017191 AA491211 AA761823 AA714555 AA768099 AA808286 AI934069 AA570223 AA574389 AA582438 AI745346 AW964510 AA319642 |
| | | | AW853758 H56414 |
| 10 | 423756 | 231725_1 | AA828125 AA834883 AA330555 |
| | 425168 | 247552_1 | R96366 AL133929 AA351636 H78818 AA477084 Z28957 H80194 |
| | 425517 | 252729_1 | AF121179 BE162736 AA358827 |
| | 426413 | 266650_1 | AA377823 AW954494 AI022688 |
| | 428002 | 285602_1 | AA418703 AA418711 BE071915 BE071920 BE071912 |
| | 428679 | 294049_1 | AA431765 AA432015 |
| 15 | 428858 | 296453_1 | AA436760 AW237453 BE327496 N47347 N56967 |
| | 429007 | 298301_1 | D80642 AA443145 AL119015 AW904500 |
| | 429163 | 300543_1 | AA884766 AW974271 AA592975 AA447312 |
| | 433532 | 368950_1 | AW975367 AA598607 AA742735 |
| 20 | 436190 | 41555_1 | AK001059 AA633055 |
| | 437034 | 431713_1 | AA742643 AA808575 AW976568 |
| | 438458 | 457837_1 | AW975186 AA807807 D29548 |
| | 438993 | 467651_1 | AA828955 AA834879 AI926361 |
| | 439566 | 47387_1 | AF086387 W77884 W72711 |
| 25 | 440322 | 491965_1 | AA879430 BE070262 BE070493 BE070272 BE070484 BE070397 BE070395 BE070201 BE070198 BE070404 BE070270 BE070400 |
| | 444584 | 611496_1 | AI168422 D80113 T59074 |
| | 447197 | 711623_1 | R36075 AI366546 R36167 |
| | 448451 | 764066_1 | AW015994 R39898 AW000978 AI598202 AI521706 |
| | 450625 | 84032_1 | AW970107 AA513951 AA010406 |
| 30 | 452453 | 918300_1 | AI902519 AI902518 AI902516 |
| | 454996 | 1248640_1 | AW350180 AW850326 |
| | 455350 | 1283853_1 | AW901809 AW901787 AW901795 AW901792 AW901744 AW901753 AW901807 AW901798 |

TABLE 8C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

| | | | | |
|----|--------|---------|--------|---|
| 40 | Pkey | Ref | Strand | NL_position |
| | 400777 | 8131663 | Plus | 70745-71121 |
| | 400780 | 8131663 | Minus | 118372-118619 |
| | 400859 | 9757499 | Minus | 91888-92018,98131-98294,99474-99570 |
| 45 | 400860 | 9757499 | Minus | 151830-152104,152649-152744 |
| | 400992 | 8098828 | Plus | 140390-140822 |
| | 401324 | 9863791 | Plus | 234057-234174 |
| | 402408 | 9796239 | Minus | 110326-110491 |
| | 402604 | 9909420 | Plus | 20393-20767 |
| 50 | 402605 | 9909420 | Minus | 47680-47973 |
| | 402693 | 8569863 | Minus | 82366-82515 |
| | 402855 | 9662953 | Minus | 59763-59909 |
| | 404029 | 7671252 | Plus | 108716-111112 |
| | 404048 | 3688074 | Minus | 54421-56808 |
| 55 | 404049 | 3688074 | Minus | 75765-78155 |
| | 404283 | 2276311 | Minus | 99460-99564 |
| | 404299 | 5738652 | Minus | 3826-4025 |
| | 404541 | 8318559 | Plus | 103456-103664 |
| | 404584 | 9857511 | Plus | 138651-139153 |
| 60 | 404593 | 9944086 | Minus | 74922-75788 |
| | 404721 | 9856648 | Minus | 173763-174294 |
| | 404819 | 4678240 | Plus | 16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578 |
| | 405238 | 7249119 | Minus | 51728-51836 |
| | 405771 | 7018349 | Plus | 91191-91254,91510-91589 |
| | 405819 | 4007557 | Plus | 2830-2967 |
| 65 | 406311 | 9211559 | Minus | 137114-139033 |

TABLE 9A: ABOUT 1202 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CENTRAL NERVOUS SYSTEM (CNS)

Table 9A lists about 1202 genes up-regulated in glioblastoma compared to normal adult central nervous system (CNS). These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" glioblastoma to "average" normal adult CNS tissues was greater than or equal to 2.0. The "average" glioblastoma level was set to the 75th percentile amongst various glioblastoma tumors. The "average" normal adult CNS tissue level was set to the 95th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of 75th percentile tumor to 95th percentile normal adult nervous system tissue

| | | | | | |
|----|--------|----------|-----------|------------------------|------|
| 80 | Pkey | ExAccn | UnigenelD | Unigene Title | R1 |
| | 452461 | N78223 | Hs.108106 | transcription factor | 20.1 |
| | 435895 | AF037335 | Hs.5338 | carbonic anhydrase XII | 15.2 |
| | 453941 | U39817 | Hs.36820 | Bloom syndrome | 14.2 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| 5 | 443247 | BE614387 | Hs.333893 | c-Myc target JPO1 | 12.4 |
| | 428330 | L22524 | Hs.2256 | matrix metalloproteinase 7 (matrilysin, | 12.0 |
| | 447342 | AI199268 | Hs.19322 | Homo sapiens, Similar to RIKEN cDNA 2010 | 11.7 |
| | 422163 | AF027208 | Hs.112360 | prominin (mouse)-like 1 | 11.4 |
| | 439451 | AF086270 | Hs.278554 | heterochromatin-like protein 1 | 11.2 |
| 10 | 424800 | AL035588 | Hs.153203 | MyoD family inhibitor | 10.2 |
| | 416111 | AA033813 | Hs.79018 | chromatin assembly factor 1, subunit A (| 10.0 |
| | 444190 | AI878918 | Hs.10526 | cysteine and glycine-rich protein 2 | 9.9 |
| | 412140 | AA219691 | Hs.73625 | RAB6 interacting, kinesin-like (rabkines | 9.9 |
| | 449340 | AW235786 | Hs.195359 | hypothetical protein MGC10954 | 9.8 |
| 15 | 409731 | AA125985 | Hs.56145 | thymosin, beta, identified in neuroblast | 9.4 |
| | 439978 | BE139460 | Hs.124673 | Homo sapiens cDNA FLJ11477 fis, clone HE | 8.9 |
| | 411411 | AA345241 | Hs.55950 | ESTs, Weakly similar to KIAA1330 protein | 8.9 |
| | 455516 | BE172704 | Hs.222746 | KIAA1610 protein | 8.2 |
| | 420092 | AA814043 | Hs.88045 | ESTs | 7.9 |
| 20 | 422631 | BE218919 | Hs.118793 | hypothetical protein FLJ10688 | 7.9 |
| | 453392 | U23752 | Hs.32964 | SRY (sex determining region Y)-box 11 | 7.9 |
| | 438527 | AI969251 | Hs.115325 | RAB7, member RAS oncogene family-like 1 | 7.9 |
| | 427581 | NM_014788 | Hs.179703 | KIAA0129 gene product | 7.8 |
| | 418661 | NM_001949 | Hs.1189 | E2F transcription factor 3 | 7.8 |
| 25 | 440584 | AI253123 | Hs.127356 | ESTs, Highly similar to S21424 nestin [H | 7.8 |
| | 429643 | AA455889 | Hs.167279 | FYVE-finger-containing Rab5 effector pro | 7.7 |
| | 409638 | AW450420 | Hs.21335 | ESTs | 7.5 |
| | 444665 | BE613126 | Hs.47783 | B aggressive lymphoma gene | 7.5 |
| | 456759 | BE259150 | Hs.127792 | della (Drosophila)-like 3 | 7.5 |
| 30 | 412777 | AI355773 | Hs.270123 | ESTs | 7.4 |
| | 436607 | AW661783 | Hs.211061 | ESTs | 7.3 |
| | 432058 | AW665996 | Hs.130729 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 7.3 |
| | 417061 | AI675944 | Hs.188691 | Homo sapiens cDNA FLJ12033 fis, clone HE | 7.3 |
| | 428976 | AL037824 | Hs.194695 | ras homolog gene family, member 1 | 7.2 |
| 35 | 433244 | AB040943 | Hs.271285 | KIAA1510 protein | 7.1 |
| | 436726 | AA324975 | Hs.128993 | ESTs, Weakly similar to T00079 hypothe | 7.1 |
| | 408432 | AW195262 | Hs.148135 | gb:mx67b05.x1 NCL_CGAP_CML1 Homo sapiens | 7.1 |
| | 434164 | AW207019 | Hs.251946 | serine/threonine kinase 33 | 7.0 |
| | 445873 | AA250970 | Hs.293707 | poly(A)-binding protein, cytoplasmic 1-I | 7.0 |
| 40 | 439726 | AW449893 | Hs.3076 | ESTs, Weakly similar to I38598 zinc fing | 7.0 |
| | 432656 | NM_000246 | Hs.250500 | MHC class II transactivator | 6.8 |
| | 431117 | AF003522 | Hs.252809 | delta (Drosophila)-like 1 | 6.8 |
| | 453387 | AI990741 | Hs.183161 | ESTs | 6.6 |
| | 418821 | AA436002 | Hs.69328 | ESTs | 6.6 |
| 45 | 437034 | AA742643 | Hs.151738 | gb:ny91c01.s1 NCL_CGAP_GCB1 Homo sapiens | 6.6 |
| | 411252 | AB018549 | Hs.271741 | MD-2 protein | 6.5 |
| | 424687 | J05070 | Hs.271741 | matrix metalloproteinase 9 (gelatinase B | 6.4 |
| | 452953 | AI932884 | Hs.38207 | ESTs, Weakly similar to A46010 X-linked | 6.3 |
| | 433532 | AW975367 | Hs.21668 | gb:EST387475 MAGE resequences, MAGN Homo | 6.3 |
| 50 | 420311 | AW445044 | Hs.21668 | Human DNA sequence from clone RP4-53015 | 6.2 |
| | 418097 | R45137 | Hs.13872 | ESTs | 6.2 |
| | 407304 | AA565832 | Hs.57471 | gb:bj32b03.s1 NCL_CGAP_AA1 Homo sapiens | 6.1 |
| | 435256 | AF193766 | | cytokine-like protein C17 | 6.1 |
| | 449448 | D60730 | | ESTs | 6.1 |
| 55 | 403790 | | | | 6.0 |
| | 425517 | AF121179 | | gb:AF121179 Homo sapiens liver (Chang L- | 6.0 |
| | 420674 | NM_000055 | Hs.1327 | butyrylcholinesterase | 6.0 |
| | 435542 | AA687376 | Hs.269533 | ESTs | 5.9 |
| | 418216 | AA662240 | Hs.283099 | AF15q14 protein | 5.8 |
| 60 | 439086 | AF085947 | | gb:Homo sapiens full length insert cDNA | 5.8 |
| | 408037 | AW271720 | Hs.42233 | hypothetical protein FLJ10300 | 5.7 |
| | 412225 | AW902042 | | gb:QV0-NN1022-170400-193-c02 NN1022 Homo | 5.7 |
| | 436109 | AA922153 | Hs.132760 | hypothetical protein MGC15729 | 5.7 |
| | 435005 | U80743 | Hs.306094 | trinucleotide repeat containing 12 | 5.7 |
| 65 | 429149 | AW193360 | Hs.197962 | ESTs, Weakly similar to I38022 hypothe | 5.7 |
| | 418113 | AI272141 | Hs.83484 | SRY (sex determining region Y)-box 4 | 5.6 |
| | 405558 | | | | 5.6 |
| | 442432 | BE093589 | Hs.38178 | hypothetical protein FLJ23468 | 5.6 |
| | 442547 | AA308997 | Hs.217484 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 5.6 |
| 70 | 413063 | AL035737 | Hs.75184 | chitinase 3-like 1 (cartilage glycoprote | 5.5 |
| | 420560 | AW207748 | Hs.59115 | ESTs | 5.5 |
| | 408096 | BE250162 | Hs.83765 | dihydrofolate reductase | 5.5 |
| | 443539 | AI076182 | Hs.134074 | ESTs, Moderately similar to ALU6_HUMAN A | 5.4 |
| | 426318 | AA375125 | Hs.147112 | Homo sapiens cDNA: FLJ22322 fis, clone H | 5.4 |
| 75 | 429115 | AA446728 | Hs.289020 | Homo sapiens cDNA FLJ14098 fis, clone MA | 5.3 |
| | 453900 | AW003582 | Hs.226414 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 5.3 |
| | 444168 | AW379879 | | gb:RC1-HT0256-081199-011 HT0256 Homo | 5.3 |
| | 432789 | D26361 | Hs.3104 | KIAA0042 gene product | 5.3 |
| | 437036 | AI571514 | Hs.133022 | ESTs | 5.2 |
| 80 | 421247 | BE391727 | Hs.102910 | general transcription factor IIH, polype | 5.2 |
| | 441523 | AW514263 | Hs.301771 | ESTs, Weakly similar to ALUF_HUMAN IIII | 5.2 |
| | 451106 | BE382701 | Hs.25960 | v-myc avian myelocytomatosis viral relat | 5.1 |
| | 457211 | AW972565 | Hs.32399 | ESTs, Weakly similar to S51797 vasodilat | 5.1 |
| | 454157 | AW162906 | Hs.312481 | ESTs, Weakly similar to S66668 hydrogen | 5.1 |
| 80 | 423343 | AA324643 | Hs.246106 | ESTs | 5.1 |
| | 425292 | NM_005824 | Hs.155545 | 37 kDa leucine-rich repeat (LRR) protein | 5.1 |
| | 406679 | AA070786 | | gb:zm66b07.r1 Stratagene neuroepithelium | 5.1 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 442671 | AI005668 | Hs.134779 | EST | 5.1 |
| | 433001 | AF217513 | Hs.279905 | clone HQ0310 PRO0310p1 | 5.0 |
| | 418819 | AA228776 | Hs.191721 | ESTs | 5.0 |
| 5 | 432946 | U60899 | Hs.279854 | mannosidase, alpha, class 2B, member 1 | 4.9 |
| | 420730 | NM_002691 | Hs.99890 | polymerase (DNA directed), delta 1, cata | 4.9 |
| | 441217 | AI922183 | Hs.213246 | ESTs | 4.9 |
| | 453385 | AW296101 | Hs.252806 | ESTs | 4.8 |
| | 418203 | X54942 | Hs.83758 | CDC28 protein kinase 2 | 4.7 |
| 10 | 450813 | AI739625 | Hs.203376 | ESTs | 4.7 |
| | 444006 | BE395085 | Hs.10086 | type I transmembrane protein Fn14 | 4.7 |
| | 412530 | AA766268 | Hs.266273 | hypothetical protein FLJ13346 | 4.7 |
| | 431070 | AW408164 | Hs.249184 | transcription factor 19 (SC1) | 4.7 |
| | 429786 | AL080232 | Hs.220696 | Homo sapiens mRNA; cDNA DKFZp586A061 (tr | 4.7 |
| | 405771 | | | | 4.6 |
| 15 | 457065 | AI476318 | Hs.192480 | ESTs | 4.6 |
| | 436190 | AK001059 | | gb:Homo sapiens cDNA FLJ10197 fis, clone | 4.6 |
| | 400859 | | | | 4.6 |
| | 435267 | N23797 | Hs.110114 | ESTs | 4.6 |
| 20 | 443454 | AI057494 | Hs.133421 | ESTs | 4.5 |
| | 452811 | AA937079 | Hs.118983 | hypothetical protein FLJ12150 | 4.5 |
| | 437267 | AW511443 | Hs.258110 | ESTs | 4.5 |
| | 435020 | AW505076 | Hs.301855 | DiGeorge syndrome critical region gene 8 | 4.5 |
| | 454269 | AI961060 | Hs.129908 | KIAA0591 protein | 4.5 |
| 25 | 422106 | D84239 | Hs.111732 | Fc fragment of IgG binding protein | 4.5 |
| | 422765 | AW409701 | Hs.1578 | baculoviral IAP repeat-containing 5 (sur | 4.5 |
| | 456534 | X91195 | Hs.100623 | phospholipase C, beta 3, neighbor pseudo | 4.5 |
| | 423756 | AA828125 | | gb:od71a09.s1 NCI_CGAP_Ov2 Homo sapiens | 4.5 |
| | 417308 | H60720 | Hs.81892 | KIAA0101 gene product | 4.5 |
| 30 | 422170 | AI791949 | Hs.112432 | anti-Mullerian hormone | 4.4 |
| | 429500 | X78565 | Hs.289114 | hexabrachion (tenascin C, cytotoxin) | 4.4 |
| | 406568 | AF088886 | Hs.11590 | cathepsin F | 4.4 |
| | 426812 | AF105365 | Hs.172513 | solute carrier family 12 (potassium/chlo | 4.4 |
| | 402516 | | | | 4.4 |
| 35 | 432865 | AI753709 | Hs.152484 | ESTs, Weakly similar to I38022 hypotheti | 4.4 |
| | 413625 | AW451103 | Hs.71371 | ESTs | 4.4 |
| | 436098 | R20597 | Hs.9739 | glycerol-3-phosphate dehydrogenase 1 (so | 4.4 |
| | 418333 | W92113 | | gb:zh48e01.r1 Soares_fetal_liver_spleen_ | 4.4 |
| | 416933 | BE561850 | Hs.80506 | small nuclear ribonucleoprotein polypept | 4.4 |
| 40 | 438192 | AI859065 | Hs.337620 | Homo sapiens AFG3L1 isoform 1 mRNA, part | 4.3 |
| | 457374 | AA493662 | | gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens | 4.3 |
| | 433159 | AB035898 | Hs.150587 | kinesin-like protein 2 | 4.3 |
| | 444386 | BE065183 | | gb:RC1-BT0314-Q20200-012-c04 BT0314 Homo | 4.3 |
| | 453202 | AW085781 | Hs.26270 | hypothetical protein FLJ11588 | 4.3 |
| 45 | 441020 | W79283 | Hs.35962 | ESTs | 4.3 |
| | 414733 | BE514535 | Hs.77171 | minichromosome maintenance deficient (S. | 4.3 |
| | 407902 | AL117474 | Hs.41181 | Homo sapiens mRNA; cDNA DKFZp727C191 (fr | 4.3 |
| | 405701 | | | | 4.3 |
| 50 | 451659 | BE379761 | Hs.14248 | ESTs | 4.3 |
| | 418845 | AA852985 | Hs.89232 | chromobox homolog 5 (Drosophila HP1 alph | 4.2 |
| | 433323 | AA805132 | Hs.30701 | ESTs | 4.2 |
| | 439811 | AA135332 | Hs.71608 | ESTs | 4.2 |
| | 415406 | T26510 | | gb:AB282F8R Infant brain, LLNL array of | 4.2 |
| | 436282 | R91913 | Hs.272104 | ESTs, Moderately similar to ALU1_HUMAN A | 4.1 |
| 55 | 441269 | AW015206 | Hs.178784 | ESTs | 4.1 |
| | 418727 | AA227609 | Hs.94834 | ESTs | 4.1 |
| | 433006 | BE242758 | Hs.190223 | ESTs, Moderately similar to T29285 hypot | 4.1 |
| | 436480 | AJ271643 | Hs.87469 | putative acid-sensing ion channel | 4.1 |
| | 430786 | AA486144 | Hs.31293 | ESTs | 4.1 |
| 60 | 445372 | N36417 | Hs.144928 | ESTs | 4.1 |
| | 410555 | U92649 | Hs.64311 | a disintegrin and metalloproteinase doma | 4.0 |
| | 457465 | AW301344 | Hs.122908 | DNA replication factor | 4.0 |
| | 422094 | AF129535 | Hs.272027 | F-box only protein 5 | 4.0 |
| | 442029 | AW956698 | Hs.14456 | neural precursor cell expressed, develop | 4.0 |
| 65 | 459321 | AW044477 | Hs.299538 | ESTs | 4.0 |
| | 421308 | AA687322 | Hs.192843 | leucine zipper protein FKSG14 | 4.0 |
| | 420567 | AK000812 | Hs.98874 | similar to proline-rich protein 48 | 4.0 |
| | 447004 | AW296968 | Hs.157539 | ESTs | 4.0 |
| | 448295 | AI381911 | Hs.334859 | KIAA1814 protein | 3.9 |
| 70 | 439699 | AF086534 | Hs.187561 | ESTs, Moderately similar to ALU1_HUMAN A | 3.9 |
| | 440704 | M69241 | Hs.162 | insulin-like growth factor binding prote | 3.9 |
| | 453096 | AW294631 | Hs.11325 | ESTs | 3.9 |
| | 457026 | AA397620 | Hs.48692 | ESTs | 3.9 |
| | 404642 | | | | 3.9 |
| 75 | 450375 | AA009647 | Hs.8850 | a disintegrin and metalloproteinase doma | 3.9 |
| | 430132 | AA204686 | Hs.234149 | hypothetical protein FLJ20647 | 3.9 |
| | 437718 | AI927288 | Hs.196779 | ESTs | 3.9 |
| | 438490 | AW593272 | Hs.301299 | ESTs | 3.9 |
| | 429919 | AA460692 | Hs.278945 | hypothetical protein FLJ23024 | 3.9 |
| 80 | 413604 | R51767 | | gb:y973g11.r1 Soares infant brain 1N1B H | 3.9 |
| | 425599 | AW366745 | Hs.214140 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.9 |
| | 448796 | AA147829 | Hs.301431 | endothelial zinc finger protein induced | 3.9 |
| | 449300 | AI656959 | Hs.222165 | ESTs | 3.8 |
| | 452203 | X57522 | Hs.158164 | transporter 1, ATP-binding cassette, sub | 3.8 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 425769 | U72513 | Hs.159486 | Human RPL13-2 pseudogene mRNA, complete | 3.8 |
| | 404295 | | | | 3.8 |
| | 410361 | BE391804 | Hs.62661 | guanylate binding protein 1, interferon- | 3.8 |
| 5 | 428728 | NM_016625 | Hs.191381 | hypothetical protein | 3.8 |
| | 409142 | AL136877 | Hs.50758 | SMC4 (structural maintenance of chromoso | 3.8 |
| | 430172 | AA468591 | Hs.161889 | ESTs | 3.8 |
| | 447499 | AW262580 | Hs.147674 | protocadherin beta 16 | 3.8 |
| | 405884 | | | | 3.8 |
| 10 | 437236 | AW137817 | Hs.244353 | ESTs | 3.7 |
| | 418883 | BE387036 | Hs.1211 | acid phosphatase 5, tartrate resistant | 3.7 |
| | 444143 | AW747996 | Hs.160999 | ESTs, Moderately similar to A56194 throm | 3.7 |
| | 425529 | NM_014656 | Hs.158282 | KIAA0040 gene product | 3.7 |
| | 425502 | R98895 | Hs.125823 | ESTs | 3.7 |
| 15 | 419741 | NM_007019 | Hs.93002 | ubiquitin carrier protein E2-C | 3.7 |
| | 402424 | | | | 3.7 |
| | 429469 | M64590 | Hs.27 | glycine dehydrogenase (decarboxylating; | 3.7 |
| | 434072 | H70854 | Hs.283059 | Homo sapiens PRO1082 mRNA, complete cds | 3.7 |
| | 414872 | U82010 | Hs.77513 | COX10 (yeast) homolog, cytochrome c oxid | 3.7 |
| 20 | 426071 | AW138057 | Hs.163835 | ESTs | 3.7 |
| | 419078 | M93119 | Hs.89584 | insulinoma-associated 1 | 3.7 |
| | 428037 | N47474 | Hs.89230 | potassium intermediate/small conductance | 3.7 |
| | 416547 | H62914 | Hs.268946 | ESTs, Weakly similar to PC4259 ferritin | 3.7 |
| | 436899 | AA764852 | Hs.291567 | ESTs | 3.6 |
| 25 | 436722 | AW975977 | | gb:EST388086 MAGE resequences, MAGN Homo | 3.6 |
| | 440652 | A1216751 | Hs.143977 | ESTs | 3.6 |
| | 428450 | NM_014791 | Hs.184339 | KIAA0175 gene product | 3.6 |
| | 452103 | R42764 | Hs.339654 | ESTs, Weakly similar to I38022 hypotheti | 3.6 |
| | 409048 | H59990 | Hs.37699 | ESTs | 3.6 |
| 30 | 439546 | AF088056 | | gb:Homo sapiens full length insert cDNA | 3.6 |
| | 443544 | A1076315 | Hs.16359 | ESTs | 3.6 |
| | 418478 | U38945 | Hs.1174 | cyclin-dependent kinase inhibitor 2A (me | 3.6 |
| | 435889 | A1249107 | Hs.269901 | ESTs | 3.6 |
| | 420301 | AA767526 | Hs.22030 | paired box gene 5 (B-cell lineage specif | 3.6 |
| 35 | 438078 | A1016377 | Hs.131693 | ESTs | 3.6 |
| | 408420 | NM_006915 | Hs.44766 | retinitis pigmentosa 2 (X-linked recessi | 3.6 |
| | 416871 | H98716 | | gb:yx13d08.s1 Soares melanocyte 2NbHM Ho | 3.5 |
| | 424085 | NM_002914 | Hs.139226 | replication factor C (activator 1) 2 (40 | 3.5 |
| | 446291 | BE397753 | Hs.14623 | interferon, gamma-inducible protein 30 | 3.5 |
| 40 | 432281 | AK001239 | Hs.274263 | hypothetical protein FLJ10377 | 3.5 |
| | 436123 | AA057484 | Hs.35406 | ESTs, Highly similar to unnamed protein | 3.5 |
| | 411256 | AW834039 | | gb:QV0-TT0010-091199-053-e09 TT0010 Homo | 3.5 |
| | 419239 | AA468183 | Hs.184598 | Homo sapiens cDNA: FLJ23241 fis, clone C | 3.5 |
| | 435065 | BE064391 | | gb:RC4-BT0310-110300-015-b08 BT0310 Homo | 3.5 |
| 45 | 435532 | AW291488 | Hs.117305 | Homo sapiens, clone IMAGE:3682908, mRNA | 3.5 |
| | 447101 | N72185 | Hs.44189 | ESTs | 3.5 |
| | 410530 | M25809 | Hs.64173 | ATPase, H+ transporting, lysosomal (vacu | 3.5 |
| | 422156 | N34524 | | gb:yy56d10.s1 Soares_multiple_sclerosis_ | 3.5 |
| 50 | 453616 | NM_003462 | Hs.33846 | dynein, axonemal, light intermediate pol | 3.5 |
| | 439743 | AL389956 | Hs.283858 | Homo sapiens mRNA full length insert cDN | 3.5 |
| | 453894 | AA355925 | Hs.36232 | KIAA0186 gene product | 3.5 |
| | 424954 | NM_000546 | Hs.1846 | tumor protein p53 (Li-Fraumeni syndrome) | 3.5 |
| | 420721 | AA927802 | Hs.159471 | ZAP3 protein | 3.5 |
| | 426764 | AA732524 | Hs.151464 | ESTs, Weakly similar to ALUC_HUMAN !!! | 3.4 |
| 55 | 420649 | A1866964 | Hs.124704 | ESTs, Moderately similar to S65657 alpha | 3.4 |
| | 448831 | AL080123 | Hs.22182 | zinc finger protein 23 (KOX 16) | 3.4 |
| | 444371 | BE540274 | Hs.239 | forkhead box M1 | 3.4 |
| | 402604 | | | | 3.4 |
| | 442407 | AW469584 | Hs.32353 | mitogen-activated protein kinase kinase | 3.4 |
| 60 | 414300 | A1304870 | Hs.188680 | ESTs | 3.4 |
| | 444670 | H58373 | Hs.332938 | hypothetical protein MGC5370 | 3.4 |
| | 414550 | BE379808 | | gb:601159567T1 NIH_MGC_53 Homo sapiens c | 3.4 |
| | 452211 | A1985513 | Hs.233420 | ESTs | 3.4 |
| | 414416 | AW409985 | Hs.76084 | hypothetical protein MGC2721 | 3.4 |
| 65 | 449961 | AW265634 | Hs.133100 | ESTs | 3.4 |
| | 413257 | BE075035 | | gb:PM3-BT0584-260300-002-g05 BT0584 Homo | 3.4 |
| | 453857 | AL080235 | Hs.35861 | DKFZP586E1621 protein | 3.4 |
| | 417404 | NM_007350 | Hs.82101 | pleckstrin homology-like domain, family | 3.4 |
| | 422846 | BE513934 | Hs.1583 | neutrophil cytosolic factor 1 (47kD, chr | 3.4 |
| 70 | 446189 | H85224 | Hs.214013 | ESTs | 3.4 |
| | 437385 | AA757055 | Hs.164060 | ESTs | 3.4 |
| | 453652 | AW009640 | Hs.28368 | ESTs, Moderately similar to S65657 alpha | 3.4 |
| | 408298 | A1745325 | Hs.271923 | Homo sapiens cDNA: FLJ22785 fis, clone K | 3.4 |
| | 455778 | BE088746 | | gb:CM2-BT0893-210300-123-d09 BT0693 Homo | 3.3 |
| 75 | 417546 | H65569 | Hs.18845 | ESTs | 3.3 |
| | 412471 | M63193 | Hs.73946 | endothelial cell growth factor 1 (platelet | 3.3 |
| | 454631 | AW811324 | | gb:IL3-ST0141-131099-017-A02 ST0141 Homo | 3.3 |
| | 454294 | AB000734 | Hs.50640 | JAK binding protein | 3.3 |
| | 457131 | AC002310 | Hs.301463 | Human Chromosome 16 BAC clone CIT987SK-A | 3.3 |
| 80 | 410102 | AW248508 | Hs.279727 | Homo sapiens cDNA FLJ14035 fis, clone HE | 3.3 |
| | 449676 | AW380579 | Hs.209657 | ESTs | 3.3 |
| | 436211 | AK001581 | Hs.334828 | hypothetical protein FLJ10719; KIAA1794 | 3.3 |
| | 453746 | AL120611 | | gb:DKFZp761H119_r1 761 (synonym: harry2) | 3.3 |
| | 452799 | A1948829 | Hs.213786 | ESTs | 3.3 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 435380 | AA679001 | Hs.192221 | ESTs | 3.3 |
| | 426746 | J03626 | Hs.2057 | uridine monophosphate synthetase (crotal | 3.3 |
| | 453362 | H14988 | Hs.107375 | ESTs | 3.3 |
| 5 | 456473 | AI202788 | Hs.25682 | Homo sapiens mRNA for KIAA1863 protein, | 3.3 |
| | 416426 | AA180256 | Hs.210473 | Homo sapiens cDNA FLJ14872 fis, clone PL | 3.3 |
| | 445777 | AI580371 | Hs.145384 | ESTs | 3.3 |
| | 423757 | AL049337 | Hs.132571 | Homo sapiens mRNA; cDNA DKFZp564P016 (fr | 3.3 |
| | 431941 | AK000106 | Hs.272227 | Homo sapiens cDNA FLJ20099 fis, clone CO | 3.3 |
| 10 | 404299 | | | | 3.3 |
| | 404108 | | | | 3.3 |
| | 425189 | H16622 | | gb:ym26c07.r1 Soares infant brain 1N1B H | 3.3 |
| | 449318 | AW236021 | Hs.78531 | Homo sapiens, Similar to RIKEN cDNA 5730 | 3.3 |
| | 450193 | AI916071 | Hs.15607 | Homo sapiens Fanconi anemia complementat | 3.2 |
| 15 | 427725 | U66839 | Hs.180533 | mitogen-activated protein kinase kinase | 3.2 |
| | 424051 | AL110203 | Hs.138411 | Homo sapiens mRNA; cDNA DKFZp586J1922 (f | 3.2 |
| | 418968 | NM_000078 | Hs.89538 | cholesteryl ester transfer protein, plas | 3.2 |
| | 449248 | M33782 | Hs.23391 | Homo sapiens, Similar to transcription f | 3.2 |
| | 439416 | W58294 | Hs.56254 | ESTs | 3.2 |
| 20 | 401596 | AA172106 | Hs.110950 | Rag C protein | 3.2 |
| | 408380 | AF123050 | Hs.44532 | diubiquitin | 3.2 |
| | 450325 | AI935962 | Hs.26289 | ESTs | 3.2 |
| | 428730 | AA625947 | Hs.25750 | ESTs | 3.2 |
| | 457536 | AA305233 | Hs.278712 | eukaryotic translation initiation factor | 3.2 |
| 25 | 426836 | N41720 | Hs.172684 | vesicle-associated membrane protein 8 (e | 3.2 |
| | 442710 | AI015631 | Hs.23210 | ESTs | 3.2 |
| | 435232 | NM_001262 | Hs.4854 | cyclin-dependent kinase inhibitor 2C (p1 | 3.2 |
| | 430970 | AI018210 | Hs.144083 | ESTs | 3.2 |
| | 416192 | NM_005036 | Hs.998 | peroxisome proliferative activated recep | 3.2 |
| 30 | 446676 | H09380 | Hs.300965 | ESTs | 3.2 |
| | 451459 | AI797515 | Hs.270560 | ESTs, Moderately similar to ALU7_HUMAN A | 3.2 |
| | 407603 | AW955705 | Hs.62604 | Homo sapiens, clone IMAGE:4299322, mRNA, | 3.2 |
| | 413840 | AI301558 | Hs.146381 | RNA binding motif protein, X chromosome | 3.2 |
| | 448751 | BE551203 | Hs.201792 | ESTs | 3.2 |
| 35 | 432593 | AW301003 | Hs.51483 | ESTs, Weakly similar to hypothetical pro | 3.2 |
| | 458786 | AI457098 | Hs.280848 | ESTs | 3.2 |
| | 455909 | BE156417 | Hs.278798 | ESTs | 3.2 |
| | 419311 | AA689591 | | gb:nv66a12.s1 NCI_CGAP_GCB1 Homo sapiens | 3.2 |
| | 439710 | AF086543 | | gb:Homo sapiens full length insert cDNA | 3.2 |
| 40 | 434559 | AF147315 | | gb:Homo sapiens full length insert cDNA | 3.1 |
| | 455800 | R22479 | Hs.167073 | Homo sapiens cDNA FLJ13047 fis, clone NT | 3.1 |
| | 436703 | AW880614 | Hs.146381 | RNA binding motif protein, X chromosome | 3.1 |
| | 414799 | AI752416 | Hs.77326 | insulin-like growth factor binding prote | 3.1 |
| | 437860 | AA333063 | Hs.279898 | Homo sapiens cDNA: FLJ23165 fis, clone L | 3.1 |
| 45 | 434182 | W20309 | Hs.118520 | G-protein gamma-12 subunit | 3.1 |
| | 417900 | BE250127 | Hs.82906 | CDC20 (cell division cycle 20, S. cerevi | 3.1 |
| | 434769 | AA648884 | Hs.134278 | Homo sapiens cDNA FLJ12676 fis, clone NT | 3.1 |
| | 414825 | X06370 | Hs.77432 | epidermal growth factor receptor (avian | 3.1 |
| | 426413 | AA377823 | | gb:EST90805 Synovial sarcoma Homo sapien | 3.1 |
| 50 | 447959 | AI452784 | Hs.270270 | ESTs, Weakly similar to 2109260A B cell | 3.1 |
| | 404589 | | | | 3.1 |
| | 421764 | AI681535 | Hs.148135 | serine/threonine kinase 33 | 3.1 |
| | 419986 | AI345455 | Hs.78915 | GA-binding protein transcription factor, | 3.1 |
| | 416941 | BE000150 | Hs.48778 | riban protein | 3.1 |
| 55 | 414761 | AU077228 | Hs.77256 | enhancer of zeste (Drosophila) homolog 2 | 3.1 |
| | 449611 | AI970394 | Hs.197075 | ESTs | 3.1 |
| | 434746 | AA648368 | Hs.295368 | ESTs | 3.1 |
| | 434274 | AA628539 | Hs.116252 | ESTs, Moderately similar to ALU1_HUMAN A | 3.1 |
| | 427899 | AA829286 | Hs.332053 | serum amyloid A1 | 3.1 |
| 60 | 417642 | BE302665 | Hs.105461 | hypothetical protein FLJ20357 | 3.1 |
| | 452472 | AW957300 | Hs.294142 | ESTs, Weakly similar to C55663 oligodend | 3.1 |
| | 446131 | NM_000929 | Hs.290 | phospholipase A2, group V | 3.1 |
| | 440052 | AI633744 | Hs.195648 | ESTs, Weakly similar to 138022 hypothe | 3.1 |
| | 426531 | AA381071 | | gb:EST94100 Activated T-cells XII Homo s | 3.1 |
| 65 | 422158 | L10343 | Hs.112341 | protease inhibitor 3, skin-derived (SKAL | 3.1 |
| | 406267 | | | | 3.1 |
| | 447039 | AV561798 | Hs.282915 | ESTs | 3.1 |
| | 404802 | | | | 3.1 |
| | 406927 | M26460 | | gb:Homo sapiens (clone 104) retinoblasto | 3.1 |
| 70 | 419314 | AW971924 | Hs.87280 | ESTs | 3.0 |
| | 435894 | AI076667 | Hs.188011 | ESTs | 3.0 |
| | 432140 | AK000404 | Hs.272688 | hypothetical protein FLJ20397 | 3.0 |
| | 443426 | AF098158 | Hs.9329 | chromosome 20 open reading frame 1 | 3.0 |
| | 425202 | AW962282 | Hs.152049 | ESTs, Weakly similar to 138022 hypothe | 3.0 |
| 75 | 407047 | X65965 | | gb:H.sapiens SOD-2 gene for manganese su | 3.0 |
| | 418241 | M26682 | Hs.1149 | LIM domain only 1 (rhombotin 1) | 3.0 |
| | 446599 | Z97832 | Hs.15476 | differentially expressed in FDCP (mouse | 3.0 |
| | 412950 | BE018581 | Hs.245342 | hypothetical protein FLJ14642 | 3.0 |
| | 428670 | AA431682 | Hs.134832 | ESTs | 3.0 |
| 80 | 446975 | BE246446 | Hs.16695 | ubiquitin-activating enzyme E1-like | 3.0 |
| | 437756 | AA767537 | Hs.197096 | ESTs | 3.0 |
| | 416084 | L16991 | Hs.79006 | deoxythymidylate kinase (thymidylate kin | 3.0 |
| | 402374 | AL135225 | Hs.301865 | dopachrome tautomerase (dopachrome della | 3.0 |
| | 443985 | H91806 | Hs.15284 | ESTs | 3.0 |

| | | | | | |
|----|--------|----------|-----------|---|-----|
| 5 | 434008 | AA740878 | Hs.112982 | ESTs | 3.0 |
| | 452568 | AA805634 | Hs.300870 | Homo sapiens mRNA; cDNA DKFZp547M072 (fr | 3.0 |
| | 414239 | AI288330 | Hs.182330 | ESTs | 3.0 |
| | 421013 | MG2397 | Hs.1345 | mutated in colorectal cancers | 3.0 |
| | 424635 | AA420687 | Hs.115455 | Homo sapiens cDNA FLJ14259 fis, clone PL | 3.0 |
| 10 | 410276 | AI554545 | Hs.68301 | ESTs | 3.0 |
| | 433865 | N29862 | Hs.44104 | ESTs | 3.0 |
| | 406028 | | | | 3.0 |
| | 401626 | | | | 3.0 |
| | 415949 | H10562 | Hs.21691 | ESTs | 3.0 |
| 15 | 418583 | AA604379 | Hs.86211 | hypothetical protein | 3.0 |
| | 417933 | X02308 | Hs.82962 | thymidylate synthetase | 3.0 |
| | 434577 | R37316 | Hs.179769 | Homo sapiens cDNA: FLJ22487 fis, clone H | 3.0 |
| | 430437 | AI768801 | Hs.169943 | Homo sapiens cDNA FLJ13569 fis, clone PL | 3.0 |
| | 427940 | AA417812 | Hs.38775 | ESTs | 2.9 |
| 20 | 456060 | C14904 | Hs.45184 | Homo sapiens cDNA FLJ12284 fis, clone MA | 2.9 |
| | 421988 | AW450481 | Hs.161333 | ESTs | 2.9 |
| | 448775 | AB025237 | Hs.388 | nudix (nucleoside diphosphate linked moi | 2.9 |
| | 438598 | AI805943 | Hs.326067 | hypothetical protein MGC5178 | 2.9 |
| | 429612 | AF062649 | Hs.252587 | pituitary tumor-transforming 1 | 2.9 |
| 25 | 451189 | AA016019 | Hs.40905 | ESTs | 2.9 |
| | 401558 | | | | 2.9 |
| | 426207 | BE390657 | Hs.30026 | HSPC182 protein | 2.9 |
| | 404721 | | | | 2.9 |
| | 401384 | | | | 2.9 |
| 30 | 417288 | AI984792 | Hs.108812 | hypothetical protein FLJ22004 | 2.9 |
| | 427648 | AI376722 | Hs.180062 | proteasome (prosome, macropain) subunit, | 2.9 |
| | 435928 | H64345 | Hs.183961 | ESTs | 2.9 |
| | 431740 | N75450 | Hs.183412 | ESTs, Moderately similar to AF116721 67 | 2.9 |
| | 428242 | H55709 | Hs.2250 | leukemia inhibitory factor (cholinergic | 2.9 |
| 35 | 439972 | AI348100 | Hs.124662 | ESTs | 2.9 |
| | 433112 | AA973801 | Hs.144553 | ESTs, Weakly similar to unnamed protein | 2.9 |
| | 423751 | AW235633 | Hs.46525 | ESTs | 2.9 |
| | 406748 | AW339106 | Hs.217493 | annexin A2 | 2.9 |
| | 422154 | T79045 | Hs.126927 | ESTs | 2.9 |
| 40 | 405588 | | | | 2.9 |
| | 440911 | AA909536 | Hs.143562 | ESTs | 2.9 |
| | 412420 | AL035668 | Hs.73853 | bone morphogenetic protein 2 | 2.9 |
| | 445043 | AW014413 | Hs.196066 | ESTs | 2.9 |
| | 410114 | AW580540 | Hs.271280 | ESTs | 2.9 |
| 45 | 419217 | AA504571 | | gb:aa60e12.r1 NCL_CGAP_GCB1 Homo sapiens | 2.9 |
| | 415849 | R20529 | Hs.6806 | ESTs | 2.9 |
| | 448140 | AF146761 | Hs.20450 | BCM-like membrane protein precursor | 2.9 |
| | 453331 | AI240665 | Hs.8895 | ESTs | 2.9 |
| | 432065 | AA401039 | Hs.2903 | protein phosphatase 4 (formerly X), cata | 2.9 |
| 50 | 438380 | T06430 | Hs.6194 | chondroitin sulfate proteoglycan BEHAB/b | 2.9 |
| | 454377 | AA076811 | | gb:7B03C12 Chromosome 7 Fetal Brain cDNA | 2.9 |
| | 421491 | H99999 | Hs.42736 | ESTs | 2.9 |
| | 452291 | AF015592 | Hs.28853 | CDC7 (cell division cycle 7, S. cerevisi | 2.8 |
| | 415446 | F08898 | Hs.66075 | ESTs | 2.8 |
| 55 | 439518 | W76326 | | gb:zd60d04.r1 Soares_fetal_heart_Nbt-H19W | 2.8 |
| | 427221 | L15409 | Hs.174007 | von Hippel-Lindau syndrome | 2.8 |
| | 422493 | AW474183 | Hs.250173 | hypothetical protein FLJ13158 | 2.8 |
| | 419451 | AI907117 | Hs.90535 | synaptobrevin binding protein 2 | 2.8 |
| | 448789 | BE539108 | Hs.22051 | hypothetical protein MGC15548 | 2.8 |
| 60 | 424126 | AA335635 | Hs.96917 | ESTs | 2.8 |
| | 458895 | AV660159 | Hs.282284 | ESTs, Weakly similar to I38022 hypothe | 2.8 |
| | 418973 | AA233056 | Hs.191518 | ESTs | 2.8 |
| | 440471 | AA886146 | Hs.307944 | ESTs | 2.8 |
| | 421016 | AA504583 | Hs.101047 | transcription factor 3 (E2A immunoglobul | 2.8 |
| 65 | 433647 | AA603367 | Hs.222294 | ESTs | 2.8 |
| | 415817 | U88967 | Hs.78867 | protein tyrosine phosphatase, receptor-t | 2.8 |
| | 421723 | AA620400 | Hs.300717 | sodium channel, voltage-gated, type III, | 2.8 |
| | 434964 | AI638850 | Hs.130746 | ESTs | 2.8 |
| | 432022 | AL162042 | Hs.272348 | Homo sapiens mRNA; cDNA DKFZp761L1212 (f | 2.8 |
| 70 | 400517 | AF242388 | Hs.149585 | lengsin | 2.8 |
| | 433023 | AW864793 | Hs.87409 | thrombospondin 1 | 2.8 |
| | 448734 | BE614070 | Hs.326416 | Homo sapiens mRNA; cDNA DKFZp564H1916 (f | 2.8 |
| | 406736 | AI254733 | Hs.182426 | ribosomal protein S2 | 2.8 |
| | 409207 | AW373564 | Hs.194637 | BANP homolog, SMAR1 homolog | 2.8 |
| 75 | 440196 | N72847 | Hs.125221 | ESTs | 2.8 |
| | 403961 | | | | 2.8 |
| | 425193 | AW965689 | Hs.22509 | ESTs | 2.8 |
| | 425268 | AI807883 | Hs.180059 | Homo sapiens cDNA FLJ20653 fis, clone KA | 2.8 |
| | 440483 | AI200835 | Hs.150386 | ESTs | 2.8 |
| 80 | 412391 | AW947710 | | gb:RC0-MT0004-130300-011-e07 MT0004 Homo | 2.8 |
| | 448769 | N66037 | Hs.38173 | ESTs | 2.8 |
| | 411632 | AW854829 | | gb:QV2-CT0261-201099-011-R1 CT0261 Homo | 2.8 |
| | 438221 | AI798853 | Hs.122224 | ESTs, Weakly similar to ALU5_HUMAN ALU S | 2.8 |
| | 457578 | AA578027 | | gb:nl20h01.s1 NCL_CGAP_HSC1 Homo sapiens | 2.8 |
| | 455510 | AA422029 | Hs.143640 | ESTs, Weakly similar to hyperpolarizatio | 2.8 |
| | 447769 | AW873704 | Hs.320831 | Homo sapiens cDNA FLJ14597 fis, clone NT | 2.8 |
| | 427701 | AA411101 | Hs.243886 | nuclear autoantigenic sperm protein (his | 2.8 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 433800 | AI034361 | Hs.135150 | lung type-I cell membrane-associated gly | 2.8 |
| | 439662 | H97552 | Hs.269060 | ESTs | 2.8 |
| | 425694 | U51333 | Hs.159237 | hexokinase 3 (white cell) | 2.8 |
| 5 | 414747 | U30872 | Hs.77204 | centromere protein F (350/400kD, mitotin | 2.8 |
| | 414598 | AI094221 | Hs.135150 | lung type-I cell membrane-associated gly | 2.8 |
| | 447752 | M73700 | Hs.105938 | lactotransferrin | 2.8 |
| | 408761 | AA057264 | Hs.238936 | ESTs, Weakly similar to (define not ava | 2.8 |
| | 453350 | AI917771 | Hs.61790 | hypothetical protein FLJ23338 | 2.7 |
| 10 | 456629 | AW891965 | Hs.279789 | histone deacetylase 3 | 2.7 |
| | 439538 | AA837323 | Hs.164047 | ESTs | 2.7 |
| | 458814 | AI498957 | Hs.170861 | ESTs, Weakly similar to Z195_HUMAN ZINC | 2.7 |
| | 456029 | BE255990 | Hs.218329 | hypothetical protein | 2.7 |
| | 451129 | BE072881 | | gb:RC2-BT0548-200300-012-e09 BT0548 Homo | 2.7 |
| 15 | 456412 | AW749617 | Hs.280776 | tankyrase, TRF1-interacting ankyrin-rela | 2.7 |
| | 453536 | AA137000 | Hs.62578 | ESTs | 2.7 |
| | 438378 | AW970529 | Hs.86434 | hypothetical protein FLJ21816 | 2.7 |
| | 425745 | U44060 | Hs.14427 | Homo sapiens cDNA: FLJ21800 fis, clone H | 2.7 |
| | 446322 | N23033 | Hs.155814 | ESTs | 2.7 |
| 20 | 451592 | AI805416 | Hs.213897 | ESTs | 2.7 |
| | 429466 | M85835 | Hs.12827 | ESTs | 2.7 |
| | 429747 | M87507 | Hs.2490 | caspase 1, apoptosis-related cysteine pr | 2.7 |
| | 455514 | AW983871 | | gb:RC1-HN0003-220300-021-h07 HN0003 Homo | 2.7 |
| | 414732 | AW410976 | Hs.77152 | minichromosome maintenance deficient (S. | 2.7 |
| 25 | 444207 | AI565004 | Hs.79572 | cathepsin D (lysosomal aspartyl protease | 2.7 |
| | 427421 | AA402414 | Hs.3059 | coatomer protein complex, subunit beta | 2.7 |
| | 449655 | AI021987 | Hs.59970 | ESTs | 2.7 |
| | 422648 | D86983 | Hs.118893 | Melanoma associated gene | 2.7 |
| | 428494 | AA233439 | Hs.184634 | hypothetical protein FLJ20005 | 2.7 |
| 30 | 406895 | X60648 | Hs.172550 | polypyrimidine tract binding protein (he | 2.7 |
| | 453255 | AA278167 | Hs.19215 | Homo sapiens, clone IMAGE:3605822, mRNA | 2.7 |
| | 427348 | NM_014137 | Hs.177258 | PRO0650 protein | 2.7 |
| | 435370 | AI964074 | Hs.225838 | ESTs | 2.7 |
| | 407862 | BE548267 | Hs.50724 | Homo sapiens cDNA FLJ10934 fis, clone OV | 2.7 |
| 35 | 411874 | AA096106 | Hs.20403 | ESTs | 2.7 |
| | 421192 | AA833718 | Hs.204529 | KIAA1806 protein | 2.7 |
| | 435899 | W89093 | Hs.189914 | ESTs | 2.7 |
| | 414603 | R58394 | Hs.25119 | ESTs, Weakly similar to YEX0_YEAST HYPOT | 2.7 |
| | 453462 | AL037291 | Hs.236605 | ESTs, Moderately similar to ALU4_HUMAN A | 2.7 |
| 40 | 436554 | AI985810 | Hs.301173 | ESTs | 2.7 |
| | 427528 | AU077143 | Hs.179565 | minichromosome maintenance deficient (S. | 2.7 |
| | 403881 | | | | 2.7 |
| | 431779 | AW971178 | Hs.268571 | apolipoprotein C-I | 2.7 |
| | 404984 | | | | 2.7 |
| 45 | 448275 | BE514434 | Hs.20830 | kinesin-like 2 | 2.7 |
| | 446839 | BE091926 | Hs.16244 | mitotic spindle coiled-coil related prot | 2.7 |
| | 411927 | BE274009 | Hs.772 | glycogen synthase 1 (muscle) | 2.7 |
| | 404756 | | | | 2.7 |
| | 447072 | D61594 | Hs.17279 | tyrosylprotein sulfotransferase 1 | 2.7 |
| 50 | 422176 | H80977 | | gb:yu89a11.s1 Soares fetal liver spleen | 2.7 |
| | 439627 | BE621702 | Hs.29076 | hypothetical protein FLJ21841 | 2.7 |
| | 436532 | AA721522 | | gb:nv54h12.r1 NCL_CGAP_Ew1 Homo sapiens | 2.7 |
| | 412833 | AIW960547 | Hs.298262 | ribosomal protein S19 | 2.7 |
| | 457245 | AI745498 | Hs.204579 | ESTs | 2.7 |
| 55 | 446861 | AI696519 | Hs.14427 | Homo sapiens cDNA: FLJ21800 fis, clone H | 2.7 |
| | 453263 | R91778 | Hs.99369 | ESTs | 2.7 |
| | 459385 | BE380047 | | gb:601159362F2 NIH_MGC_53 Homo sapiens c | 2.7 |
| | 438764 | AA824524 | Hs.336452 | ESTs | 2.7 |
| | 429285 | AI971081 | Hs.20432 | ESTs, Weakly similar to I38022 hypothei | 2.7 |
| 60 | 424853 | BE549737 | Hs.132967 | Human EST clone 122887 mariner transposo | 2.7 |
| | 430037 | BE409649 | Hs.227789 | mitogen-activated protein kinase-activat | 2.7 |
| | 449892 | N73608 | Hs.50309 | ESTs | 2.7 |
| | 454201 | AB023191 | Hs.44131 | KIAA0974 protein | 2.7 |
| | 452279 | AA286844 | Hs.61260 | hypothetical protein FLJ13164 | 2.7 |
| 65 | 427954 | J03060 | Hs.247551 | melanin 1 | 2.7 |
| | 400371 | U80740 | | | 2.7 |
| | 452449 | AW068658 | Hs.20943 | ESTs | 2.7 |
| | 431114 | AA492400 | Hs.291015 | ESTs | 2.7 |
| | 417088 | M54915 | Hs.81170 | pim-1 oncogene | 2.7 |
| 70 | 447674 | BE270640 | Hs.19192 | cyclin-dependent kinase 2 | 2.7 |
| | 403680 | | | | 2.7 |
| | 454679 | AW813110 | | gb:CM4-ST0189-051099-021-R05 ST0189 Homo | 2.7 |
| | 411968 | AI207410 | Hs.69280 | Homo sapiens, clone IMAGE:3636299, mRNA, | 2.6 |
| | 422240 | R60594 | Hs.29002 | KIAA1706 protein | 2.6 |
| 75 | 424368 | AB037766 | Hs.146085 | KIAA1345 protein | 2.6 |
| | 405808 | | | | 2.6 |
| | 419700 | AF084935 | Hs.92357 | galactokinase 1 | 2.6 |
| | 435972 | W95088 | Hs.114198 | ESTs | 2.6 |
| | 433568 | S70782 | Hs.557 | adrenergic, alpha-1D-, receptor | 2.6 |
| 80 | 443725 | AW245680 | Hs.9701 | growth arrest and DNA-damage-inducible, | 2.6 |
| | 444156 | AW500059 | Hs.86437 | ESTs, Highly similar to AF219140 1 gastr | 2.6 |
| | 428209 | AA424197 | Hs.98947 | ESTs, Weakly similar to S33496 trypsin | 2.6 |
| | 437640 | AA764893 | Hs.272155 | ESTs, Weakly similar to I38022 hypothei | 2.6 |
| | 453948 | AI970797 | Hs.64859 | ESTs | 2.6 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 415402 | AA164687 | Hs.177576 | mannosyl (alpha-1,3)-glycoprotein beta- | 2.6 |
| | 425397 | J04088 | Hs.156346 | topoisomerase (DNA) II alpha (170kD) | 2.6 |
| | 418228 | AA962181 | Hs.111219 | ESTs, Moderately similar to ALU1_HUMAN A | 2.6 |
| 5 | 401324 | | | | 2.6 |
| | 425234 | AW152225 | Hs.165909 | ESTs, Weakly similar to I38022 hypothei | 2.6 |
| | 443210 | AI692649 | Hs.9451 | hypothetical protein MGC13168 | 2.6 |
| | 457244 | AA581385 | Hs.162473 | ESTs, Weakly similar to I38022 hypothei | 2.6 |
| | 417144 | AA382104 | Hs.81337 | lectin, galactoside-binding, soluble, 9 | 2.6 |
| 10 | 433933 | AI754389 | Hs.133494 | Homo sapiens clone TCCCA00164 mRNA sequ | 2.6 |
| | 437437 | AA226869 | Hs.16520 | hypothetical protein DKFZp762L0311 | 2.6 |
| | 434206 | AW136973 | Hs.288516 | ESTs, Weakly similar to S89890 mitogen i | 2.6 |
| | 400992 | | | | 2.6 |
| | 455530 | AW984744 | | gb:RC1-HN0015-040400-011-d03 HN0015 Homo | 2.6 |
| 15 | 436139 | AA765786 | Hs.120936 | ESTs | 2.6 |
| | 448330 | AL036449 | Hs.207163 | ESTs | 2.6 |
| | 412942 | AL120344 | Hs.75074 | mitogen-activated protein kinase-activat | 2.6 |
| | 432753 | NM_014075 | Hs.336938 | Homo sapiens PRO0593 mRNA, complete cds | 2.6 |
| 20 | 433430 | AI863735 | Hs.186755 | ESTs | 2.6 |
| | 436693 | AW973223 | Hs.303197 | B-cell CLL/lymphoma 7C | 2.6 |
| | 429482 | AF076974 | Hs.203952 | transformation/transcription domain-asso | 2.6 |
| | 432715 | AA247152 | Hs.200483 | ESTs, Weakly similar to KIAA1074 protein | 2.6 |
| | 414217 | AI309298 | Hs.279898 | Homo sapiens cDNA: FLJ23165 fis, clone L | 2.6 |
| | 434165 | AA971328 | Hs.95361 | myosin VIIA (Usher syndrome 1B (autosoma | 2.6 |
| 25 | 414835 | AA156720 | Hs.185342 | ESTs | 2.6 |
| | 424489 | T48851 | Hs.149250 | D-siglec precursor, | 2.6 |
| | 436496 | AA281959 | Hs.5210 | glia maturation factor, gamma | 2.6 |
| | 403797 | | | | 2.6 |
| | 434573 | AW372340 | Hs.159717 | ESTs | 2.6 |
| 30 | 418841 | NM_002332 | Hs.89137 | low density lipoprotein-related protein | 2.6 |
| | 415785 | R82419 | Hs.23603 | ESTs, Moderately similar to ALU8_HUMAN A | 2.6 |
| | 450608 | AA010365 | Hs.193229 | ESTs | 2.6 |
| | 425304 | AA463844 | Hs.31339 | fibroblast growth factor 11 | 2.6 |
| | 432268 | BE311856 | Hs.274230 | 3'-phosphoadenosine 5'-phosphosulfate sy | 2.6 |
| 35 | 410507 | AA355288 | Hs.40834 | transitional epithelia response protein | 2.6 |
| | 427343 | AI880044 | Hs.176977 | protein kinase C binding protein 2 | 2.6 |
| | 420917 | AW135716 | Hs.117330 | ESTs | 2.6 |
| | 414399 | L47345 | Hs.155202 | transcription elongation factor B (SIII) | 2.6 |
| | 446089 | AI860021 | Hs.270651 | ESTs, Moderately similar to A47582 B-cel | 2.6 |
| 40 | 440829 | AF136407 | Hs.7446 | chromosome 6 open reading frame 5 | 2.6 |
| | 408475 | AA315514 | Hs.47986 | hypothetical protein MGC10940 | 2.6 |
| | 450946 | AA374569 | Hs.127698 | ESTs, Moderately similar to Z109260A B c | 2.6 |
| | 421462 | AF016495 | Hs.104624 | aquaporin 9 | 2.6 |
| | 434846 | AW295389 | Hs.119768 | ESTs | 2.6 |
| 45 | 422887 | AI751848 | Hs.49215 | ESTs | 2.6 |
| | 417435 | NM_005181 | Hs.82129 | carbonic anhydrase III, muscle specific | 2.6 |
| | 437389 | AL359587 | Hs.271586 | hypothetical protein DKFZp762M115 | 2.5 |
| | 408981 | AW500797 | Hs.49427 | Gem-interacting protein | 2.5 |
| | 432180 | Y18418 | Hs.272822 | RuvB (E coli homolog)-like 1 | 2.5 |
| 50 | 418079 | R40058 | Hs.6911 | ESTs | 2.5 |
| | 437820 | AA769062 | Hs.323836 | ESTs, Weakly similar to alternatively sp | 2.5 |
| | 439685 | AW956781 | Hs.293937 | ESTs, Weakly similar to FXD2_HUMAN FORKH | 2.5 |
| | 425681 | AB018297 | Hs.159183 | KIAA0754 protein | 2.5 |
| | 435177 | AI018174 | Hs.42936 | ESTs | 2.5 |
| 55 | 437323 | AA371145 | Hs.226627 | leptin receptor | 2.5 |
| | 422114 | AW194851 | Hs.111801 | arsenate resistance protein ARS2 | 2.5 |
| | 448478 | AI523218 | Hs.203456 | ESTs | 2.5 |
| | 426623 | AA382826 | Hs.132793 | ESTs | 2.5 |
| | 448764 | AI568807 | Hs.182112 | ESTs | 2.5 |
| 60 | 458385 | AI051489 | Hs.246214 | ESTs | 2.5 |
| | 403726 | N28939 | Hs.13434 | Homo sapiens clone 24418 mRNA sequence | 2.5 |
| | 444888 | AI651039 | Hs.148559 | ESTs | 2.5 |
| | 456179 | H75490 | Hs.271930 | ESTs | 2.5 |
| | 424840 | D79987 | Hs.153479 | extra spindle poles, S. cerevisiae, homo | 2.5 |
| 65 | 406273 | NM_000919 | Hs.83920 | peptidylglycine alpha-amidating monooxyg | 2.5 |
| | 418054 | NM_002318 | Hs.83354 | lysyl oxidase-like 2 | 2.5 |
| | 445936 | BE543594 | Hs.61478 | hypothetical protein FLJ22329 | 2.5 |
| | 454967 | AW848276 | | gb:LL3-CT0214-150200-074-E06 CT0214 Homo | 2.5 |
| | 442303 | AA989289 | Hs.129169 | ESTs | 2.5 |
| 70 | 456583 | AF179897 | Hs.104105 | Meis (mouse) homolog 2 | 2.5 |
| | 434263 | N34895 | Hs.44648 | ESTs | 2.5 |
| | 416892 | L24498 | Hs.80409 | growth arrest and DNA-damage-inducible, | 2.5 |
| | 424528 | AW073971 | Hs.238954 | ESTs, Weakly similar to KIAA1204 protein | 2.5 |
| | 406038 | Y14443 | Hs.88219 | zinc finger protein 200 | 2.5 |
| 75 | 413495 | Y12395 | Hs.315177 | interferon-related developmental regulat | 2.5 |
| | 423098 | AA321980 | Hs.204682 | ESTs | 2.5 |
| | 410817 | AI262789 | Hs.93659 | protein disulfide isomerase related prot | 2.5 |
| | 439841 | AF038961 | Hs.6710 | mannose-P-dolichol utilization defect 1 | 2.5 |
| | 453828 | AW970960 | Hs.293821 | ESTs | 2.5 |
| 80 | 445034 | AW293376 | Hs.143659 | ESTs | 2.5 |
| | 449620 | BE407797 | Hs.23794 | checkpoint with forkhead and ring finger | 2.5 |
| | 406876 | AI382286 | Hs.180842 | ribosomal protein L13 | 2.5 |
| | 412370 | AW946614 | | gb:RC2-ET0021-280400-011-c05 ET0021 Homo | 2.5 |
| | 423642 | AW452650 | Hs.157148 | hypothetical protein MGC13204 | 2.5 |

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|----|--------|-----------|-----------|--|-----|
| | 430357 | AW976789 | Hs.165607 | ESTs | 2.5 |
| | 414853 | U31116 | Hs.77501 | sarcoglycan, beta (43kD dystrophin-assoc | 2.5 |
| | 416097 | BE387371 | Hs.118964 | hypothetical protein FLJ120085 | 2.5 |
| 5 | 428619 | AK002140 | Hs.187378 | hypothetical protein FLJ11278 | 2.5 |
| | 413976 | BE295452 | Hs.75655 | procollagen-proline, 2-oxoglutarate 4-di | 2.5 |
| | 445223 | AW291553 | Hs.254983 | ESTs | 2.5 |
| | 423926 | X03833 | Hs.1722 | interleukin 1, alpha | 2.5 |
| | 410165 | BE560228 | Hs.71869 | apoptosis-associated speck-like protein | 2.5 |
| | 406474 | | | | 2.5 |
| 10 | 433908 | AW298141 | Hs.157975 | ESTs | 2.5 |
| | 439755 | AW748482 | Hs.77873 | B7 homolog 3 | 2.5 |
| | 437528 | N59646 | Hs.169745 | crumbs (Drosophila) homolog 1 | 2.5 |
| | 420734 | AW972872 | Hs.293736 | ESTs | 2.5 |
| | 415345 | Z43108 | | gb:HSC13E071 normalized infant brain cDN | 2.5 |
| 15 | 419337 | AW291112 | Hs.209978 | ESTs | 2.5 |
| | 444606 | R09478 | Hs.18041 | ESTs | 2.5 |
| | 430061 | AB037817 | Hs.230188 | KIAA1396 protein | 2.5 |
| | 413407 | AI356293 | Hs.75339 | inositol polyphosphate phosphatase-like | 2.5 |
| | 411965 | BE467339 | Hs.280115 | ESTs | 2.5 |
| 20 | 409278 | AA346683 | Hs.52763 | anaphase-promoting complex subunit 7 | 2.5 |
| | 403142 | | | | 2.5 |
| | 401714 | | | | 2.5 |
| | 425081 | X74794 | Hs.154443 | minichromosome maintenance deficient (S. | 2.5 |
| 25 | 416505 | H66470 | Hs.16004 | ESTs | 2.5 |
| | 431518 | AA743462 | Hs.165337 | ESTs | 2.5 |
| | 448623 | BE613468 | Hs.107515 | ESTs, Weakly similar to T00329 hypotheti | 2.5 |
| | 428301 | AW628666 | Hs.98440 | ESTs, Weakly similar to I38022 hypotheti | 2.5 |
| | 404366 | | | | 2.5 |
| 30 | 449733 | R74546 | Hs.29438 | Homo sapiens cDNA FLJ12094 fis, clone HE | 2.5 |
| | 459583 | AI907673 | | gb:IL-BT152-080399-004 BT152 Homo sapien | 2.5 |
| | 402856 | AW939659 | | gb:RC0-DT0076-110100-031-c09 DT0076 Homo | 2.5 |
| | 420751 | J03019 | Hs.99913 | adrenergic, beta-1-, receptor | 2.4 |
| | 436805 | AA731533 | Hs.270751 | ESTs | 2.4 |
| 35 | 420285 | AA258124 | Hs.293878 | ESTs, Moderately similar to ZN91_HUMAN Z | 2.4 |
| | 453496 | AA442103 | Hs.330084 | solute carrier family 2 (facilitated glu | 2.4 |
| | 453853 | AL040600 | Hs.188083 | ESTs | 2.4 |
| | 407909 | AW103986 | | gb:xd63e06.x1 NCL_CGAP_Ov23 Homo sapiens | 2.4 |
| | 454630 | BE142075 | | gb:CM3-HT0137-170999-012-02 HT0137 Homo | 2.4 |
| 40 | 451026 | AA013218 | Hs.157492 | cer-d4 (mouse) homolog | 2.4 |
| | 420779 | L12398 | Hs.99922 | dopamine receptor D4 | 2.4 |
| | 438322 | AA804170 | Hs.221349 | ESTs | 2.4 |
| | 455908 | BE156306 | | gb:QV0-HT0367-150200-114-h04 HT0367 Homo | 2.4 |
| | 419625 | U91616 | Hs.91640 | nuclear factor of kappa light polypeptid | 2.4 |
| 45 | 440773 | AA352702 | Hs.332541 | Homo sapiens, Similar to RIKEN cDNA 2700 | 2.4 |
| | 450823 | T81223 | Hs.22011 | complement-c1q tumor necrosis factor-rel | 2.4 |
| | 447247 | AW369351 | Hs.287955 | Homo sapiens cDNA FLJ13090 fis, clone NT | 2.4 |
| | 429109 | AL008637 | Hs.196352 | neutrophil cytosolic factor 4 (40kD) | 2.4 |
| | 451802 | AI817711 | Hs.209374 | ESTs | 2.4 |
| 50 | 419417 | R92491 | Hs.39429 | ESTs | 2.4 |
| | 407094 | AF000574 | Hs.22405 | leukocyte immunoglobulin-like receptor, | 2.4 |
| | 423567 | BE252949 | Hs.69331 | hypothetical protein FLJ13633 | 2.4 |
| | 427501 | AI369280 | Hs.131743 | ESTs | 2.4 |
| | 451773 | Z42044 | Hs.26996 | KIAA1278 protein | 2.4 |
| 55 | 436845 | AA732297 | Hs.113928 | ESTs | 2.4 |
| | 431584 | AW296121 | Hs.266263 | Homo sapiens cDNA FLJ14115 fis, clone MA | 2.4 |
| | 440614 | AA781530 | Hs.127236 | hypothetical protein FLJ12879 | 2.4 |
| | 423721 | AF176911 | Hs.132004 | cardiotrophin-like cytokine; neurotrophi | 2.4 |
| | 452125 | BE312642 | Hs.28077 | GDP-mannose pyrophosphorylase B | 2.4 |
| 60 | 419508 | AW997938 | Hs.90786 | ATP-binding cassette, sub-family C (CFTR | 2.4 |
| | 453446 | BE299996 | | gb:600944574F1 NIH_MGC_17 Homo sapiens c | 2.4 |
| | 419792 | AA250890 | Hs.190037 | ESTs | 2.4 |
| | 452786 | R61362 | Hs.106642 | ESTs, Weakly similar to T09052 hypotheti | 2.4 |
| | 410447 | AW816134 | | gb:MR3-ST0220-290100-016-e04 ST0220 Homo | 2.4 |
| 65 | 438662 | AA223599 | Hs.6351 | cleavage and polyadenylation specific fa | 2.4 |
| | 402408 | | | | 2.4 |
| | 443950 | NM_001425 | Hs.9999 | epithelial membrane protein 3 | 2.4 |
| | 414625 | AA335738 | Hs.76686 | glutathione peroxidase 1 | 2.4 |
| | 403048 | | | | 2.4 |
| 70 | 432088 | AA525454 | | gb:ni85c09.s1 NCL_CGAP_Pr20 Homo sapiens | 2.4 |
| | 431692 | AL021331 | Hs.267749 | unc93 (C.elegans) homolog A | 2.4 |
| | 455023 | AW850907 | | gb:IL3-CT0220-310100-065-H11 CT0220 Homo | 2.4 |
| | 426249 | F05422 | Hs.168352 | nucleoporin-like protein 1 | 2.4 |
| | 446795 | AI797713 | Hs.156471 | ESTs | 2.4 |
| 75 | 414774 | X02419 | Hs.77274 | plasminogen activator, urokinase | 2.4 |
| | 414252 | AA346483 | Hs.126191 | ESTs | 2.4 |
| | 417918 | AA209205 | Hs.163754 | hypothetical protein FLJ12606 | 2.4 |
| | 427550 | BE242818 | Hs.179606 | nuclear RNA helicase, DECD variant of DE | 2.4 |
| | 404020 | | | | 2.4 |
| 80 | 407846 | AA426202 | Hs.40403 | Cbp/p300-interacting transactivator, wit | 2.4 |
| | 417222 | AI525424 | Hs.42053 | hypothetical protein MGC2383 | 2.4 |
| | 443639 | BE269042 | Hs.9661 | proteasome (prosome, macropain) subunit, | 2.4 |
| | 452706 | AW449390 | Hs.257150 | ESTs, Moderately similar to SUR1_HUMAN S | 2.4 |
| | 401676 | | | | 2.4 |

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|----|--------|-----------|-----------|--|-----|
| | 428882 | AA436915 | Hs.131748 | ESTs, Moderately similar to ALU7_HUMAN A | 2.4 |
| | 436277 | R88520 | Hs.120917 | ESTs | 2.4 |
| | 426271 | AF026547 | Hs.169047 | chondroitin sulfate proteoglycan 3 (neur | 2.4 |
| 5 | 405353 | | | | 2.4 |
| | 409193 | AA131483 | | gb:zo08e05.r1 Stratagene neuroepithelium | 2.4 |
| | 431431 | AL096711 | Hs.252953 | Human DNA sequence from clone RP3-403A15 | 2.4 |
| | 407889 | R34556 | Hs.30800 | ESTs, Weakly similar to S65657 alpha-1C- | 2.4 |
| | 453335 | AW857376 | Hs.169238 | fucosyltransferase 3 (galactoside 3(4)-L | 2.4 |
| 10 | 450621 | AW297288 | Hs.55918 | hypothetical protein FLJ11354 | 2.4 |
| | 419652 | AL157485 | Hs.91973 | hypothetical protein | 2.4 |
| | 421151 | BE174431 | Hs.63386 | ESTs | 2.4 |
| | 437846 | AA773866 | Hs.244569 | esophagus cancer-related gene-2 | 2.4 |
| | 420681 | AA847602 | Hs.106510 | ESTs, Moderately similar to ALU2_HUMAN A | 2.4 |
| 15 | 405288 | | | | 2.4 |
| | 453527 | R49570 | Hs.180236 | ESTs | 2.4 |
| | 429875 | AI091815 | | gb:qa58b06.s1 Soares_NhHMPu_S1 Homo sapi | 2.4 |
| | 436360 | AI962796 | Hs.136754 | ESTs | 2.4 |
| | 418592 | X99226 | Hs.284153 | Fanconi anemia, complementation group A | 2.4 |
| 20 | 419991 | AJ000098 | Hs.94210 | eyes absent (Drosophila) homolog 1 | 2.4 |
| | 449539 | W80363 | Hs.58446 | ESTs | 2.4 |
| | 419870 | AW403911 | Hs.265175 | phosphoprotein associated with GEMs | 2.4 |
| | 404584 | | | | 2.4 |
| | 454276 | AW294996 | Hs.255374 | ESTs | 2.4 |
| 25 | 423746 | AW361817 | Hs.132370 | NADPH oxidase 1 | 2.4 |
| | 415558 | AA885143 | Hs.125719 | ESTs | 2.4 |
| | 428141 | D50402 | Hs.182611 | solute carrier family 11 (proton-coupled | 2.4 |
| | 406953 | L36847 | | gb:Human (clone p17/90) rearranged iduro | 2.4 |
| | 444471 | AB020684 | Hs.11217 | KIAA0877 protein | 2.4 |
| 30 | 451031 | AI360187 | Hs.4254 | ESTs | 2.4 |
| | 455302 | AW97641 | | gb:RC6-BN0052-170200-011-D06 BN0052 Homo | 2.4 |
| | 449063 | AI627352 | Hs.236547 | Homo sapiens, clone IMAGE:2905978, mRNA, | 2.4 |
| | 401048 | | | | 2.4 |
| | 434420 | AA688278 | Hs.194864 | hypothetical protein FLJ22578 | 2.4 |
| 35 | 425848 | BE242709 | Hs.159637 | valyl-tRNA synthetase 2 | 2.4 |
| | 449086 | AI628357 | Hs.208037 | ESTs | 2.4 |
| | 415238 | R37780 | Hs.21422 | ESTs | 2.4 |
| | 448337 | AW206453 | Hs.3782 | ESTs | 2.4 |
| | 416991 | N35389 | Hs.141296 | KIAA0226 gene product | 2.3 |
| 40 | 412600 | L28824 | Hs.74101 | spleen tyrosine kinase | 2.3 |
| | 418385 | AW590613 | Hs.301040 | Homo sapiens, clone IMAGE:3357127, mRNA, | 2.3 |
| | 440769 | BE561793 | Hs.21446 | KIAA1716 protein | 2.3 |
| | 450437 | X13956 | Hs.24998 | hypothetical protein MGC10471 | 2.3 |
| | 412035 | N78559 | Hs.293629 | hypothetical protein MGC3121 | 2.3 |
| 45 | 406739 | AI566709 | Hs.182426 | ribosomal protein S2 | 2.3 |
| | 418506 | AA084248 | Hs.85339 | G protein-coupled receptor 39 | 2.3 |
| | 410286 | AI739159 | Hs.61898 | DKFZP586N2124 protein | 2.3 |
| | 443740 | R56434 | Hs.21062 | ESTs | 2.3 |
| | 405605 | | | | 2.3 |
| 50 | 416913 | AW934714 | | gb:RC1-DT0001-031299-011-a11 DT0001 Homo | 2.3 |
| | 426509 | M31166 | Hs.2050 | pentaxin-related gene, rapidly induced b | 2.3 |
| | 445828 | F05802 | Hs.81907 | ESTs | 2.3 |
| | 457195 | AB011099 | Hs.195647 | KIAA0527 protein | 2.3 |
| | 420372 | AW960049 | Hs.293660 | Homo sapiens, clone IMAGE:3535476, mRNA, | 2.3 |
| 55 | 423198 | M81933 | Hs.1634 | cell division cycle 25A | 2.3 |
| | 457730 | AW753613 | | gb:RC1-CT0268-060100-013-e01 CT0268 Homo | 2.3 |
| | 412014 | AI620650 | Hs.43761 | ESTs, Weakly similar to A46010 X-linked | 2.3 |
| | 447131 | NM_004585 | Hs.17466 | retinoic acid receptor responder (tazaro | 2.3 |
| | 446288 | AW189209 | Hs.149708 | ESTs | 2.3 |
| 60 | 436954 | AA740151 | Hs.130425 | ESTs | 2.3 |
| | 411658 | AW855598 | | gb:CM1-CT0278-031199-032-e08 CT0278 Homo | 2.3 |
| | 404240 | | | | 2.3 |
| | 458094 | H95091 | | gb:yw57a09.r1 Soares_placenta_8to9weeks_ | 2.3 |
| | 416951 | AA190926 | Hs.190785 | ESTs, Moderately similar to S65657 alpha | 2.3 |
| 65 | 406737 | AI356586 | | gb:qy15h09.x1 NCL_CGAP_Bm23 Homo sapien | 2.3 |
| | 458453 | AI097452 | Hs.135095 | ESTs | 2.3 |
| | 452330 | AI879127 | Hs.191979 | KIAA1733 protein | 2.3 |
| | 408523 | AW833259 | Hs.314287 | ESTs | 2.3 |
| | 455470 | AW947992 | | gb:PMO-MT0011-240300-001-c09 MT0011 Homo | 2.3 |
| 70 | 436323 | R17697 | Hs.140963 | ESTs, Weakly similar to I38022 hypotheti | 2.3 |
| | 450000 | AI952797 | Hs.10886 | hypothetical protein FLJ21709 | 2.3 |
| | 416171 | H23896 | Hs.125790 | leucine-rich repeat-containing 2 | 2.3 |
| | 419134 | T89863 | Hs.221771 | ESTs | 2.3 |
| | 445933 | AV655733 | Hs.293860 | spintex-like protein | 2.3 |
| 75 | 422089 | AA523172 | Hs.103135 | ESTs, Weakly similar to SFR4_HUMAN SPLIC | 2.3 |
| | 449911 | AI262106 | Hs.12653 | ESTs | 2.3 |
| | 417079 | U65590 | Hs.81134 | interleukin 1 receptor antagonist | 2.3 |
| | 411742 | AW247593 | Hs.71819 | eukaryotic translation initiation factor | 2.3 |
| | 435615 | Y15065 | Hs.4975 | potassium voltage-gated channel, KQT-lik | 2.3 |
| 80 | 423491 | AA191765 | Hs.129673 | eukaryotic translation initiation factor | 2.3 |
| | 407182 | AA312551 | Hs.230157 | ESTs | 2.3 |
| | 411448 | AA178955 | Hs.271439 | ESTs, Weakly similar to I38022 hypotheti | 2.3 |
| | 438644 | AI126162 | Hs.129037 | ESTs | 2.3 |
| | 432691 | U29725 | Hs.3080 | mitogen-activated protein kinase 7 | 2.3 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 452198 | AI097560 | Hs.61210 | ESTs, Weakly similar to I38022 hypotheti | 2.3 |
| | 411125 | AA151647 | Hs.68877 | cytochrome b-245, alpha polypeptide | 2.3 |
| | 404054 | | | | 2.3 |
| 5 | 430458 | AA479300 | Hs.225706 | ESTs, Weakly similar to I38022 hypotheti | 2.3 |
| | 440210 | AW674562 | Hs.125296 | ESTs | 2.3 |
| | 446727 | AB011095 | Hs.16032 | KIAA0523 protein | 2.3 |
| | 453775 | NM_002916 | Hs.35120 | replication factor C (activator 1) 4 (37 | 2.3 |
| | 438379 | N23018 | Hs.171391 | C-terminal binding protein 2 | 2.3 |
| 10 | 449919 | AI674685 | Hs.200141 | ESTs | 2.3 |
| | 415293 | R49462 | Hs.106541 | ESTs | 2.3 |
| | 441126 | NM_000429 | Hs.323715 | methionine adenosyltransferase I, alpha | 2.3 |
| | 408203 | AA053137 | Hs.42390 | nasopharyngeal carcinoma susceptibility | 2.3 |
| | 434941 | AW073202 | Hs.334825 | Homo sapiens cDNA FLJ14752 fis, clone NT | 2.3 |
| 15 | 450748 | AI733093 | Hs.130016 | ESTs | 2.3 |
| | 404185 | | | | 2.3 |
| | 418327 | U70370 | Hs.84136 | paired-like homeodomain transcription fa | 2.3 |
| | 451370 | AI791929 | Hs.300782 | ESTs | 2.3 |
| | 400034 | | | | 2.3 |
| 20 | 407723 | AW071161 | Hs.252873 | ESTs | 2.3 |
| | 431320 | AW969474 | Hs.183070 | ESTs | 2.3 |
| | 429271 | AF039850 | Hs.198515 | dead ringer (Drosophila)-like 1 | 2.3 |
| | 453707 | AW003879 | Hs.126522 | Homo sapiens, clone MGC:16722, mRNA, com | 2.3 |
| | 419225 | U70073 | | gb:HSU70073 Human Homo sapiens cDNA clon | 2.3 |
| 25 | 444656 | AI277924 | Hs.145199 | ESTs | 2.3 |
| | 405741 | | | | 2.3 |
| | 400917 | | | | 2.3 |
| | 432567 | AA736777 | Hs.293770 | ESTs | 2.3 |
| | 437949 | U78519 | Hs.41654 | ESTs, Weakly similar to A46010 X-linked | 2.3 |
| 30 | 450514 | AC005785 | Hs.25069 | A kinase (PRKA) anchor protein 8 | 2.3 |
| | 418400 | BE243026 | Hs.301989 | KIAA0246 protein | 2.3 |
| | 444019 | BE173977 | Hs.10098 | putative nucleolar RNA helicase | 2.3 |
| | 406326 | | | | 2.3 |
| | 412077 | N51107 | Hs.47199 | ESTs, Weakly similar to FLJ00004 protein | 2.3 |
| 35 | 427647 | W19744 | Hs.180059 | Homo sapiens cDNA FLJ20653 fs, clone KA | 2.3 |
| | 414528 | AA148950 | Hs.188836 | ESTs | 2.3 |
| | 414854 | BE546797 | Hs.51483 | ESTs, Weakly similar to hypothetical pro | 2.3 |
| | 420352 | BE258835 | | gb:601117374F1 NIH_MGC_16 Homo sapiens c | 2.3 |
| | 439467 | AW292275 | Hs.158355 | ESTs | 2.3 |
| 40 | 402627 | | | | 2.3 |
| | 451711 | AK000461 | Hs.26890 | cat eye syndrome chromosome region, cand | 2.3 |
| | 424308 | AW975531 | Hs.154443 | minichromosome maintenance deficient (S. | 2.3 |
| | 423869 | BE409301 | Hs.134012 | C1q-related factor | 2.3 |
| | 405915 | | | | 2.3 |
| 45 | 431503 | NM_012129 | Hs.258576 | claudin 12 | 2.3 |
| | 423306 | W88562 | Hs.108198 | ESTs | 2.3 |
| | 443232 | AF161521 | Hs.9081 | phenylalanyl-tRNA synthetase beta-subuni | 2.3 |
| | 433064 | D79991 | Hs.30002 | SH3-containing protein SH3GLB2; KIAA1848 | 2.3 |
| | 434437 | AI912566 | Hs.187813 | ESTs | 2.3 |
| 50 | 436191 | BE407866 | Hs.170253 | hypothetical protein FLJ23282 | 2.3 |
| | 420006 | H14429 | Hs.94300 | serologically defined colon cancer antig | 2.3 |
| | 447942 | F12628 | Hs.334786 | hypothetical protein MGC16040 | 2.3 |
| | 403166 | | | | 2.3 |
| | 422119 | AI277829 | Hs.111862 | KIAA0590 gene product | 2.3 |
| | 403751 | | | | 2.3 |
| 55 | 426451 | AI908165 | Hs.169946 | GATA-binding protein 3 | 2.3 |
| | 427413 | BE547647 | Hs.177781 | hypothetical protein MGC5618 | 2.3 |
| | 409091 | AW970386 | Hs.269423 | ESTs | 2.3 |
| | 440491 | R35252 | Hs.24944 | ESTs, Weakly similar to 2109260A B cell | 2.3 |
| 60 | 427722 | AK000123 | Hs.180479 | hypothetical protein FLJ20116 | 2.3 |
| | 405747 | | | | 2.3 |
| | 438210 | AA780519 | Hs.311601 | EST | 2.3 |
| | 404652 | | | | 2.3 |
| 65 | 423524 | AF055989 | Hs.129738 | potassium voltage-gated channel, Shaw-re | 2.2 |
| | 426793 | X89887 | Hs.172350 | HIR (histone cell cycle regulation defec | 2.2 |
| | 444424 | AI654684 | Hs.196377 | ESTs | 2.2 |
| | 434031 | BE384165 | Hs.23723 | pseudouridylyl synthase 1 | 2.2 |
| | 427650 | AW501245 | Hs.252259 | ribosomal protein S3 | 2.2 |
| | 435220 | D50030 | Hs.104 | HGF activator | 2.2 |
| 70 | 438279 | AA805166 | Hs.154762 | HIV-1 rev binding protein 2 | 2.2 |
| | 424668 | D83702 | Hs.151573 | cryptochrome 1 (photolyase-like) | 2.2 |
| | 429961 | BE246829 | Hs.226770 | DKFZP566C0424 protein | 2.2 |
| | 442065 | AI831229 | Hs.128417 | hypothetical protein FLJ14009 | 2.2 |
| | 415198 | AW009480 | Hs.943 | natural killer cell transcript 4 | 2.2 |
| 75 | 420536 | AL117455 | Hs.275438 | histone deacetylase 7A | 2.2 |
| | 411263 | BE297802 | Hs.69360 | kinesin-like 6 (mitotic centromere-assoc | 2.2 |
| | 443753 | AW367578 | Hs.134749 | ESTs | 2.2 |
| | 423243 | AA351938 | Hs.23964 | sin3-associated polypeptide, 18kD | 2.2 |
| | 446572 | AV659151 | Hs.282961 | ESTs | 2.2 |
| 80 | 412247 | AF022375 | Hs.73793 | vascular endothelial growth factor | 2.2 |
| | 421040 | AA715026 | Hs.135280 | ESTs | 2.2 |
| | 426212 | S71824 | Hs.167988 | neural cell adhesion molecule 1 | 2.2 |
| | 455584 | BE007420 | | gb:PM3-BN0142-200300-001-c04 BN0142 Homo | 2.2 |
| | 406851 | AA609784 | Hs.180255 | major histocompatibility complex, class | 2.2 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 444153 | AK001610 | Hs.10414 | hypothetical protein FLJ10748 | 2.2 |
| | 419575 | U43431 | Hs.91175 | topoisomerase (DNA) III alpha | 2.2 |
| | 418672 | L44284 | Hs.159743 | ESTs | 2.2 |
| 5 | 456261 | AA210718 | Hs.104157 | ESTs, Weakly similar to KIAA0694 protein | 2.2 |
| | 415737 | AA167626 | Hs.118743 | ESTs | 2.2 |
| | 447554 | AI391598 | Hs.36119 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.2 |
| | 405159 | | | | 2.2 |
| | 442177 | AW661820 | Hs.211413 | ESTs | 2.2 |
| 10 | 446139 | H77395 | Hs.39749 | ESTs | 2.2 |
| | 458339 | AW976853 | Hs.172843 | ESTs | 2.2 |
| | 401876 | | | | 2.2 |
| | 439566 | AF086387 | | gb:Homo sapiens full length insert cDNA | 2.2 |
| | 425079 | H09963 | Hs.2257 | vitronectin (serum spreading factor, som | 2.2 |
| 15 | 441837 | AA361743 | Hs.179881 | core-binding factor, beta subunit | 2.2 |
| | 430644 | AB015419 | Hs.247710 | preprolactin-releasing peptide | 2.2 |
| | 431474 | AL133990 | Hs.190642 | ESTs | 2.2 |
| | 407739 | NM_002285 | Hs.38070 | lymphoid nuclear protein related to AF4 | 2.2 |
| | 424244 | AV647184 | Hs.143601 | hypothetical protein hCLA-iso | 2.2 |
| 20 | 438057 | AW294544 | Hs.125785 | ESTs, Weakly similar to CORB MOUSE CORN1 | 2.2 |
| | 412715 | NM_000947 | Hs.74519 | primase, polypeptide 2A (58kD) | 2.2 |
| | 422365 | AF035537 | Hs.115521 | REV3 (yeast homolog)-like, catalytic sub | 2.2 |
| | 404170 | | | | 2.2 |
| | 406902 | M32074 | | gb:Human retinoic acid receptor gamma 2 | 2.2 |
| 25 | 437902 | AA770599 | Hs.144055 | ESTs | 2.2 |
| | 401012 | | | | 2.2 |
| | 446502 | AI302654 | Hs.208024 | ESTs | 2.2 |
| | 442554 | AW467376 | Hs.129640 | ESTs | 2.2 |
| | 443021 | AA368546 | Hs.8904 | Ig superfamily protein | 2.2 |
| 30 | 421141 | AW117261 | Hs.125914 | ESTs | 2.2 |
| | 443070 | BE388662 | Hs.8984 | Homo sapiens chromosome 14 BAC 98L12 | 2.2 |
| | 446566 | H95741 | Hs.17914 | membrane-spanning 4-domains, subfamily A | 2.2 |
| | 427695 | R88483 | Hs.172662 | ESTs | 2.2 |
| | 426503 | AA380153 | | gb:EST93093 Skin tumor I Homo sapiens cD | 2.2 |
| 35 | 431468 | AW248431 | Hs.256526 | nuclear prelamin A recognition factor | 2.2 |
| | 416185 | AW975861 | Hs.47367 | KIAA1785 protein | 2.2 |
| | 437319 | BE410958 | Hs.56406 | Homo sapiens cDNA FLJ13549 fis, clone PL | 2.2 |
| | 402054 | | | | 2.2 |
| | 413335 | AI613318 | Hs.48442 | ESTs | 2.2 |
| 40 | 408212 | AA297567 | Hs.43728 | hypothetical protein | 2.2 |
| | 406169 | | | | 2.2 |
| | 451099 | R52795 | Hs.25954 | interleukin 13 receptor, alpha 2 | 2.2 |
| | 407335 | AA631047 | Hs.158761 | Homo sapiens cDNA FLJ13054 fis, clone NT | 2.2 |
| | 409715 | W42591 | Hs.23892 | ESTs | 2.2 |
| 45 | 431921 | N46466 | Hs.58879 | ESTs | 2.2 |
| | 443823 | BE089782 | Hs.9877 | hypothetical protein | 2.2 |
| | 432458 | AI968598 | Hs.78768 | malignant cell expression-enhanced gene/ | 2.2 |
| | 419726 | U50330 | Hs.1274 | bone morphogenetic protein 1 | 2.2 |
| 50 | 423178 | AI033140 | Hs.124983 | Homo sapiens mRNA; cDNA DKFZp564C142 (fr | 2.2 |
| | 451089 | AA903705 | Hs.4190 | Homo sapiens cDNA: FLJ23269 fis, clone C | 2.2 |
| | 415216 | AI825905 | Hs.193211 | Homo sapiens cDNA FLJ11421 fis, clone HE | 2.2 |
| | 442242 | AV647908 | Hs.90424 | Homo sapiens cDNA: FLJ23285 fis, clone H | 2.2 |
| | 441830 | AA383104 | Hs.42954 | hypothetical protein DKFZp564D0372 | 2.2 |
| | 406660 | X65371 | Hs.172550 | polypyrimidine tract binding protein (he | 2.2 |
| 55 | 443378 | AW392550 | Hs.9280 | proteasome (prosome, macropain) subunit, | 2.2 |
| | 432558 | R97268 | Hs.177269 | ESTs | 2.2 |
| | 408146 | R45621 | Hs.81057 | hypothetical protein MGC2718 | 2.2 |
| | 419865 | NM_007020 | Hs.93502 | U1-snRNP binding protein homolog (70kD) | 2.2 |
| | 439444 | AI277652 | Hs.54578 | ESTs, Weakly similar to I38022 hypothe | 2.2 |
| 60 | 438407 | AI457122 | Hs.129673 | eukaryotic translation initiation factor | 2.2 |
| | 450184 | W31096 | Hs.237617 | Homo sapiens, clone IMAGE:3447394, mRNA, | 2.2 |
| | 409130 | BE076601 | Hs.75658 | phosphorylase, glycogen; brain | 2.2 |
| | 428844 | AW972635 | Hs.301904 | hypothetical protein FLJ12671 | 2.2 |
| | 429489 | AF008203 | Hs.204039 | aristae-like homeobox 3 | 2.2 |
| 65 | 433042 | AW193534 | Hs.281895 | Homo sapiens cDNA FLJ11660 fis, clone HE | 2.2 |
| | 440658 | H29142 | Hs.143032 | ESTs, Weakly similar to neuronal thread | 2.2 |
| | 408204 | AA454501 | Hs.43666 | protein tyrosine phosphatase type IVA, m | 2.2 |
| | 427498 | NM_003926 | Hs.178728 | methyl-CpG binding domain protein 3 | 2.2 |
| | 408006 | H57654 | Hs.303345 | ESTs, Weakly similar to I38022 hypothe | 2.2 |
| 70 | 445703 | AV654845 | Hs.27 | glycine dehydrogenase (decarboxylating; | 2.2 |
| | 431446 | AW294929 | Hs.255369 | Homo sapiens cDNA FLJ10265 fis, clone HE | 2.2 |
| | 456660 | AA909249 | Hs.112282 | solute carrier family 30 (zinc transport | 2.2 |
| | 433099 | NM_002504 | Hs.3187 | nuclear transcription factor, X-box bind | 2.2 |
| | 415857 | AA866115 | Hs.127797 | Homo sapiens cDNA FLJ11381 fis, clone HE | 2.2 |
| 75 | 415245 | N59650 | Hs.27252 | ESTs | 2.2 |
| | 443657 | R14973 | | gb:y42f10.s1 Soares fetal liver spleen | 2.2 |
| | 402521 | AW501216 | Hs.108945 | KIAA0515 protein | 2.2 |
| | 414819 | BE177320 | Hs.156148 | hypothetical protein FLJ13231 | 2.2 |
| | 446530 | AV658909 | Hs.282642 | ESTs | 2.2 |
| 80 | 415797 | AI291896 | Hs.72800 | ESTs | 2.2 |
| | 414812 | X72755 | Hs.77367 | monokine induced by gamma interferon | 2.2 |
| | 453028 | AB006532 | Hs.31442 | RacQ protein-like 4 | 2.2 |
| | 412133 | U83460 | Hs.73614 | solute carrier family 31 (copper transpo | 2.2 |
| | 407881 | AW072003 | Hs.40968 | heparan sulfate (glucosamine) 3-O-sulfot | 2.2 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 437033 | AW248364 | Hs.5409 | RNA polymerase I subunit | 2.2 |
| | 422732 | AA577455 | Hs.24937 | transformer-2 alpha (htra-2 alpha) | 2.2 |
| | 416388 | AI417358 | Hs.73677 | ESTs | 2.2 |
| 5 | 452849 | AF044924 | Hs.30792 | hook2 protein | 2.2 |
| | 446615 | BE513202 | Hs.15589 | PPAR binding protein | 2.2 |
| | 428361 | NM_015905 | Hs.183858 | transcriptional intermediary factor 1 | 2.2 |
| | 446279 | AA490770 | Hs.182382 | ESTs | 2.2 |
| | 422938 | NM_001809 | Hs.1594 | centromere protein A (17kD) | 2.2 |
| | 403969 | | | | 2.2 |
| 10 | 410423 | AW402432 | Hs.63489 | protein tyrosine phosphatase, non-recept | 2.2 |
| | 429736 | AF125304 | Hs.212680 | tumor necrosis factor receptor superfam | 2.2 |
| | 447091 | AW089648 | Hs.157779 | ESTs, Weakly similar to CA17_HUMAN COLLA | 2.2 |
| | 422017 | NM_003877 | Hs.110776 | STAT induced STAT inhibitor-2 | 2.2 |
| | 426728 | NM_007118 | Hs.171957 | triple functional domain (PTPRF interact | 2.2 |
| 15 | 438726 | AB033103 | Hs.6385 | KIAA1277 protein | 2.2 |
| | 453315 | BE544203 | Hs.24831 | ESTs | 2.2 |
| | 423244 | AL039379 | Hs.209602 | ESTs, Weakly similar to ubiquitous TPR m | 2.2 |
| | 433610 | AA806822 | Hs.112547 | ESTs | 2.2 |
| 20 | 429451 | BE409861 | Hs.202833 | heme oxygenase (decycling) 1 | 2.2 |
| | 417980 | R32235 | | gb:yh67f08.r1 Soares placenta Nb2HP Homo | 2.2 |
| | 406347 | | | | 2.2 |
| | 414406 | BE297904 | | gb:601177814F1 NIH_MGC_17 Homo sapiens c | 2.2 |
| | 401827 | | | | 2.2 |
| 25 | 446913 | AA430650 | Hs.16529 | transmembrane 4 superfamily member (tetr | 2.2 |
| | 452294 | AI871925 | Hs.117895 | ESTs, Moderately similar to A47582 B-cel | 2.2 |
| | 404084 | | | | 2.2 |
| | 456786 | AK002084 | Hs.132851 | hypothetical protein FLJ11222 | 2.2 |
| | 435031 | AI632091 | Hs.116877 | ESTs | 2.2 |
| 30 | 442609 | AL020996 | Hs.8518 | selenoprotein N | 2.1 |
| | 439732 | AW629604 | Hs.167641 | hypothetical protein from EUROIMAGE 1703 | 2.1 |
| | 421506 | BE302796 | Hs.105097 | thymidine kinase 1, soluble | 2.1 |
| | 439253 | AF086064 | Hs.332252 | ESTs | 2.1 |
| | 409669 | AW177551 | Hs.220255 | hypothetical protein MGC13098 | 2.1 |
| 35 | 429574 | BE268321 | Hs.208912 | hypothetical protein MGC861 | 2.1 |
| | 437470 | AL390147 | Hs.134742 | hypothetical protein DKFZp547D065 | 2.1 |
| | 408945 | AW015089 | Hs.4964 | DKFZP586J1624 protein | 2.1 |
| | 447687 | AI627947 | Hs.150186 | hypothetical protein DKFZp566K1946 | 2.1 |
| | 459584 | AI910884 | Hs.207898 | ESTs | 2.1 |
| 40 | 439130 | AA306090 | Hs.124707 | ESTs | 2.1 |
| | 428180 | AI129767 | Hs.182874 | guanine nucleotide binding protein (G pr | 2.1 |
| | 442028 | AI239437 | Hs.48945 | ESTs | 2.1 |
| | 430958 | AW972830 | | gb:EST384925 MAGE resequences, MAGL Homo | 2.1 |
| | 443609 | AV650231 | Hs.282941 | ESTs, Highly similar to A Chain A, Human | 2.1 |
| 45 | 417164 | AA338283 | Hs.81361 | heterogeneous nuclear ribonucleoprotein | 2.1 |
| | 444534 | AW271626 | Hs.42294 | ESTs | 2.1 |
| | 438391 | AI262248 | Hs.25027 | ESTs | 2.1 |
| | 442003 | AW297497 | Hs.201891 | ESTs | 2.1 |
| | 456278 | BE300369 | Hs.289038 | hypothetical protein MGC4126 | 2.1 |
| 50 | 416976 | BE243985 | Hs.80680 | major vault protein | 2.1 |
| | 417810 | D28419 | Hs.82609 | hydroxymethylbilane synthase | 2.1 |
| | 445242 | BE156478 | Hs.21108 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.1 |
| | 452712 | AW838616 | | gb:RCS-LT0054-140200-013-D01 LT0054 Homo | 2.1 |
| | 434926 | BE543269 | Hs.50252 | mitochondrial ribosomal protein L32 | 2.1 |
| 55 | 421564 | AB007864 | Hs.105850 | KIAA0404 protein | 2.1 |
| | 424927 | AW973666 | Hs.153850 | hypothetical protein C321D2.4 | 2.1 |
| | 432742 | AA564453 | Hs.162339 | ESTs | 2.1 |
| | 435958 | H98180 | Hs.117975 | ESTs | 2.1 |
| | 421531 | AA713505 | Hs.291769 | ESTs | 2.1 |
| 60 | 410431 | BE261320 | Hs.158196 | transcriptional adaptor 3 (ADA3, yeast h | 2.1 |
| | 420503 | AI570943 | Hs.337546 | ESTs | 2.1 |
| | 448127 | AI478416 | Hs.282883 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.1 |
| | 452897 | BE066058 | Hs.269233 | ESTs, Moderately similar to I78885 serin | 2.1 |
| | 447112 | H17800 | Hs.7154 | ESTs | 2.1 |
| 65 | 406577 | | | | 2.1 |
| | 437162 | AW005505 | Hs.5464 | thyroid hormone receptor coactivating pr | 2.1 |
| | 451460 | AI797550 | Hs.209652 | ESTs | 2.1 |
| | 447402 | H54520 | Hs.18490 | hypothetical protein FLJ20452 | 2.1 |
| | 435828 | AA700705 | Hs.13852 | ESTs | 2.1 |
| 70 | 436396 | AI683487 | Hs.152213 | wingless-type MMTV integration site fami | 2.1 |
| | 420582 | BE047878 | Hs.99093 | Homo sapiens chromosome 19, cosmid R2837 | 2.1 |
| | 450200 | AA722012 | Hs.255757 | ESTs, Weakly similar to AT2A_HUMAN POTEN | 2.1 |
| | 415586 | Z45481 | | gb:HSC2QE041 normalized infant brain cDN | 2.1 |
| | 452620 | AA436504 | Hs.119286 | ESTs | 2.1 |
| 75 | 457066 | BE244613 | Hs.158272 | ESTs, Weakly similar to CA13 MOUSE COLLA | 2.1 |
| | 435472 | AW972330 | Hs.283022 | triggering receptor expressed on myeloid | 2.1 |
| | 431741 | AA514783 | Hs.191701 | ESTs | 2.1 |
| | 446840 | AW294828 | Hs.209203 | ESTs | 2.1 |
| | 440818 | AI147060 | Hs.146726 | ESTs | 2.1 |
| 80 | 410174 | AA306007 | Hs.59461 | DKFZP434C245 protein | 2.1 |
| | 400822 | | | | 2.1 |
| | 412760 | AW379030 | Hs.41324 | ESTs | 2.1 |
| | 410653 | BE383768 | Hs.65238 | 95 kDa retinoblastoma protein binding pr | 2.1 |
| | 426925 | NM_001196 | Hs.315689 | Homo sapiens cDNA: FLJ22373 fs, clone H | 2.1 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 424242 | AA337476 | Hs.293984 | hypothetical protein MGC13102 | 2.1 |
| | 452560 | BE077084 | Hs.336432 | ESTs | 2.1 |
| | 456437 | AJ924228 | Hs.115185 | ESTs, Moderately similar to PC4259 ferri | 2.1 |
| 5 | 458922 | BE501831 | Hs.282053 | ESTs | 2.1 |
| | 439231 | AW581935 | Hs.141480 | Homo sapiens mRNA; cDNA DKFZp434N079 (fr | 2.1 |
| | 419488 | AA316241 | Hs.90691 | nucleophosmin/nucleoplasm 3 | 2.1 |
| | 411829 | AW865749 | | gb:QV3-SN0021-100500-185-c03 SN0021 Homo | 2.1 |
| | 457192 | AL135682 | Hs.22452 | Homo sapiens mRNA for KIAA1737 protein, | 2.1 |
| 10 | 422128 | AW881145 | | gb:QV0-OT0033-010400-182-a07 OT0033 Homo | 2.1 |
| | 452571 | W31518 | Hs.34665 | ESTs | 2.1 |
| | 423699 | H41850 | Hs.131846 | PCAF associated factor 65 alpha | 2.1 |
| | 406610 | | | | 2.1 |
| | 453638 | AW814996 | | gb:MR1-ST0206-170400-024-h09 ST0206 Homo | 2.1 |
| | 418856 | AA362858 | | gb:EST72900 Ovary II Homo sapiens cDNA 5 | 2.1 |
| 15 | 437623 | D63880 | Hs.5719 | chromosome condensation-related SMC-asso | 2.1 |
| | 410908 | AA121686 | Hs.10592 | ESTs | 2.1 |
| | 420221 | N25991 | Hs.43725 | ESTs | 2.1 |
| | 424739 | AA346108 | Hs.221610 | ESTs | 2.1 |
| 20 | 425398 | AL049689 | Hs.156369 | hypothetical protein similar to tenascin | 2.1 |
| | 424901 | Z11933 | Hs.182505 | POU domain, class 3, transcription facto | 2.1 |
| | 411096 | U80034 | Hs.68583 | mitochondrial intermediate peptidase | 2.1 |
| | 415635 | F13168 | | gb:HSC3JF101 normalized infant brain cDN | 2.1 |
| | 418181 | U37012 | Hs.83727 | cleavage and polyadenylation specific fa | 2.1 |
| 25 | 407103 | AA424881 | Hs.256301 | hypothetical protein MGC13170 | 2.1 |
| | 454389 | AW752571 | | gb:IL3-CT0213-170100-055-F02 CT0213 Homo | 2.1 |
| | 400021 | | | | 2.1 |
| | 439228 | N51700 | | gb:yy72d01.s1 Soares_multiple_sclerosis_ | 2.1 |
| | 456505 | AA504595 | Hs.111418 | ESTs | 2.1 |
| 30 | 405258 | | | | 2.1 |
| | 444645 | AI184564 | Hs.101654 | ESTs | 2.1 |
| | 430246 | AI269069 | Hs.109268 | hypothetical protein FLJ12552 | 2.1 |
| | 458687 | AW024815 | Hs.170088 | GLUT4 enhancer factor | 2.1 |
| | 403857 | | | | 2.1 |
| 35 | 400258 | | | | 2.1 |
| | 422221 | AA306649 | Hs.169370 | FYN oncogene related to SRC, FGR, YES | 2.1 |
| | 441054 | AA913591 | Hs.126480 | ESTs | 2.1 |
| | 452700 | AI859390 | Hs.288940 | five-span transmembrane protein M83 | 2.1 |
| | 454606 | AW809752 | | gb:MR4-ST0124-181299-020-b06 ST0124 Homo | 2.1 |
| 40 | 448954 | AB014564 | Hs.22616 | KIAA0664 protein | 2.1 |
| | 443148 | AI034357 | Hs.211194 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 2.1 |
| | 453486 | AL039201 | Hs.173554 | ubiquinol-cytochrome c reductase core pr | 2.1 |
| | 437695 | AA769202 | Hs.192142 | ESTs | 2.1 |
| | 425449 | XS2056 | Hs.157441 | spleen focus forming virus (SFFV) provir | 2.1 |
| 45 | 447270 | AC002551 | Hs.331 | general transcription factor IIIC, polyp | 2.1 |
| | 435677 | AA694142 | Hs.293726 | ESTs, Weakly similar to TSGA RAT TESTIS | 2.1 |
| | 436382 | AW977063 | Hs.250181 | ESTs | 2.1 |
| | 435837 | AI689210 | Hs.187276 | Homo sapiens cDNA FLJ11431 fis, clone HE | 2.1 |
| | 458287 | AA987556 | Hs.12867 | ESTs | 2.1 |
| 50 | 423794 | BE551781 | Hs.231895 | ESTs | 2.1 |
| | 408049 | AW076098 | Hs.74316 | desmoplakin (DPI, DPII) | 2.1 |
| | 402721 | | | | 2.1 |
| | 451999 | AW176401 | Hs.27424 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypep | 2.1 |
| | 417541 | AI992191 | Hs.180040 | hypothetical protein FLJ22439 | 2.1 |
| 55 | 414857 | AW402389 | Hs.920 | modulator recognition factor I | 2.1 |
| | 435760 | AF231922 | Hs.213004 | chromosome 21 open reading frame 62 | 2.1 |
| | 428086 | AL110193 | Hs.224137 | hypothetical protein | 2.1 |
| | 447853 | AI434204 | Hs.164285 | ESTs, Weakly similar to AFG1_YEAST AFG1 | 2.1 |
| | 419034 | NM_002110 | Hs.89555 | hemopoietic cell kinase | 2.1 |
| 60 | 431019 | NM_005249 | Hs.2714 | forkhead box G1B | 2.1 |
| | 421064 | AI245432 | Hs.101382 | tumor necrosis factor, alpha-induced pro | 2.1 |
| | 416435 | AI431301 | Hs.179703 | KIAA0129 gene product | 2.1 |
| | 437014 | AA808757 | Hs.222531 | ESTs, Weakly similar to S59501 interfero | 2.1 |
| | 459369 | T83080 | | gb:yd40e03.r1 Soares fetal liver spleen | 2.1 |
| 65 | 402239 | | | | 2.1 |
| | 412280 | AW205116 | Hs.272814 | hypothetical protein DKFZp434E1723 | 2.1 |
| | 426012 | AA367507 | Hs.75874 | pregnancy-associated plasma protein A | 2.1 |
| | 438885 | AI886558 | Hs.184987 | ESTs | 2.1 |
| | 426076 | AW962714 | | gb:EST374787 MAGE resequences, MAGG Homo | 2.1 |
| 70 | 404561 | | | | 2.1 |
| | 442932 | AA457211 | Hs.8858 | bromodomain adjacent to zinc finger doma | 2.1 |
| | 408175 | W29089 | Hs.19066 | hypothetical protein DKFZp667O2416 | 2.1 |
| | 423867 | AA331886 | | gb:EST35757 Embryo, 8 week I Homo sapien | 2.1 |
| | 458604 | W37944 | Hs.4007 | Sarcolemmal-associated protein | 2.1 |
| 75 | 409650 | T08490 | Hs.288969 | HSCARG protein | 2.1 |
| | 401729 | | | | 2.1 |
| | 433675 | AW977653 | Hs.75319 | ribonucleotide reductase M2 polypeptide | 2.1 |
| | 456741 | W37608 | Hs.184492 | ESTs | 2.1 |
| | 417037 | BE083936 | Hs.80976 | antigen identified by monoclonal antibod | 2.1 |
| 80 | 415079 | R43179 | Hs.22895 | hypothetical protein FLJ23548 | 2.1 |
| | 439262 | AA832333 | Hs.333045 | ESTs | 2.1 |
| | 403108 | | | | 2.1 |
| | 436718 | AW015227 | Hs.289053 | hypothetical protein FLJ14733 | 2.1 |
| | 440696 | AI762757 | Hs.187660 | putative Rab5 GDP/GTP exchange factor ho | 2.1 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 409745 | AA077391 | | gb:7B14E12 Chromosome 7 Fetal Brain cDNA | 2.1 |
| | 453485 | BE620712 | Hs.33026 | hypothetical protein PP2447 | 2.1 |
| | 418177 | N44967 | Hs.5663 | ESTs | 2.1 |
| 5 | 457292 | AI921270 | Hs.334882 | hypothetical protein FLJ14251 | 2.1 |
| | 454434 | AA083558 | Hs.261286 | ESTs | 2.1 |
| | 406085 | | | | 2.1 |
| | 424441 | X14850 | Hs.147097 | H2A histone family, member X | 2.1 |
| | 422726 | U11690 | Hs.1572 | faciogenital dysplasia (Aarskog-Scott sy | 2.1 |
| 10 | 424576 | BE154142 | Hs.96833 | ESTs | 2.1 |
| | 423660 | AL045228 | Hs.130831 | Homo sapiens mRNA; cDNA DKFZp434L137 (fr | 2.1 |
| | 403509 | AF231919 | Hs.18759 | KIAA0539 gene product | 2.1 |
| | 441940 | AW298115 | Hs.128152 | ESTs | 2.1 |
| | 439190 | AW978693 | Hs.293811 | ESTs | 2.1 |
| 15 | 417791 | AW965339 | Hs.111471 | ESTs | 2.1 |
| | 423701 | AA329856 | Hs.143022 | ESTs | 2.1 |
| | 427239 | BE270447 | Hs.174070 | ubiquitin carrier protein | 2.1 |
| | 459642 | BE243103 | | gb:TCAAP2E0949 Pediatric acute myelogeno | 2.1 |
| | 450385 | AI631024 | Hs.24948 | synuclein, alpha interacting protein (sy | 2.1 |
| 20 | 425159 | NM_004341 | Hs.154868 | carbamoyl-phosphate synthetase 2, aspart | 2.1 |
| | 425591 | AW294734 | Hs.279727 | Homo sapiens cDNA FLJ14035 fis, clone HE | 2.1 |
| | 445101 | T75202 | Hs.12314 | Homo sapiens mRNA; cDNA DKFZp586C1019 (f | 2.1 |
| | 412811 | H06382 | Hs.21400 | ESTs | 2.1 |
| | 426369 | AF134157 | Hs.169487 | Kreisler (mouse) maf-related leucine zip | 2.1 |
| 25 | 435924 | AW029203 | Hs.191952 | ESTs | 2.1 |
| | 418388 | R72332 | Hs.29258 | Homo sapiens cDNA FLJ11364 fis, clone HE | 2.1 |
| | 452235 | AL039743 | Hs.28514 | testes development-related NYD-SP21 | 2.1 |
| | 452313 | Y00486 | Hs.28914 | adenine phosphoribosyltransferase | 2.1 |
| | 450704 | H85157 | Hs.40696 | ESTs | 2.1 |
| 30 | 427539 | AA405205 | Hs.97960 | ESTs, Weakly similar to T51146 ring-box | 2.1 |
| | 402028 | | | | 2.1 |
| | 405362 | | | | 2.1 |
| | 414718 | H95348 | Hs.107987 | ESTs | 2.1 |
| | 433424 | R68252 | Hs.163566 | ESTs | 2.1 |
| 35 | 444875 | AI200759 | Hs.44737 | ESTs | 2.0 |
| | 449523 | NM_000579 | Hs.54443 | chemokine (C-C motif) receptor 5 | 2.0 |
| | 456072 | H54381 | | gb:yq89a03.s1 Soares fetal liver spleen | 2.0 |
| | 436331 | AI239495 | Hs.120189 | ESTs | 2.0 |
| | 448418 | Z43704 | Hs.21192 | Homo sapiens clone 25155 mRNA sequence | 2.0 |
| 40 | 447250 | AI878909 | Hs.17883 | protein phosphatase 1G (formerly 2C), ma | 2.0 |
| | 448192 | R43915 | Hs.4958 | ESTs | 2.0 |
| | 448966 | AW372914 | Hs.86149 | phosphoinositol 3-phosphate-binding prot | 2.0 |
| | 408605 | AF025374 | Hs.45465 | T-cell, immune regulator 1 | 2.0 |
| | 410790 | AW803357 | | gb:IL2-UM0079-090300-050-A08 UM0079 Homo | 2.0 |
| 45 | 436872 | X15624 | | gb:Human H1 RNA | 2.0 |
| | 432238 | AL133057 | Hs.274135 | Homo sapiens mRNA; cDNA DKFZp434K1815 (f | 2.0 |
| | 446307 | T50083 | Hs.9094 | ESTs | 2.0 |
| | 436588 | AA759233 | Hs.126506 | ESTs | 2.0 |
| | 452487 | AW207659 | Hs.6630 | Homo sapiens cDNA FLJ13329 fis, clone OV | 2.0 |
| 50 | 430420 | AW140027 | Hs.26373 | Homo sapiens cDNA: FLJ23449 fis, clone H | 2.0 |
| | 432036 | AF224266 | Hs.272373 | interleukin 20 | 2.0 |
| | 414460 | L00727 | Hs.898 | dystrophin myotonic-protein kinase | 2.0 |
| | 433507 | AI817336 | Hs.191791 | ESTs | 2.0 |
| | 427964 | AA418082 | Hs.98286 | ESTs, Weakly similar to T20655 hypotheti | 2.0 |
| 55 | 443108 | W86975 | Hs.203707 | ESTs | 2.0 |
| | 434504 | AI887341 | Hs.121590 | hypothetical protein FLJ12827 | 2.0 |
| | 454310 | AW818390 | Hs.175613 | homolog of Xenopus Caspin | 2.0 |
| | 443566 | AI290284 | Hs.159872 | ESTs | 2.0 |
| | 449722 | BE280074 | Hs.23960 | cyclin B1 | 2.0 |
| 60 | 452682 | AA456193 | Hs.9071 | progesterone membrane binding protein | 2.0 |
| | 412362 | AW945484 | Hs.184252 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 2.0 |
| | 429341 | X73874 | Hs.2393 | phosphorylase kinase, alpha 1 (muscle) | 2.0 |
| | 435863 | AF255346 | Hs.62919 | Jun dimerization protein p21SNFT | 2.0 |
| | 400774 | R58624 | Hs.2186 | eukaryotic translation elongation factor | 2.0 |
| 65 | 453944 | AW975369 | Hs.292570 | Homo sapiens, clone IMAGE:3502107, mRNA, | 2.0 |
| | 419227 | BE537383 | Hs.89739 | cholinergic receptor, nicotinic, beta po | 2.0 |
| | 448529 | T26460 | Hs.22550 | ESTs | 2.0 |
| | 443206 | AB011420 | Hs.9075 | serine/threonine kinase 17a (apoptosis-i | 2.0 |
| | 439360 | AA448488 | Hs.336629 | ribosomal protein L44 | 2.0 |
| 70 | 436660 | AI658870 | Hs.184513 | ESTs | 2.0 |
| | 449030 | AI365582 | Hs.57100 | Homo sapiens mRNA for FLJ00016 protein, | 2.0 |
| | 411048 | AK001742 | Hs.67991 | hypothetical protein DKFZp434G0522 | 2.0 |
| | 406624 | AF052762 | | gb:Homo sapiens clone csneg8-1 immunoglo | 2.0 |
| | 450666 | T99968 | Hs.18799 | ESTs, Weakly similar to I38022 hypotheti | 2.0 |
| 75 | 446143 | BE245342 | Hs.306079 | sec61 homolog | 2.0 |
| | 437698 | R61837 | Hs.7990 | ESTs, Moderately similar to I84505 calci | 2.0 |
| | 426607 | AA382330 | Hs.124223 | ESTs | 2.0 |
| | 449246 | AW411209 | Hs.23363 | hypothetical protein FLJ10983 | 2.0 |
| | 422564 | AI148006 | Hs.222120 | ESTs | 2.0 |
| 80 | 432682 | AI376400 | Hs.159588 | ESTs | 2.0 |
| | 422140 | BE295918 | Hs.112193 | mutS (E. coli) homolog 5 | 2.0 |
| | 408215 | BE614290 | Hs.43812 | syntaxin 10 | 2.0 |
| | 417129 | AI381800 | Hs.300684 | calcitonin gene-related peptide-receptor | 2.0 |
| | 442772 | AW503680 | Hs.5957 | Homo sapiens clone 24416 mRNA sequence | 2.0 |

| | | | | | |
|----|-------------|---------------------------------------|---|--|-----|
| 5 | 434928 | AW015595 | Hs.4267 | Homo sapiens clones 24714 and 24715 mRNA | 2.0 |
| | 411380 | AW841619 | | gb:RC1-CN0017-120200-012-b09 CN0017 Homo | 2.0 |
| | 430603 | AA148164 | Hs.247280 | HBV associated factor | 2.0 |
| | 425905 | AB032959 | Hs.318584 | novel C3HC4 type Zinc finger (ring finger) | 2.0 |
| | 401125 | | | | 2.0 |
| 10 | 412939 | AW411491 | Hs.2186 | eukaryotic translation elongation factor | 2.0 |
| | 448740 | BE250632 | Hs.8026 | sestrin 2 | 2.0 |
| | 454390 | AB020713 | Hs.56966 | KIAA0906 protein | 2.0 |
| | 415012 | NM_004383 | Hs.77793 | c-src tyrosine kinase | 2.0 |
| | 410407 | X66839 | Hs.63287 | carbonic anhydrase IX | 2.0 |
| 15 | 403478 | | | | 2.0 |
| | 456485 | AI393037 | Hs.97871 | Homo sapiens, clone IMAGE:3845253, mRNA, | 2.0 |
| | 430294 | AI538226 | Hs.32976 | guanine nucleotide binding protein 4 | 2.0 |
| | 411669 | BE612676 | Hs.303116 | stromal cell-derived factor 2-like 1 | 2.0 |
| | 451944 | AW445218 | Hs.210876 | ESTs | 2.0 |
| 20 | 436395 | AJ227900 | | gb:Homo sapiens partial mRNA; ID EE2-16B | 2.0 |
| | 456457 | AA252905 | Hs.194477 | E3 ubiquitin ligase SMURF2 | 2.0 |
| | 449123 | D50920 | Hs.23106 | KIAA0130 gene product | 2.0 |
| | 409214 | AW405967 | Hs.333388 | Homo sapiens, clone IMAGE:3957135, mRNA, | 2.0 |
| | 437619 | AW351491 | Hs.334853 | hypothetical protein FLJ123544 | 2.0 |
| 25 | 453348 | BE272318 | Hs.8595 | hypothetical protein FLJ12438 | 2.0 |
| | 424382 | AA351898 | Hs.23539 | ESTs | 2.0 |
| | 447079 | AA280057 | Hs.105280 | ESTs, Weakly similar to dJ963K23.2 [Hsa | 2.0 |
| | 449501 | AI652924 | Hs.231942 | ESTs | 2.0 |
| | 422893 | X98411 | Hs.121555 | myosin IF | 2.0 |
| 30 | 412125 | Y17114 | Hs.73393 | eyes absent (Drosophila) homolog 4 | 2.0 |
| | 434845 | BE267057 | Hs.325321 | hypothetical protein R32184_1 | 2.0 |
| | 410422 | AL042014 | Hs.334698 | Homo sapiens, clone MGC:15203, mRNA, com | 2.0 |
| | 430255 | AK000703 | Hs.323822 | Homo sapiens mRNA for KIAA1551 protein, | 2.0 |
| | 451656 | BE327088 | Hs.212752 | ESTs | 2.0 |
| 35 | 442068 | BE312873 | Hs.314932 | ESTs | 2.0 |
| | 446846 | AW197626 | Hs.271901 | ESTs, Moderately similar to S08686 finger | 2.0 |
| | 442690 | AI014727 | Hs.160047 | ESTs, Weakly similar to B28096 line-1 pr | 2.0 |
| | 454277 | AW295069 | Hs.31743 | ESTs, Weakly similar to Z157_HUMAN ZINC | 2.0 |
| | 426910 | AA470023 | Hs.190089 | ESTs, Moderately similar to ALU1_HUMAN A | 2.0 |
| 40 | 402798 | | | | 2.0 |
| | 404554 | | | | 2.0 |
| | TABLE 9B: | | | | |
| | Pkey: | Unique Eos probeset identifier number | | | |
| | CAT number: | Gene cluster number | | | |
| | Accession: | Genbank accession numbers | | | |
| 45 | Pkey | CAT Number | Accession | | |
| | 407909 | 1025254_1 | AW103986 BE156395 BE156391 BE156190 BE156184 BE156388 BE156394 | | |
| | 408432 | 1058667_1 | AW195262 R27868 AW811262 | | |
| | 409193 | 110747_1 | AA131483 AA065156 AA076448 | | |
| | 409745 | 115237_1 | AA077391 AI347618 AI361453 AI088754 AW207491 AW960912 AA921874 AA286833 AA150722 BE152353 AW188822 BE152450 | | |
| 50 | 410447 | 1203929_1 | AW816134 BE063456 AW748795 BE150839 | | |
| | 410790 | 1221131_1 | AW803357 AW803423 AW812233 R06814 | | |
| | 411256 | 1236790_1 | AW834039 AW834040 AW834047 AW845410 BE003128 AW852479 | | |
| | 411380 | 1242343_1 | AW841619 AW851958 AW851851 AW851985 | | |
| | 411632 | 1252361_1 | AW854829 AW854805 AW854841 AW854825 AW854822 AW854830 AW854835 AW854826 | | |
| 55 | 411658 | 1252987_1 | AW855598 AW855608 BE148763 BE148764 AW855645 AW855615 AW855596 AW855610 AW855601 AW855605 | | |
| | 411829 | 1260309_1 | AW865749 BE179419 BE179492 | | |
| | 412225 | 1284108_1 | AW902042 N77591 | | |
| | 412370 | 1291952_1 | AW946614 AW946622 AW946663 AW946667 AW946615 AW946619 | | |
| | 412391 | 1292625_1 | AW947710 AW947698 AW947697 AW947713 | | |
| 60 | 413257 | 1355963_1 | BE075035 BE074999 BE075006 BE075005 BE075032 BE075008 BE075037 | | |
| | 413604 | 1379715_1 | RS1767 BE152515 Z44834 H23397 | | |
| | 414406 | 1443333_1 | BE297904 BE294312 | | |
| | 414550 | 1460990_1 | BE379808 | | |
| | 415346 | 1534581_1 | Z43108 F06295 R13085 | | |
| 65 | 415406 | 1536026_1 | T26510 F07926 R53367 | | |
| | 415586 | 1540116_1 | Z45481 F12393 T74437 | | |
| | 415635 | 1540853_1 | F13168 R21289 T77628 | | |
| | 416871 | 1626761_1 | H98716 N90792 N24283 | | |
| | 416913 | 163001_1 | AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499 | | |
| 70 | 417980 | 1712954_1 | R32235 R32247 R32219 | | |
| | 418333 | 173_2 | W92113 AA702794 BE044316 W91984 AA679375 T94184 AA679335 BE503126 AW502118 BE467367 AA584550 AW139964 R93353 AW088477 | | |
| | | | AI887846 AW502624 W81697 W81696 AA447817 AA447667 F13631 AW268271 AA055366 AW629027 AA677404 AA831618 AI124782 AA889402 | | |
| | | | AA765804 AA765530 AA055698 AA594019 AI267358 AA456946 R93354 AF264624 AW668618 AA601493 | | |
| | | | AA362858 AW863761 AA229428 | | |
| 75 | 418856 | 179649_1 | AA504571 AA235243 AA411737 AW969068 AA406543 | | |
| | 419217 | 182954_1 | U70073 | | |
| | 419225 | 1830274_1 | AA689591 AW974261 AA236240 AI077451 AA631399 AW974262 | | |
| | 419311 | 183793_1 | BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280 | | |
| | 420352 | 192979_1 | AW881145 AA490718 M85637 AA304575 T06067 AA331991 | | |
| 80 | 422128 | 211994_1 | N34524 AA305071 AW954803 AA502335 AI433430 AI203597 AW026670 AW265323 AW850787 AA317554 AW993643 AW835572 AW385512 | | |
| | 422155 | 212379_1 | AI334966 W32951 H62656 H53902 R88904 AW835732 | | |
| | | | H80977 BE147695 AA305496 AW962366 AA436754 | | |
| | 422176 | 212714_1 | AA828125 AA834883 AA330555 | | |
| | 423756 | 231725_1 | AA331886 AW962659 AW962655 T89441 | | |
| | 423867 | 232732_1 | | | |

| | | | |
|----|--------|-----------|--|
| 5 | 425189 | 247825_1 | H16622 R17322 AA351959 |
| | 425517 | 252729_1 | AF121179 BE162736 AA358827 |
| | 426076 | 260504_1 | AW962714 AA369277 AA369278 |
| | 426413 | 266650_1 | AA377823 AW954494 A1022688 |
| | 426503 | 268283_1 | AA380153 AA380233 AW963529 |
| | 426531 | 268760_1 | AA381071 AA381084 AA380862 |
| | 429875 | 310034_1 | A1091815 AA460162 AA460761 |
| | 430968 | 326269_1 | AW972830 AA527647 AA489820 AA570362 |
| 10 | 432088 | 341195_1 | AA525454 H74039 R89502 T77379 |
| | 433532 | 368950_1 | AW975367 AA598607 AA742735 |
| | 434559 | 38889_1 | AF147315 AW173079 T53029 |
| | 435065 | 399329_1 | BE064391 BE064395 AA663613 N99644 |
| | 436190 | 41555_1 | AK001059 AA633055 |
| 15 | 436395 | 41905_1 | AJ227900 A1094933 AW051119 F00947 |
| | 436532 | 421802_1 | AA721522 AW975443 T93070 |
| | 436722 | 425758_1 | AW975977 AA729469 AA747132 |
| | 436872 | 42851_1 | X15624 |
| | 437034 | 431713_1 | AA742643 AA808575 AW976668 |
| 20 | 439086 | 46852_1 | AF085947 H70981 H78989 |
| | 439228 | 47001_1 | N51700 AF086051 N51792 |
| | 439518 | 47334_1 | W76326 AF086341 W72300 |
| | 439546 | 47360_1 | AF088056 W76297 W72448 |
| | 439566 | 47387_1 | AF086387 W77884 W72711 |
| 25 | 439710 | 47550_1 | AF086543 W96291 W96225 |
| | 443657 | 576685_1 | R14973 R14967 A1081006 |
| | 444168 | 593829_1 | AW379879 A1126285 H12014 |
| | 444386 | 604004_1 | BE065183 A1144398 BE065367 |
| | 451129 | 859870_1 | BE072881 BE072946 A1762181 |
| 30 | 452712 | 928309_1 | AW838616 AW838660 BE144343 A1914520 AW888910 BE184854 BE184784 |
| | 453446 | 967533_1 | BE299996 BE297115 BE270415 BE295214 BE296526 |
| | 453638 | 975649_1 | AW814996 AL047199 AW850979 |
| | 453746 | 979731_1 | AL120611 BE006190 BE006189 |
| | 454377 | 114761_1 | AA076811 AW814764 |
| 35 | 454389 | 115682_1 | AW752571 AW847602 AA077979 |
| | 454606 | 1226149_2 | AW809752 AW810271 AW809944 AW810319 AW810215 AW810368 AW810167 |
| | 454630 | 1227352_1 | BE142075 BE142148 BE142189 AW816249 BE142147 BE142002 BE142406 BE142094 BE142020 BE142074 BE142347 BE142000 BE142375 |
| | | | AW811189 BE142133 |
| | 454631 | 1227443_1 | AW811324 AW811325 AW811326 AW811333 AW811329 AW811328 AW811332 AW811339 AW811335 |
| 40 | 454679 | 1228929_1 | AW813110 AW813113 |
| | 454967 | 1247021_1 | AW848276 AW848416 AW847945 AW847947 AW848063 AW848113 |
| | 455023 | 1249188_1 | AW850907 AW850901 AW850877 |
| | 455302 | 1276542_1 | AW997641 AW891777 |
| | 455470 | 1292849_1 | AW947992 AW947967 AW947950 AW947957 AW947953 AW947973 AW947966 AW947971 AW947947 AW947970 AW947995 AW947979 AW947952 |
| 45 | 455514 | 1321649_1 | AW947956 |
| | 455530 | 1322298_1 | AW983871 BE090302 AW983867 AW983845 AW983860 AW983853 AW983852 |
| | 455584 | 1334741_1 | AW984744 AW984759 |
| | 455778 | 1364506_1 | BE007420 BE007419 BE007421 BE007422 |
| | 455908 | 1382301_1 | BE088746 BE088802 BE088755 BE088876 BE088947 BE088881 BE088952 |
| 50 | 456072 | 1470256_1 | BE156306 BE156188 BE156298 BE156377 BE156374 |
| | 456094 | 1504780_1 | H54381 H54463 BE393262 |
| | 457374 | 328758_1 | H95091 C01228 |
| | 457578 | 359618_1 | AA493662 AW897396 BE154814 |
| 55 | 457730 | 393905_1 | AA578027 |
| | | | AW753613 AW753857 BE150374 BE150693 BE150394 AA808851 AA650159 AA654653 BE150419 |

TABLE 9C:

| | |
|--------------|---|
| Pkey: | Unique number corresponding to an Eos probeset |
| Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. |
| Strand: | Indicates DNA strand from which exons were predicted. |
| NI_position: | Indicates nucleotide positions of predicted exons. |

| | | | | |
|----|--------|---------|--------|-------------------------------------|
| 65 | Pkey | Ref | Strand | NI_position |
| | 400822 | 7465000 | Plus | 186223-186402,186878-187275 |
| | 400859 | 9757499 | Minus | 91888-92018,98131-98294,99474-99570 |
| | 400917 | 7283186 | Minus | 173258-173631 |
| | 400992 | 8096828 | Plus | 140390-140822 |
| | 401012 | 7230838 | Minus | 736-1137 |
| 70 | 401048 | 7232177 | Plus | 132430-132761 |
| | 401125 | 8570296 | Minus | 126863-126984 |
| | 401324 | 9863791 | Plus | 234057-234174 |
| | 401384 | 6850939 | Minus | 58360-58545 |
| | 401558 | 7139678 | Plus | 103510-104090 |
| 75 | 401626 | 8575943 | Minus | 238100-238432 |
| | 401676 | 9965536 | Plus | 3891-4691 |
| | 401714 | 6715702 | Plus | 96484-96681 |
| | 401729 | 8134856 | Minus | 90651-90878 |
| | 401827 | 2262095 | Plus | 94725-94860,98452-98660 |
| 80 | 401876 | 8099107 | Plus | 95913-96641 |
| | 402028 | 7139781 | Plus | 88749-89237 |
| | 402064 | 8117294 | Plus | 100159-100350,100445-100912 |
| | 402239 | 7690131 | Plus | 38175-38304,42133-42266 |
| | 402408 | 9796239 | Minus | 110326-110491 |

| | | | | |
|----|--------|---------|-------|---|
| 5 | 402424 | 9796344 | Minus | 64925-65073 |
| | 402516 | 9798099 | Minus | 195342-195511 |
| | 402604 | 9909420 | Plus | 20393-20767 |
| | 402627 | 9931216 | Plus | 12136-12272,16487-16628,17654-17798,18494-18621,18933-19089,20669-20790,21134-21298,22866-22973,23686-23820,26626-26895,29279-29469 |
| 10 | 402721 | 8969253 | Minus | 144428-144715 |
| | 402798 | 3355547 | Plus | 23596-23867 |
| | 402856 | 9801288 | Minus | 90119-90411 |
| | 403048 | 4210991 | Plus | 44275-44592,49656-49955 |
| 15 | 403108 | 8980955 | Plus | 93253-93667 |
| | 403142 | 9444521 | Plus | 89286-90131 |
| | 403166 | 9838127 | Minus | 67762-67940,68695-68856,70394-70507 |
| | 403478 | 9958258 | Plus | 116458-116564 |
| 20 | 403680 | 7331517 | Minus | 157184-157415 |
| | 403751 | 7229815 | Minus | 158794-160929 |
| | 403790 | 8084957 | Minus | 87826-87947,89835-90002 |
| | 403797 | 8099896 | Minus | 123065-125008 |
| 25 | 403857 | 7708910 | Minus | 2524-3408 |
| | 403881 | 7710245 | Minus | 107250-107685,108924-109213 |
| | 403961 | 7596976 | Minus | 110393-110603 |
| | 403969 | 8569909 | Plus | 31237-31375,32405-32506 |
| 30 | 404020 | 8655966 | Minus | 174449-174663 |
| | 404054 | 3548785 | Plus | 66713-69175 |
| | 404084 | 9944055 | Plus | 2795-2969 |
| | 404108 | 8247074 | Minus | 63603-64942 |
| 35 | 404170 | 9930793 | Plus | 168836-169248 |
| | 404185 | 4572584 | Minus | 129171-129327 |
| | 404240 | 5002624 | Minus | 116132-116407,116653-116922 |
| | 404295 | 9856663 | Minus | 75747-75947 |
| 40 | 404299 | 5738652 | Minus | 3826-4025 |
| | 404366 | 9964977 | Plus | 96589-96801 |
| | 404554 | 7243881 | Plus | 42637-42839 |
| | 404561 | 9795980 | Minus | 69039-70100 |
| 45 | 404584 | 9857511 | Plus | 138651-139153 |
| | 404589 | 9931665 | Minus | 32824-32985 |
| | 404642 | 9796810 | Plus | 102999-103145 |
| | 404652 | 9796969 | Minus | 108172-108296 |
| 50 | 404721 | 9856648 | Minus | 173763-174294 |
| | 404756 | 7706327 | Plus | 82849-83627 |
| | 404802 | 4581357 | Minus | 30093-30600 |
| | 404984 | 6939882 | Plus | 87221-87505 |
| 55 | 405159 | 9966252 | Plus | 79659-79804 |
| | 405258 | 7329310 | Plus | 129930-130076 |
| | 405288 | 6139075 | Minus | 126268-126436 |
| | 405353 | 2811095 | Plus | 118525-118892 |
| 60 | 405362 | 2337862 | Minus | 105008-105142,105980-106091,140445-140556,142519-142641 |
| | 405558 | 1621110 | Plus | 4502-4644,5983-6083 |
| | 405588 | 5002511 | Plus | 46180-46366 |
| | 405605 | 5836195 | Minus | 117070-117270 |
| 65 | 405701 | 4263751 | Plus | 93243-93364 |
| | 405741 | 9966947 | Minus | 156747-156875,156936-157208 |
| | 405747 | 8469069 | Minus | 153933-154060 |
| | 405771 | 7018349 | Plus | 91191-91254,91510-91589 |
| 70 | 405808 | 9929207 | Plus | 109758-111166 |
| | 405884 | 6758747 | Plus | 62383-62583 |
| | 405915 | 7712162 | Minus | 43717-43859 |
| | 406028 | 8312303 | Minus | 177469-177829 |
| 75 | 406085 | 9123888 | Plus | 18665-18843 |
| | 406169 | 6684220 | Minus | 12620-14251 |
| | 406267 | 7528342 | Minus | 2570-2731 |
| | 406326 | 9212385 | Plus | 84508-84655 |
| 80 | 406347 | 9255981 | Plus | 90900-91091 |
| | 406474 | 9795567 | Plus | 52758-53211 |
| | 406577 | 7711730 | Plus | 11377-11509 |
| | 406610 | 8312226 | Plus | 13096-13334 |

TABLE 10A: ABOUT 582 GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS TISSUES

Table 10A lists about 582 genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 59680 probesets on the Affymetrix/Eos HuD3 GeneChip array such that the ratio of "average" normal CNS to "average" glioblastoma was greater than or equal to 3. The "average" normal CNS level was set to the 75th percentile amongst various normal CNS tissues. The "average" glioblastoma level was set to the 85th percentile amongst various tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Key: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of 75th percentile normal central nervous system tissue to 85th percentile tumor

| Key | ExAccn | UnigeneID | Unigene Title | R1 |
|--------|----------|-----------|--|-------|
| 453655 | AW960427 | Hs.79059 | transforming growth factor, beta recepto | 136.7 |
| 417275 | X63578 | Hs.295449 | parvalbumin | 29.0 |
| 430829 | AW451999 | Hs.194024 | ESTs | 25.7 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 410657 | AF063228 | Hs.65248 | dynein, cytoplasmic, intermediate polype | 22.6 |
| | 419954 | D14720 | Hs.93883 | myelin protein zero (Charcot-Marie-Tooth | 21.2 |
| | 459247 | N46243 | Hs.110373 | ESTs, Highly similar to T42626 secreted | 18.5 |
| 5 | 416133 | NM_001683 | Hs.89512 | ATPase, Ca++ transporting, plasma membra | 15.5 |
| | 416018 | AW138239 | Hs.78977 | proprotein convertase subtilisin/kexin 1 | 15.2 |
| | 417167 | AW206437 | Hs.4290 | ESTs | 14.8 |
| | 433940 | H05129 | Hs.7459 | cyclic AMP-regulated phosphoprotein, 21 | 13.4 |
| | 413324 | V00571 | Hs.75294 | corticotropin releasing hormone | 13.1 |
| 10 | 439830 | AA846666 | Hs.151489 | ESTs, Weakly similar to XE7_HUMAN PROTEI | 12.6 |
| | 408068 | AW148652 | Hs.167398 | ESTs | 12.6 |
| | 412636 | NM_004415 | Hs.74316 | desmoptakin (DPI, DPII) | 12.5 |
| | 429096 | AB011106 | Hs.196012 | KIAA0534 protein | 12.2 |
| | 412638 | AA910199 | Hs.203838 | ESTs | 12.2 |
| 15 | 423690 | AA329648 | Hs.23804 | ESTs, Weakly similar to PN0099 son3 prot | 12.1 |
| | 456844 | AI264155 | Hs.152981 | ODP-diacylglycerol synthase (phosphatida | 11.9 |
| | 418318 | U47732 | Hs.84072 | transmembrane 4 superfamily member 3 | 10.9 |
| | 442593 | R39804 | Hs.31961 | ESTs | 10.8 |
| | 446353 | AI290919 | Hs.153661 | ESTs | 10.4 |
| 20 | 420290 | AW977318 | Hs.194480 | ESTs | 10.3 |
| | 414220 | BE298094 | | gb:601118231F1 NIH_MGC_17 Homo sapiens c | 10.3 |
| | 414290 | AI568801 | Hs.71721 | ESTs | 10.2 |
| | 426365 | AA376667 | Hs.10283 | RNA binding motif protein 88 | 10.0 |
| | 414937 | R38698 | Hs.12382 | ESTs | 10.0 |
| 25 | 419643 | F06066 | Hs.91791 | chromosome 11 open reading frame 25 | 9.5 |
| | 407173 | T64349 | | gb:yc10d08.s1 Stratagene lung (937210) H | 9.5 |
| | 412454 | R55745 | Hs.167330 | ESTs | 9.5 |
| | 439366 | AF100143 | Hs.6540 | fibroblast growth factor 13 | 9.4 |
| | 415315 | F12240 | Hs.250655 | prothymosin, alpha (gene sequence 28) | 9.3 |
| 30 | 441790 | AW294909 | Hs.132208 | ESTs | 9.2 |
| | 448117 | H49129 | Hs.172982 | ESTs | 9.1 |
| | 400661 | | | | 9.0 |
| | 433558 | AA833757 | Hs.201769 | ESTs, Weakly similar to T24435 hypotheti | 9.0 |
| | 412453 | R20205 | Hs.167330 | ESTs | 9.0 |
| 35 | 408920 | AL120071 | Hs.48998 | fibronectin leucine rich transmembrane p | 8.9 |
| | 409031 | AA376836 | Hs.76728 | ESTs | 8.7 |
| | 428106 | BE620016 | Hs.182470 | PTD010 protein | 8.3 |
| | 446544 | AI631932 | Hs.7047 | ESTs, Weakly similar to Unknown [Hsapie | 8.2 |
| | 423479 | NM_014326 | Hs.129208 | death-associated protein kinase 2 | 8.2 |
| 40 | 439480 | AL038511 | Hs.125316 | ESTs, Weakly similar to S33990 finger pr | 8.2 |
| | 418036 | Z37976 | Hs.83337 | latent transforming growth factor beta b | 8.0 |
| | 456490 | UB3171 | Hs.97203 | small inducible cytokine subfamily A (Cy | 8.0 |
| | 410200 | AA082557 | Hs.101915 | Stargardt disease 3 (autosomal dominant) | 8.0 |
| | 414602 | AW630088 | Hs.76550 | Homo sapiens mRNA; cDNA DKFZp564B1264 (I | 8.0 |
| 45 | 408428 | NM_014787 | Hs.44896 | DnaJ (Hsp40) homolog, subfamily B, membe | 7.9 |
| | 437073 | AI885608 | Hs.94122 | ESTs | 7.9 |
| | 408434 | AW195317 | Hs.107716 | hypothetical protein FLJ22344 | 7.9 |
| | 438150 | AA037534 | Hs.79059 | transforming growth factor, beta recepto | 7.9 |
| | 440209 | H05049 | Hs.22269 | neurexin 3 | 7.8 |
| 50 | 408119 | W26213 | Hs.101672 | ESTs, Weakly similar to T00331 hypotheti | 7.8 |
| | 417421 | AL138201 | Hs.82120 | nuclear receptor subfamily 4, group A, m | 7.8 |
| | 410587 | AA370706 | Hs.86412 | chromosome 9 open reading frame 5 | 7.8 |
| | 429611 | AI889077 | Hs.211388 | Homo sapiens BAC clone CTB-60N22 from 7q | 7.7 |
| | 405800 | | | | 7.7 |
| 55 | 421750 | AK000768 | Hs.107872 | hypothetical protein FLJ20761 | 7.7 |
| | 426356 | BE536836 | Hs.98682 | hypothetical protein FKSG32 | 7.7 |
| | 423440 | R25234 | Hs.143434 | contactin 1 | 7.7 |
| | 445148 | AI214510 | Hs.146304 | ESTs | 7.6 |
| | 416294 | D86980 | Hs.79170 | KIAA0227 protein | 7.6 |
| 60 | 424087 | N69333 | Hs.143434 | contactin 1 | 7.6 |
| | 437479 | R61866 | Hs.101277 | ESTs | 7.5 |
| | 405071 | | | | 7.5 |
| | 421224 | AW402154 | Hs.125812 | ESTs | 7.4 |
| | 442025 | AW887434 | Hs.11810 | CDA11 protein | 7.4 |
| 65 | 459476 | BE185844 | | gb:IL5-HT0731-110500-087-c08 HT0731 Homo | 7.2 |
| | 430573 | AA744550 | Hs.136345 | ESTs | 7.1 |
| | 401836 | | | | 7.1 |
| | 448958 | AB020651 | Hs.22653 | KIAA0844 protein | 7.1 |
| | 430152 | AB001325 | Hs.234642 | aquaporin 3 | 7.1 |
| 70 | 419474 | AW968619 | Hs.155849 | ESTs | 7.1 |
| | 401780 | | | | 7.1 |
| | 446052 | AA358760 | | gb:EST67699 Fetal lung II Homo sapiens c | 7.0 |
| | 423605 | AF047826 | Hs.129887 | cadherin 19, type 2 | 7.0 |
| | 433098 | AW190593 | Hs.151143 | ESTs | 7.0 |
| 75 | 445511 | AI436187 | Hs.295261 | guanine nucleotide binding protein (G pr | 6.9 |
| | 451285 | AW137912 | Hs.227583 | Homo sapiens chromosome X map Xp11.23 L- | 6.8 |
| | 428414 | AL049980 | Hs.184216 | DKFZP564C152 protein | 6.8 |
| | 419273 | BE271180 | Hs.293490 | ESTs, Weakly similar to I38022 hypotheti | 6.8 |
| | 443155 | R54485 | Hs.23772 | ESTs | 6.8 |
| 80 | 450561 | R49674 | Hs.25909 | ESTs | 6.8 |
| | 433068 | NM_006456 | Hs.288215 | sialyltransferase | 6.8 |
| | 440729 | AA904739 | Hs.128204 | ESTs | 6.8 |
| | 448426 | BE018315 | Hs.280776 | tankyrase, TRF1-interacting ankyrin-rela | 6.7 |
| | 423589 | AA328082 | Hs.209569 | ESTs | 6.6 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 415681 | AI379882 | Hs.72630 | ESTs | |
| | 413510 | F13044 | | gb:HSC3HH101 normalized infant brain cDN | 6.5 |
| | 427992 | Y15014 | Hs.181353 | UDP-Gal:betaGlcNAc beta 1,3-galactosyltr | 6.4 |
| 5 | 453344 | BE349075 | Hs.44571 | ESTs | 6.4 |
| | 450642 | R39773 | Hs.7130 | copine IV | 6.4 |
| | 432251 | AW972983 | Hs.232165 | polycythemia rubra vera 1; cell surface | 6.4 |
| | 429322 | D86984 | Hs.199243 | KIAA0231 protein | 6.4 |
| | 444927 | AW016637 | Hs.199425 | ESTs | 6.4 |
| 10 | 447482 | AB033059 | Hs.18705 | KIAA1233 protein | 6.4 |
| | 400332 | S66407 | Hs.248032 | FLT4 | 6.4 |
| | 440703 | AL137663 | Hs.7378 | Homo sapiens mRNA; cDNA DKFZp434G227 (fr | 6.3 |
| | 446129 | AW244073 | Hs.145946 | ESTs | 6.3 |
| | 454076 | AW204712 | Hs.61957 | ESTs | 6.3 |
| 15 | 425526 | AA359933 | | gb:EST69040 Fetal lung II Homo sapiens c | 6.3 |
| | 421913 | AI934365 | Hs.109439 | osteoglycin (osteoinductive factor, mime | 6.3 |
| | 434273 | AA913143 | Hs.26303 | ESTs | 6.3 |
| | 408480 | AI350337 | Hs.164568 | fibroblast growth factor 7 (keratinocyte | 6.2 |
| | 451301 | AI769514 | Hs.209890 | EST | 6.2 |
| 20 | 430754 | AW862610 | Hs.157068 | ESTs | 6.2 |
| | 438356 | AA805530 | Hs.48527 | ESTs | 6.2 |
| | 422743 | BE304678 | Hs.119598 | ribosomal protein L3 | 6.2 |
| | 453355 | AW295374 | Hs.31412 | Homo sapiens cDNA FLJ11422 fis, clone HE | 6.2 |
| | 426388 | AW081394 | Hs.97103 | ESTs | 6.2 |
| 25 | 452502 | AI904296 | | gb:PM-BT046-220199-286_1 BT046 Homo sapi | 6.1 |
| | 402546 | | | | 6.1 |
| | 457534 | AI761307 | Hs.232226 | ESTs | 6.1 |
| | 408165 | AL137573 | Hs.43143 | Homo sapiens mRNA; cDNA DKFZp564A2463 (f | 6.1 |
| | 404958 | | | | 6.1 |
| 30 | 432501 | BE546532 | Hs.25682 | Homo sapiens mRNA for KIAA1863 protein, | 6.1 |
| | 442979 | AW440782 | Hs.174743 | ESTs | 6.1 |
| | 422262 | AL022315 | Hs.113987 | lectin, galactoside-binding, soluble, 2 | 6.0 |
| | 408713 | NM_001248 | Hs.47042 | ectonucleoside triphosphate diphosphohyd | 6.0 |
| | 454065 | BE394588 | | gb:601311808F1 NIH_MGC_44 Homo sapiens c | 6.0 |
| 35 | 430004 | U27768 | Hs.227571 | regulator of G-protein signalling 4 | 5.9 |
| | 401521 | | | | 5.9 |
| | 425087 | R62424 | Hs.126059 | ESTs | 5.9 |
| | 446298 | AF187813 | Hs.14637 | kidney- and liver-specific gene | 5.9 |
| | 417761 | R13727 | Hs.21435 | ESTs | 5.9 |
| 40 | 424806 | AA382523 | Hs.105689 | MSTP031 protein | 5.9 |
| | 441695 | T12411 | Hs.183745 | hypothetical protein FLJ13456 | 5.9 |
| | 457483 | AB034694 | Hs.272558 | endomucin-1 | 5.9 |
| | 417175 | R44558 | Hs.94002 | ESTs | 5.9 |
| | 437483 | AL390174 | | gb:Homo sapiens mRNA; cDNA DKFZp547J184 | 5.8 |
| 45 | 436427 | AI344378 | Hs.143399 | ESTs | 5.8 |
| | 411939 | AI365585 | Hs.146246 | ESTs | 5.8 |
| | 459053 | AI807052 | Hs.210361 | ESTs | 5.8 |
| | 411052 | AW814950 | | gb:MR1-ST0205-130400-023-d06 ST0206 Homo | 5.7 |
| | 431063 | Z98949 | Hs.326843 | hypothetical protein bk125H2.1 | 5.7 |
| 50 | 450382 | AA397658 | Hs.60257 | Homo sapiens cDNA FLJ13598 fis, clone PL | 5.7 |
| | 408478 | NM_000806 | Hs.45740 | gamma-aminobutyric acid (GABA) A recepto | 5.7 |
| | 442676 | AI733585 | Hs.130897 | ESTs | 5.7 |
| | 446443 | AV659082 | Hs.134228 | ESTs | 5.7 |
| | 400865 | | | | 5.7 |
| 55 | 459080 | AW192083 | Hs.290855 | ESTs | 5.7 |
| | 407952 | AI215902 | Hs.88845 | ESTs, Highly similar to T50835 hypotheti | 5.6 |
| | 431984 | AL080239 | Hs.272284 | Human DNA sequence from clone GS1-256022 | 5.6 |
| | 425705 | AF007833 | Hs.159265 | kruppel-related zinc finger protein hckr | 5.6 |
| | 442238 | AW135374 | Hs.270949 | ESTs, Moderately similar to F41925 hypot | 5.6 |
| 60 | 422994 | AW891802 | Hs.296276 | ESTs | 5.6 |
| | 457148 | AF091035 | Hs.184627 | KIAA0118 protein | 5.6 |
| | 428356 | AL046991 | Hs.10338 | ESTs | 5.6 |
| | 415927 | AL120168 | Hs.78919 | Kell blood group precursor (McLeod pheno | 5.5 |
| | 402092 | | | | 5.5 |
| 65 | 440526 | AI832243 | Hs.211471 | ESTs | 5.5 |
| | 444409 | AI792140 | Hs.49265 | ESTs | 5.5 |
| | 417877 | AI025829 | Hs.86320 | ESTs | 5.5 |
| | 458238 | AW071521 | Hs.333541 | beta-amyloid binding protein precursor | 5.4 |
| | 430702 | U56979 | Hs.250651 | H factor 1 (complement) | 5.4 |
| 70 | 456189 | H91010 | Hs.44940 | ESTs | 5.4 |
| | 427424 | AA402453 | Hs.113011 | ESTs | 5.4 |
| | 437354 | AA749215 | Hs.291886 | ESTs | 5.4 |
| | 455617 | BE078070 | | gb:CM1-BT0614-160300-149-f02 BT0614 Homo | 5.4 |
| | 429290 | AF203032 | Hs.198760 | neurofilament, heavy polypeptide (200kD) | 5.3 |
| 75 | 427861 | AA813185 | Hs.98183 | ESTs | 5.3 |
| | 408556 | U49516 | Hs.46362 | 5-hydroxytryptamine (serotonin) receptor | 5.3 |
| | 444209 | AI753134 | Hs.146494 | ESTs | 5.3 |
| | 422831 | R02504 | Hs.332943 | ESTs | 5.3 |
| | 403180 | | | | 5.3 |
| 80 | 418026 | BE379727 | Hs.83213 | fatty acid binding protein 4, adipocyte | 5.3 |
| | 430339 | W26608 | Hs.239625 | integral membrane protein 2B | 5.2 |
| | 431596 | T34708 | Hs.272927 | Sec23 (S. cerevisiae) homolog A | 5.2 |
| | 431930 | AB035301 | Hs.272211 | cadherin 7, type 2 | 5.2 |
| | 437403 | AI208149 | Hs.121196 | ESTs | 5.2 |

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|----|--------|-----------|-----------|--|-----|
| | 438285 | AA782845 | Hs.22790 | ESTs | 5.2 |
| | 439901 | N73885 | Hs.124169 | ESTs | 5.2 |
| | 438507 | AA809052 | Hs.211275 | ESTs | 5.2 |
| | 449222 | AW293984 | Hs.197621 | ESTs | 5.2 |
| 5 | 402834 | AK001507 | Hs.306084 | Homo sapiens clone FLB6914 PRO1821 mRNA, | 5.2 |
| | 419042 | T81429 | Hs.221065 | ESTs | 5.2 |
| | 436777 | AA731199 | Hs.293130 | ESTs | 5.2 |
| | 445071 | AI280246 | Hs.149504 | ESTs | 5.1 |
| 10 | 408016 | AW136827 | Hs.256096 | ESTs | 5.1 |
| | 412047 | AA934589 | Hs.49696 | ESTs | 5.1 |
| | 436953 | AW959074 | Hs.23648 | Homo sapiens cDNA FLJ13097 fis, clone NT | 5.1 |
| | 436773 | AW078629 | Hs.82110 | PC4 and SFRS1 interacting protein 1 | 5.1 |
| | 409263 | AA069573 | Hs.50319 | ESTs | 5.1 |
| 15 | 453830 | AA534296 | Hs.20953 | ESTs | 5.1 |
| | 459580 | AA022888 | Hs.176055 | ESTs | 5.1 |
| | 417616 | R07728 | Hs.268658 | ESTs | 5.1 |
| | 423457 | F08208 | Hs.283844 | similar to rat tricarboxylate carrier-6 | 5.1 |
| | 441535 | AL135735 | Hs.7885 | phosphatidylinositol binding clathrin as | 5.0 |
| | 416490 | AF090116 | Hs.79348 | regulator of G-protein signalling 7 | 5.0 |
| 20 | 417284 | N52889 | Hs.107242 | Homo sapiens cDNA FLJ12965 fis, clone NT | 5.0 |
| | 447135 | T58148 | | gb:yb98g06.s1 Stratagene lung (937210) H | 5.0 |
| | 448605 | AL109678 | Hs.21597 | Homo sapiens mRNA full length insert cDN | 5.0 |
| | 442240 | AI791883 | Hs.292719 | ESTs | 4.9 |
| 25 | 459399 | BE407712 | Hs.153998 | creatine kinase, mitochondrial 1 (ubiqui | 4.9 |
| | 427972 | AA864870 | Hs.181304 | putative gene product | 4.9 |
| | 432944 | AA570687 | Hs.38512 | ESTs | 4.9 |
| | 440198 | BE560093 | | gb:601345159F1 NIH_MGC_8 Homo sapiens cD | 4.9 |
| | 444047 | AI097452 | Hs.135095 | ESTs | 4.9 |
| 30 | 416040 | AW819158 | Hs.289044 | Homo sapiens cDNA FLJ12048 fis, clone HE | 4.9 |
| | 444922 | AI921750 | Hs.144871 | Homo sapiens cDNA FLJ13752 fis, clone PL | 4.8 |
| | 436670 | AI690021 | Hs.201536 | ESTs | 4.8 |
| | 448072 | AI459306 | Hs.24908 | ESTs | 4.8 |
| | 408936 | AL138043 | Hs.293549 | ESTs | 4.8 |
| 35 | 412622 | AW664708 | Hs.171959 | ESTs | 4.8 |
| | 414943 | D80647 | Hs.124193 | ESTs | 4.8 |
| | 429254 | H10133 | Hs.91846 | hypothetical protein DKFZp761C121 | 4.8 |
| | 453567 | AI742835 | Hs.33368 | hypothetical protein FLJ11175 | 4.8 |
| | 407906 | AA369665 | Hs.41185 | Homo sapiens mRNA; cDNA DKFZp564O1262 (f | 4.8 |
| 40 | 441028 | AI333660 | Hs.17558 | Homo sapiens cDNA FLJ14446 fis, clone HE | 4.7 |
| | 405130 | | | | 4.7 |
| | 455225 | AW996689 | | gb:QV3-BN0046-150400-151-g09 BN0046 Homo | 4.7 |
| | 446218 | AV657159 | | gb:AV657159 GLC Homo sapiens cDNA clone | 4.7 |
| | 443347 | AI052543 | Hs.133244 | melanoma-derived leucine zipper, extra-n | 4.7 |
| | 402176 | | | | 4.7 |
| 45 | 416577 | BE063207 | Hs.79381 | grancalcin | 4.7 |
| | 436221 | AK001781 | Hs.296543 | Homo sapiens cDNA FLJ10919 fis, clone OV | 4.7 |
| | 420480 | AL137361 | Hs.98173 | hypothetical protein | 4.7 |
| | 400800 | Y10262 | Hs.46925 | eyes absent (Drosophila) homolog 3 | 4.6 |
| 50 | 435161 | AF124150 | Hs.272091 | ESTs | 4.6 |
| | 404793 | | | | 4.6 |
| | 430895 | U66581 | Hs.248121 | G protein-coupled receptor 22 | 4.6 |
| | 438571 | AW020775 | Hs.56022 | ESTs | 4.6 |
| | 445924 | AI264671 | Hs.164166 | ESTs | 4.6 |
| 55 | 444585 | AW170015 | Hs.6594 | ESTs | 4.6 |
| | 421044 | AF061871 | Hs.311736 | Human DNA sequence from clone RP1-238D15 | 4.6 |
| | 418274 | AI458587 | Hs.128677 | Human DNA sequence from clone RP1-50O24 | 4.6 |
| | 425475 | W56339 | Hs.107057 | ESTs | 4.6 |
| | 434311 | BE543469 | Hs.266263 | Homo sapiens cDNA FLJ14115 fis, clone MA | 4.5 |
| 60 | 414272 | AI651603 | Hs.46988 | ESTs | 4.5 |
| | 445235 | AI564022 | Hs.138207 | ESTs | 4.5 |
| | 414327 | BE408145 | Hs.185254 | ESTs, Weakly similar to T24435 hypotheti | 4.5 |
| | 414630 | BE410857 | | gb:601301177F1 NIH_MGC_21 Homo sapiens c | 4.5 |
| | 414456 | H74314 | | gb:yu56e10.r1 Soares fetal liver spleen | 4.5 |
| | 401024 | | | | 4.5 |
| 65 | 414699 | AI815523 | Hs.76930 | synuclein, alpha (non A4 component of am | 4.5 |
| | 423449 | AI497900 | Hs.33067 | ESTs | 4.5 |
| | 405138 | | | | 4.5 |
| | 413544 | BE147225 | | gb:PM2-HT0225-031299-003-f11 HT0225 Homo | 4.5 |
| 70 | 453880 | AI803166 | Hs.28462 | ESTs, Weakly similar to I38022 hypotheti | 4.5 |
| | 433521 | T66087 | Hs.112482 | Homo sapiens unknown mRNA sequence | 4.4 |
| | 441184 | AA922009 | Hs.150269 | ESTs | 4.4 |
| | 429876 | AB028977 | Hs.225974 | KIAA1054 protein | 4.4 |
| | 445481 | AW661846 | Hs.148836 | ESTs | 4.4 |
| 75 | 452340 | NM_002202 | Hs.505 | ISL1 transcription factor, LIM/homeodoma | 4.4 |
| | 404769 | | | | 4.4 |
| | 444331 | AW193342 | Hs.24144 | ESTs | 4.4 |
| | 429726 | AW628326 | Hs.27151 | ESTs | 4.4 |
| | 449093 | AB035356 | Hs.22998 | neurexin 1 | 4.4 |
| 80 | 451959 | AA056203 | Hs.27337 | hypothetical protein FLJ20623 | 4.4 |
| | 415716 | N59294 | Hs.179662 | nucleosome assembly protein 1-like 1 | 4.4 |
| | 417888 | R23053 | | gb:yh31a05.r1 Soares placenta Nb2HP Homo | 4.4 |
| | 419656 | AB002314 | Hs.92025 | KIAA0316 gene product | 4.4 |
| | 425864 | U56420 | Hs.159903 | olfactory receptor, family 5, subfamily | 4.4 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 435078 | AW518888 | Hs.40937 | ESTs | 4.4 |
| | 413493 | BE144444 | | gb:MR0-HT0168-141199-002-f09 HT0168 Homo | 4.3 |
| | 432712 | AB016247 | Hs.288031 | sterol-C5-desaturase (fungal ERG3, delta | 4.3 |
| 5 | 459650 | R25754 | Hs.301185 | ESTs | 4.3 |
| | 404828 | | | | 4.3 |
| | 423782 | AA72209 | Hs.323117 | ESTs | 4.3 |
| | 426867 | AA460967 | Hs.22668 | ESTs | 4.3 |
| | 426802 | AA385182 | Hs.46699 | ESTs | 4.3 |
| 10 | 457353 | X65633 | Hs.248144 | melanocortin 2 receptor (adrenocorticotr | 4.3 |
| | 412112 | BE180342 | | gb:RC3-HT0622-130400-012-a07 HT0622 Homo | 4.3 |
| | 401522 | N47812 | Hs.306198 | CGI-35 protein | 4.3 |
| | 419055 | AI365384 | Hs.11571 | Homo sapiens cDNA FLJ11570 fis, clone HE | 4.3 |
| | 410171 | H07892 | Hs.12431 | ESTs | 4.3 |
| 15 | 419564 | U08989 | Hs.91139 | solute carrier family 1 (neuronal/epithe | 4.3 |
| | 458789 | AL157468 | Hs.325825 | Homo sapiens cDNA FLJ20848 fis, clone AD | 4.3 |
| | 455040 | AW852286 | | gb:QV0-CT0225-100400-187-d08 CT0225 Homo | 4.3 |
| | 438533 | AI440266 | Hs.170673 | ESTs, Weakly similar to T24832 hypothe | 4.3 |
| | 459005 | AA447679 | Hs.144558 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 4.2 |
| 20 | 418489 | U76421 | Hs.85302 | adenosine deaminase, RNA-specific, B1 (h | 4.2 |
| | 433389 | AF038171 | | gb:Homo sapiens clone 23671 mRNA sequenc | 4.2 |
| | 454356 | AW390363 | Hs.11522 | hypothetical protein from Xq28 | 4.2 |
| | 442339 | BE299668 | Hs.227591 | ESTs, Weakly similar to 1901303A Leu zip | 4.2 |
| | 421249 | AA285362 | | gb:HTH277 HTCDL1 Homo sapiens cDNA 5'3' | 4.2 |
| 25 | 443998 | AI620661 | Hs.296276 | ESTs | 4.2 |
| | 452197 | AW023595 | Hs.232048 | ESTs | 4.2 |
| | 451117 | AA015752 | Hs.205173 | ESTs | 4.2 |
| | 404501 | AW247252 | Hs.75514 | nucleoside phosphorylase | 4.2 |
| 30 | 410378 | R23324 | Hs.41693 | DnaJ (Hsp40) homolog, subfamily B, membe | 4.2 |
| | 422528 | AB011182 | Hs.118087 | KIAA0612 protein | 4.2 |
| | 440323 | AA970614 | Hs.127992 | ESTs | 4.1 |
| | 425767 | AF054176 | Hs.159483 | chromosome 1 open reading frame 7 | 4.1 |
| | 434460 | AA478486 | Hs.3852 | KIAA0368 protein | 4.1 |
| | 410362 | H04811 | Hs.93164 | proprotein convertase subtilisin/kexin 1 | 4.1 |
| 35 | 413121 | T96090 | Hs.142678 | ESTs | 4.1 |
| | 409403 | AA668224 | Hs.6634 | Homo sapiens cDNA: FLJ22547 fis, clone H | 4.1 |
| | 450235 | AA007512 | Hs.17538 | ESTs | 4.1 |
| | 449754 | H00820 | Hs.30977 | ESTs, Weakly similar to B34087 hypothe | 4.1 |
| 40 | 421813 | BE048255 | | gb:tz49b05.y1 NCL_CGAP_Bm52 Homo sapien | 4.1 |
| | 408496 | AI683802 | Hs.136182 | ESTs | 4.1 |
| | 430261 | AA305127 | Hs.237225 | hypothetical protein HT023 | 4.1 |
| | 434101 | AA625205 | Hs.259599 | KIAA1622 protein | 4.1 |
| | 451837 | T92157 | Hs.16970 | ESTs | 4.1 |
| | 411772 | BE170301 | | gb:QV4-HT0536-040500-193-f05 HT0536 Homo | 4.1 |
| 45 | 437630 | AI252782 | Hs.153026 | SWAP-70 protein | 4.1 |
| | 430212 | AA469153 | | gb:nc67f04.s1 NCL_CGAP_Pr1 Homo sapiens | 4.0 |
| | 400216 | | | | 4.0 |
| | 429830 | AI537278 | Hs.225841 | DKFZP434D193 protein | 4.0 |
| 50 | 453165 | S74727 | Hs.32042 | aspartoacylase (aminoacylase 2, Canavan | 4.0 |
| | 418047 | R37633 | Hs.4847 | ESTs | 4.0 |
| | 405354 | | | | 4.0 |
| | 427931 | AW206512 | Hs.186996 | ESTs | 4.0 |
| | 428775 | AA434579 | Hs.143691 | ESTs | 4.0 |
| | 449422 | AA001373 | Hs.59821 | ESTs | 4.0 |
| 55 | 453864 | AW021407 | Hs.21058 | hypothetical protein | 4.0 |
| | 456407 | AW968614 | | gb:EST380690 MAGE resequences, MAGJ Homo | 4.0 |
| | 441869 | NM_003947 | Hs.8004 | huntingtin-associated protein interactin | 4.0 |
| | 420784 | T65158 | Hs.102399 | ESTs, Moderately similar to S65657 alpha | 4.0 |
| | 425195 | AA352026 | Hs.94319 | VPS10 domain receptor protein | 4.0 |
| 60 | 429628 | H09604 | Hs.13268 | ESTs | 4.0 |
| | 410087 | F12079 | Hs.332579 | ESTs | 4.0 |
| | 409840 | AW502122 | | gb:UL-HF-BR0p-ajr-c-08-0-ULr1 NIH_MGC_5 | 4.0 |
| | 452854 | AA437061 | Hs.14060 | prokineticin 1 precursor | 4.0 |
| | 419910 | AA662913 | Hs.190173 | ESTs, Weakly similar to A46010 X-linked | 4.0 |
| 65 | 427443 | AA402713 | Hs.97872 | ESTs | 4.0 |
| | 414990 | C17758 | Hs.221652 | Homo sapiens cDNA FLJ14323 fis, clone PL | 3.9 |
| | 412678 | AA115575 | Hs.114914 | ESTs | 3.9 |
| | 405629 | | | | 3.9 |
| | 420299 | AI056871 | Hs.15276 | ESTs | 3.9 |
| 70 | 453098 | Z25935 | Hs.86379 | ESTs | 3.9 |
| | 435752 | AF230801 | | gb:Homo sapiens growth hormone receptor | 3.9 |
| | 441005 | Z41305 | Hs.303172 | Homo sapiens mRNA: cDNA DKFZp547G133 (fr | 3.9 |
| | 414516 | AI307802 | Hs.135560 | ESTs, Weakly similar to T43458 hypothe | 3.9 |
| | 442257 | AW503831 | Hs.323370 | Human EST clone 25267 mariner transposon | 3.9 |
| 75 | 422563 | BE299342 | Hs.19348 | hypothetical protein FLJ13119 | 3.9 |
| | 406697 | M21388 | Hs.123017 | Human unproductively rearranged Ig mu-ch | 3.9 |
| | 443850 | AW014723 | Hs.334612 | ESTs | 3.9 |
| | 412677 | AW029608 | Hs.17384 | ESTs | 3.9 |
| | 422788 | AL117352 | Hs.120828 | Human DNA sequence from clone RPS-876B10 | 3.9 |
| | 405377 | | | | 3.9 |
| 80 | 414376 | BE393856 | Hs.66915 | ESTs, Weakly similar to 16.7Kd protein [| 3.9 |
| | 453341 | AI758912 | Hs.296341 | adenylyl cyclase-associated protein 2 | 3.9 |
| | 431960 | AW241821 | Hs.301927 | c6.1A | 3.9 |
| | 416854 | H40164 | Hs.80296 | Purkinje cell protein 4 | 3.9 |

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|----|--------|-----------|-----------|--|-----|
| | 427264 | AA400117 | Hs.125747 | ESTs | 3.9 |
| | 422746 | NM_004484 | Hs.119651 | glypican 3 | 3.9 |
| | 452346 | BE243534 | | gb:TCBAP1D0885 Pediatric pre-B cell acut | 3.9 |
| 5 | 414666 | NM_004466 | Hs.76828 | glypican 5 | 3.8 |
| | 418217 | AI910647 | Hs.13442 | ESTs | 3.8 |
| | 419118 | AA234223 | Hs.139204 | ESTs | 3.8 |
| | 445017 | AI205493 | Hs.176860 | ESTs | 3.8 |
| | 405867 | | | | 3.8 |
| 10 | 422760 | BE409561 | | gb:601299865F1 NIH_MGC_21 Homo sapiens c | 3.8 |
| | 453863 | X02544 | Hs.572 | orosomucoid 1 | 3.8 |
| | 457821 | H47166 | Hs.124322 | ESTs, Weakly similar to A47582 B-cell gr | 3.8 |
| | 457330 | AB013818 | Hs.247220 | peroxisome biogenesis factor 10 | 3.8 |
| | 435600 | AL047034 | Hs.119747 | ESTs | 3.8 |
| 15 | 456083 | U46922 | Hs.77252 | fragile histidine triad gene | 3.8 |
| | 413341 | H78472 | Hs.191325 | ESTs, Weakly similar to T18967 hypothesi | 3.8 |
| | 449057 | AB037784 | Hs.22941 | KIAA1363 protein | 3.8 |
| | 421855 | F06504 | Hs.27384 | ESTs, Moderately similar to ALU4_HUMAN A | 3.8 |
| | 414764 | AW013887 | Hs.72047 | ESTs | 3.8 |
| | 404391 | | | | 3.7 |
| 20 | 433629 | R13140 | Hs.13359 | ESTs | 3.7 |
| | 424738 | AI963740 | Hs.46826 | ESTs | 3.7 |
| | 401315 | | | | 3.7 |
| | 407706 | AA191085 | Hs.26612 | ESTs, Moderately similar to S23650 retro | 3.7 |
| 25 | 440530 | AA888646 | Hs.174187 | ESTs | 3.7 |
| | 433930 | AA620338 | Hs.273781 | ESTs | 3.7 |
| | 409662 | AW452320 | Hs.279726 | ESTs | 3.7 |
| | 437268 | AI754847 | Hs.227571 | regulator of G-protein signalling 4 | 3.7 |
| | 445688 | AI248205 | Hs.153244 | ESTs | 3.7 |
| 30 | 408593 | R19566 | Hs.197617 | ESTs | 3.7 |
| | 417091 | AA193283 | Hs.291990 | ESTs | 3.7 |
| | 448556 | AW885606 | Hs.5064 | ESTs | 3.7 |
| | 423135 | N67655 | Hs.26411 | ESTs | 3.7 |
| | 400135 | | | | 3.7 |
| 35 | 459150 | BE155356 | | gb:PM1-HT0350-160300-009-d06 HT0350 Homo | 3.7 |
| | 457221 | AW383197 | Hs.218260 | ESTs | 3.7 |
| | 451660 | AI807927 | Hs.249601 | ESTs | 3.7 |
| | 401600 | BE247275 | Hs.151787 | U5 snRNP-specific protein, 116 kD | 3.7 |
| | 446818 | AI342668 | Hs.279765 | ESTs | 3.7 |
| 40 | 447795 | AW295151 | Hs.163612 | ESTs | 3.7 |
| | 427562 | R56424 | Hs.26534 | ESTs | 3.6 |
| | 412258 | AA376768 | Hs.324841 | hypothetical protein FLJ22622 | 3.6 |
| | 454339 | AW381980 | | gb:QV4-HT0316-091199-028-d05 HT0316 Homo | 3.6 |
| | 439274 | AF086092 | Hs.48372 | ESTs | 3.6 |
| 45 | 452381 | H23329 | Hs.290880 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.6 |
| | 422897 | AA679784 | Hs.4290 | ESTs | 3.6 |
| | 429656 | X05608 | Hs.211584 | neurofilament, light polypeptide (68kD) | 3.6 |
| | 421908 | AW935200 | Hs.285814 | sprouty (Drosophila) homolog 4 | 3.6 |
| | 407978 | AW385129 | Hs.41717 | phosphodiesterase 1A, calmodulin-depende | 3.6 |
| 50 | 426452 | AW614271 | Hs.121647 | ESTs, Highly similar to AC006014 8 simil | 3.6 |
| | 400685 | | | | 3.6 |
| | 417154 | AI674701 | Hs.21388 | ESTs | 3.6 |
| | 447176 | Z42549 | Hs.160893 | ESTs | 3.6 |
| | 423893 | AL031709 | Hs.134846 | Human DNA sequence from clone 316G12 on | 3.6 |
| 55 | 449231 | BE410360 | Hs.298573 | KIAA1720 protein | 3.6 |
| | 411607 | AW853498 | | gb:RC1-CT0252-170200-025-h02 CT0252 Homo | 3.6 |
| | 405977 | | | | 3.6 |
| | 441470 | BE503874 | Hs.301986 | ESTs | 3.6 |
| 60 | 423568 | NM_005256 | Hs.129818 | growth arrest-specific 2 | 3.6 |
| | 441235 | AI884586 | Hs.135570 | Homo sapiens cDNA: FLJ21268 fis, clone C | 3.6 |
| | 450236 | AW162998 | Hs.24684 | KIAA1376 protein | 3.6 |
| | 425364 | AF052150 | Hs.155959 | Homo sapiens clone 24533 mRNA sequence | 3.6 |
| | 426775 | AA384564 | Hs.108829 | ESTs | 3.6 |
| | 414831 | M31158 | Hs.77439 | protein kinase, cAMP-dependent, regulato | 3.6 |
| 65 | 416876 | AW501916 | Hs.117897 | ESTs | 3.6 |
| | 400878 | | | | 3.6 |
| | 425153 | AW023193 | Hs.27046 | ESTs | 3.6 |
| | 432222 | AI204995 | | gb:an03c03.x1 Stratagene schizo brain S1 | 3.5 |
| | 415047 | F13142 | | gb:HSC3JD031 normalized infant brain cDN | 3.5 |
| 70 | 401532 | | | | 3.5 |
| | 446495 | D60923 | Hs.153460 | ESTs | 3.5 |
| | 431325 | AW026751 | Hs.5794 | ESTs, Weakly similar to 2109260A B cell | 3.5 |
| | 445898 | AF070623 | Hs.13423 | Homo sapiens clone 24468 mRNA sequence | 3.5 |
| | 455901 | BE155527 | | gb:PM1-HT0350-190400-013-b08 HT0350 Homo | 3.5 |
| 75 | 416421 | AA134006 | Hs.79306 | eukaryotic translation initiation factor | 3.5 |
| | 455697 | BE067952 | | gb:CM0-BT0365-061299-122-g09 BT0365 Homo | 3.5 |
| | 405678 | | | | 3.5 |
| | 418207 | C14685 | Hs.34772 | ESTs | 3.5 |
| | 425383 | D83407 | Hs.156007 | Down syndrome critical region gene 1-lik | 3.5 |
| 80 | 417027 | AA192306 | Hs.23926 | triadin | 3.5 |
| | 408367 | AK001178 | Hs.44424 | homolog of rat orphan transporter v7-3 | 3.5 |
| | 417702 | R09935 | Hs.191146 | ESTs | 3.5 |
| | 445687 | WB0382 | Hs.149297 | ESTs | 3.5 |
| | 408776 | AA057365 | Hs.63356 | ESTs, Weakly similar to I38022 hypothesi | 3.5 |

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|----|--------|-----------|-----------|--|-----|
| | 413164 | BE068494 | | gb:MR1-BT0371-050500-009-a12 BT0371 Homo | 3.5 |
| | 414593 | BE386764 | | gb:601273249F1 NIH_MGC_20 Homo sapiens c | 3.5 |
| | 453220 | AB033089 | Hs.32452 | Homo sapiens mRNA for KIAA1263 protein, | 3.5 |
| 5 | 415621 | AJ648602 | Hs.55468 | ESTs | 3.5 |
| | 454437 | AJ248173 | Hs.191460 | hypothetical protein MGC12936 | 3.5 |
| | 446066 | AJ343931 | Hs.149383 | ESTs | 3.5 |
| | 423374 | AB037770 | Hs.127656 | KIAA1349 protein | 3.5 |
| | 419347 | C15944 | Hs.90005 | superiorcervical ganglia, neural specifi | 3.5 |
| 10 | 418516 | NM_006218 | Hs.85701 | phosphoinositide-3-kinase, catalytic, al | 3.5 |
| | 451776 | W45679 | Hs.169854 | hypothetical protein SP192 | 3.5 |
| | 432305 | M62402 | Hs.274313 | insulin-like growth factor binding prote | 3.5 |
| | 456995 | T89832 | Hs.170278 | ESTs | 3.5 |
| | 403323 | | | | 3.5 |
| 15 | 425022 | M95724 | Hs.154207 | centromere protein C 1 | 3.5 |
| | 439394 | AA149250 | Hs.56105 | ESTs | 3.5 |
| | 433803 | AJ823593 | Hs.27688 | ESTs | 3.4 |
| | 450715 | AJ266484 | Hs.31570 | ESTs, Weakly similar to KIAA1324 protein | 3.4 |
| | 411474 | AW848427 | | gb:IL3-CT0214-150200-075-H10 CT0214 Homo | 3.4 |
| 20 | 415076 | NM_000857 | Hs.77890 | guanylate cyclase 1, soluble, beta 3 | 3.4 |
| | 423826 | U20325 | Hs.1707 | cocaine- and amphetamine-regulated trans | 3.4 |
| | 459495 | BE544158 | | gb:601076707F1 NIH_MGC_12 Homo sapiens c | 3.4 |
| | 427173 | BE255017 | Hs.97540 | ESTs | 3.4 |
| | 408112 | AW451982 | Hs.248613 | ESTs | 3.4 |
| 25 | 446092 | N33522 | Hs.145894 | ESTs | 3.4 |
| | 416868 | AJ656856 | Hs.292597 | ESTs | 3.4 |
| | 458234 | BE551408 | Hs.127196 | ESTs | 3.4 |
| | 419555 | AA244416 | | gb:nc07d11.s1 NCI_CGAP_Pr1 Homo sapiens | 3.4 |
| | 414314 | BE312991 | | gb:601150275F1 NIH_MGC_19 Homo sapiens c | 3.4 |
| 30 | 400425 | AY004252 | Hs.287385 | PR domain containing 12 | 3.4 |
| | 414366 | BE549143 | | gb:601076456F1 NIH_MGC_12 Homo sapiens c | 3.4 |
| | 434053 | AW445136 | Hs.134946 | ESTs | 3.4 |
| | 449997 | AJ683052 | Hs.201577 | KIAA1829 protein | 3.4 |
| | 433461 | AJ636047 | Hs.197623 | ESTs | 3.4 |
| 35 | 428006 | AA418743 | Hs.98306 | KIAA1862 protein | 3.4 |
| | 424695 | U58331 | Hs.151899 | sarcoglycan, delta (35kD dystrophin-asso | 3.4 |
| | 443294 | AJ733625 | Hs.133053 | ESTs | 3.4 |
| | 428212 | AW444451 | Hs.134812 | ESTs | 3.4 |
| | 457673 | AA551569 | Hs.272034 | hypothetical protein PRO2822 | 3.4 |
| 40 | 446390 | AA233393 | Hs.14992 | hypothetical protein FLJ11151 | 3.4 |
| | 428536 | AJ143139 | Hs.2288 | visinin-like 1 | 3.3 |
| | 426597 | AA382250 | Hs.145601 | ESTs | 3.3 |
| | 410366 | AJ267589 | Hs.302689 | hypothetical protein | 3.3 |
| | 458258 | AW406546 | Hs.127971 | ESTs | 3.3 |
| | 401738 | | | | 3.3 |
| 45 | 409038 | T97490 | Hs.50002 | small inducible cytokine subfamily A (Cy | 3.3 |
| | 425785 | T27017 | Hs.159528 | Homo sapiens clone 24400 mRNA sequence | 3.3 |
| | 433328 | AW298159 | Hs.23644 | ESTs, Weakly similar to S65824 reverse t | 3.3 |
| | 414541 | BE293116 | Hs.76392 | aldehyde dehydrogenase 1 family, member | 3.3 |
| 50 | 434998 | AW975157 | Hs.26037 | ESTs | 3.3 |
| | 456359 | AJ967991 | Hs.93574 | homeo box D3 | 3.3 |
| | 426527 | NM_001037 | Hs.170238 | sodium channel, voltage-gated, type I, b | 3.3 |
| | 454267 | AA437199 | Hs.656 | cell division cycle 25C | 3.3 |
| | 400302 | N48056 | Hs.1915 | folate hydrolase (prostate-specific memb | 3.3 |
| 55 | 434077 | AF116659 | Hs.321151 | Homo sapiens PRO1412 mRNA, complete cds | 3.3 |
| | 436602 | AJ793222 | Hs.166817 | ESTs | 3.3 |
| | 449204 | AB000099 | Hs.23251 | Down syndrome critical region gene 4 | 3.3 |
| | 417935 | R53697 | Hs.170044 | ESTs | 3.3 |
| | 423310 | AA325225 | Hs.124023 | Homo sapiens cDNA FLJ14218 fis, clone NT | 3.3 |
| 60 | 436524 | T64297 | Hs.5241 | fatty acid binding protein 1, liver | 3.3 |
| | 453406 | AJ192987 | Hs.61784 | hypothetical protein FLJ14451 | 3.3 |
| | 420164 | AW339037 | Hs.24908 | ESTs | 3.3 |
| | 447826 | AW779317 | Hs.258556 | ESTs | 3.3 |
| | 419875 | AA853410 | Hs.93557 | proenkephalin | 3.3 |
| 65 | 444612 | AW138111 | Hs.22902 | ESTs | 3.3 |
| | 418504 | BE159718 | Hs.85335 | Homo sapiens mRNA; cDNA DKFZp564D1462 (I | 3.2 |
| | 415242 | R45986 | Hs.295014 | ESTs | 3.2 |
| | 418188 | AW139413 | Hs.151880 | ESTs | 3.2 |
| | 430355 | NM_006219 | Hs.239818 | phosphoinositide-3-kinase, catalytic, be | 3.2 |
| 70 | 421640 | AW966652 | | gb:EST378726 MAGE resequences, MAGI Homo | 3.2 |
| | 432359 | AA076049 | Hs.274415 | Homo sapiens cDNA FLJ10229 fis, clone HE | 3.2 |
| | 408806 | AW847814 | Hs.289005 | Homo sapiens cDNA: FLJ21532 fis, clone C | 3.2 |
| | 400409 | AF153341 | Hs.283954 | Homo sapiens winged helix/forkhead trans | 3.2 |
| | 446015 | T30968 | Hs.13531 | hypothetical protein FLJ10971 | 3.2 |
| 75 | 425495 | AA358454 | Hs.78026 | ESTs, Weakly similar to similar to ankyr | 3.2 |
| | 403092 | | | | 3.2 |
| | 452971 | AJ873878 | Hs.91789 | ESTs | 3.2 |
| | 454186 | BE141030 | | gb:MR0-HT0067-201099-002-h11 HT0067 Homo | 3.2 |
| | 401485 | | | | 3.2 |
| | 401949 | | | | 3.2 |
| 80 | 457452 | AW972675 | | gb:EST384766 MAGE resequences, MAGL Homo | 3.2 |
| | 454100 | AJ693231 | Hs.126043 | chromosome 21 open reading frame 51 | 3.2 |
| | 448440 | AA173467 | Hs.62402 | p21/Cdc42/Rac1-activated kinase 1 (yeast | 3.2 |
| | 421200 | AA284811 | Hs.264433 | ESTs | 3.2 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 430142 | NM_000437 | Hs.234392 | platelet-activating factor acetylhydrolase | 3.2 |
| | 433197 | AB040889 | Hs.281022 | KIAA1456 protein | 3.2 |
| | 443509 | AV645470 | | gb:AV645470 GLC Homo sapiens cDNA clone | 3.2 |
| 5 | 440827 | AI733110 | Hs.128128 | ESTs | 3.2 |
| | 432799 | NM_016161 | Hs.278960 | alpha-1,4-N-acetylglucosaminyltransferase | 3.2 |
| | 409257 | AW370362 | | gb:RC1-BT0255-181099-012-d07 BT0255 Homo | 3.2 |
| | 459235 | BE246010 | Hs.271468 | Homo sapiens mRNA for FLJ00038 protein, | 3.2 |
| | 416789 | AA223439 | Hs.79933 | cyclin I | 3.2 |
| 10 | 429809 | AL162010 | Hs.223603 | Homo sapiens mRNA; cDNA DKFZp761D09121 (| 3.2 |
| | 420156 | AW449258 | Hs.6187 | ESTs | 3.2 |
| | 455577 | BE006341 | | gb:RC2-BN0127-240300-011-b05 BN0127 Homo | 3.2 |
| | 400617 | AF151064 | Hs.36069 | hypothetical protein | 3.2 |
| | 437129 | AL049327 | Hs.302057 | Homo sapiens mRNA; cDNA DKFZp564E016 (fr | 3.2 |
| 15 | 451820 | AW058357 | Hs.337353 | ESTs | 3.2 |
| | 457535 | AA609685 | Hs.278672 | membrane component, chromosome 11, surfa | 3.2 |
| | 419956 | AL137939 | Hs.40096 | ESTs | 3.1 |
| | 456235 | AA203637 | | gb:zx58b12.r1 Soares_fetal_liver_spleen_ | 3.1 |
| | 423930 | AA332697 | Hs.42721 | ESTs | 3.1 |
| | 403796 | | | | 3.1 |
| 20 | 414085 | AA114016 | Hs.75746 | aldehyde dehydrogenase 1 family, member | 3.1 |
| | 445886 | AI793176 | Hs.145596 | ESTs | 3.1 |
| | 414401 | AI760159 | Hs.124833 | ESTs | 3.1 |
| | 441573 | BE563966 | Hs.6529 | ESTs, Weakly similar to I78885 serine/th | 3.1 |
| 25 | 450725 | R71389 | Hs.175951 | ESTs | 3.1 |
| | 458805 | AI282933 | Hs.23294 | hypothetical protein FLJ14393 | 3.1 |
| | 417868 | AI078534 | Hs.122592 | ESTs | 3.1 |
| | 458391 | AI792628 | Hs.133273 | ESTs | 3.1 |
| | 423346 | AI267677 | Hs.127416 | synaptotagmin 1 | 3.1 |
| 30 | 454486 | AW857077 | | gb:RC1-CT0302-140300-016-f04 CT0302 Homo | 3.1 |
| | 408341 | AW182952 | Hs.249957 | ESTs | 3.1 |
| | 410669 | AW805749 | Hs.318885 | superoxide dismutase 2, mitochondrial | 3.1 |
| | 404907 | | | | 3.1 |
| | 434910 | AI333863 | Hs.215474 | ESTs, Moderately similar to alternative1 | 3.1 |
| 35 | 436990 | AI149729 | Hs.120557 | ESTs | 3.1 |
| | 441921 | AI733376 | Hs.164478 | hypothetical protein FLJ21939 similar to | 3.1 |
| | 454673 | AW812807 | | gb:RC3-ST0186-070100-016-c04 ST0186 Homo | 3.1 |
| | 429470 | AI878901 | Hs.203862 | guanine nucleotide binding protein (G pr | 3.1 |
| 40 | 404345 | AA730407 | Hs.159156 | protocadherin 11 | 3.1 |
| | 408217 | AI433201 | Hs.279860 | tumor protein, translationally-controlled | 3.1 |
| | 417313 | AA195602 | | gb:zr32f09.r1 Soares_NhHMPu_S1 Homo sapi | 3.1 |
| | 427322 | AK002017 | Hs.176227 | hypothetical protein FLJ11155 | 3.1 |
| | 411003 | AA181018 | Hs.13056 | hypothetical protein FLJ13920 | 3.1 |
| | 425339 | AA936330 | Hs.198113 | ESTs | 3.1 |
| 45 | 426716 | NM_006379 | Hs.171921 | sema domain, immunoglobulin domain (Ig), | 3.1 |
| | 449078 | AK001256 | Hs.22975 | KIAA1576 protein | 3.1 |
| | 429608 | U49250 | Hs.210862 | T-box, brain, 1 | 3.1 |
| | 442308 | AA989402 | Hs.111 | fibroblast growth factor 9 (glia-activat | 3.1 |
| 50 | 428465 | AW970976 | Hs.293653 | ESTs | 3.1 |
| | 411666 | AF106564 | Hs.71346 | neurofilament 3 (150kD medium) | 3.1 |
| | 447965 | AW292577 | Hs.94445 | ESTs | 3.1 |
| | 413918 | AW015898 | Hs.71245 | ESTs | 3.1 |
| | 419682 | H13139 | Hs.92282 | paired-like homeodomain transcription fa | 3.1 |
| | 425810 | AI923627 | Hs.31903 | ESTs | 3.1 |
| 55 | 427865 | AA416931 | Hs.126065 | ESTs | 3.1 |
| | 429060 | AW139155 | Hs.194995 | hypothetical protein DKFZp434C0320 | 3.1 |
| | 430708 | U78308 | Hs.278485 | olfactory receptor, family 1, subfamily | 3.1 |
| | 448084 | AI467800 | Hs.271000 | ESTs, Weakly similar to I38022 hypotheti | 3.1 |
| | 454506 | AW847346 | | gb:RC0-CT0205-240999-021-e01 CT0205 Homo | 3.1 |
| 60 | 414629 | AA345824 | Hs.76688 | carboxylesterase 1 (monocyte/macrophage | 3.0 |
| | 422963 | M79141 | Hs.13234 | ESTs | 3.0 |
| | 417696 | BE241624 | Hs.82401 | CD69 antigen (p60, early T-cell activati | 3.0 |
| | 448175 | BE296174 | Hs.225160 | hypothetical protein FLJ13102 | 3.0 |
| | 414686 | BE409757 | Hs.23189 | ESTs, Moderately similar to TBB2_HUMAN T | 3.0 |
| 65 | 458360 | AI027207 | Hs.132253 | ESTs | 3.0 |
| | 451829 | AW964081 | Hs.247377 | ESTs | 3.0 |
| | 445179 | AI949743 | Hs.224768 | ESTs | 3.0 |
| | 433090 | AI720050 | Hs.145362 | immortalization-upregulated protein | 3.0 |
| | 432018 | AA524447 | Hs.152377 | ESTs | 3.0 |
| 70 | 407988 | N47760 | Hs.285107 | hypothetical protein FLJ13397 | 3.0 |
| | 405911 | | | | 3.0 |
| | 418808 | AI821836 | Hs.10359 | ESTs | 3.0 |
| | 431900 | AW972048 | Hs.192534 | ESTs | 3.0 |
| | 452893 | H18017 | Hs.22869 | ESTs, Moderately similar to KIAA1395 pro | 3.0 |
| 75 | 423952 | AW877787 | Hs.136102 | KIAA0853 protein | 3.0 |
| | 412000 | AW576555 | Hs.15780 | ATP-binding cassette, sub-family A (ABC1 | 3.0 |
| | 405793 | | | | 3.0 |
| | 410711 | AB002316 | Hs.65746 | KIAA0318 protein | 3.0 |
| | 411279 | AW884776 | | gb:QV4-OT0067-010300-121-d01 OT0067 Homo | 3.0 |
| 80 | 423957 | AW978309 | Hs.136235 | Homo sapiens cDNA FLJ13542 fis, clone PL | 3.0 |
| | 427071 | AA397958 | Hs.192719 | ESTs | 3.0 |
| | 434961 | AW974956 | | gb:EST387061 MAGE resequences, MAGN Homo | 3.0 |

TABLE 108:

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| | | | | |
|----|--------|---------|-------|---|
| 5 | 400685 | 8118768 | Minus | 72969-73050,73713-73800 |
| | 400865 | 1945037 | Minus | 44482-45526 |
| | 400878 | 9864757 | Plus | 31493-32842 |
| | 401024 | 8117489 | Plus | 60551-60802 |
| | 401315 | 9212516 | Minus | 198960-199619 |
| | 401485 | 7341723 | Plus | 68009-68209,68841-69077 |
| | 401521 | 7705251 | Plus | 9127-9234 |
| | 401532 | 7798785 | Plus | 124414-124950,125050-125418 |
| 10 | 401738 | 2982169 | Minus | 41547-41757 |
| | 401780 | 7249190 | Minus | 28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573 |
| | 401836 | 7534063 | Plus | 71981-72084 |
| | 401949 | 3492889 | Plus | 160728-161660 |
| | 402092 | 7249154 | Minus | 107533-108094 |
| 15 | 402176 | 7543687 | Minus | 10-750 |
| | 402546 | 7637348 | Plus | 24673-25170 |
| | 403092 | 8954241 | Plus | 174720-175016,175104-175406,175508-175813 |
| | 403180 | 7523976 | Minus | 63603-63759 |
| | 403323 | 8348082 | Minus | 120366-120845 |
| 20 | 403796 | 8099896 | Minus | 75073-77664 |
| | 404391 | 3135305 | Minus | 26030-26173,27852-27997 |
| | 404769 | 8099713 | Minus | 175801-176823 |
| | 404793 | 7232206 | Minus | 61087-61590 |
| | 404828 | 6580415 | Minus | 26291-27253 |
| 25 | 404907 | 7331453 | Minus | 102880-103828 |
| | 404958 | 7407941 | Minus | 2731-4531 |
| | 405071 | 7708797 | Minus | 11115-11552 |
| | 405130 | 8516045 | Plus | 150235-150449 |
| | 405138 | 8576241 | Plus | 90303-90516 |
| 30 | 405354 | 2642452 | Plus | 52213-53089 |
| | 405377 | 5649375 | Plus | 216656-216848 |
| | 405629 | 4508116 | Minus | 101678-101866 |
| | 405678 | 4079670 | Plus | 151821-152027 |
| | 405793 | 1405887 | Minus | 89197-89453 |
| 35 | 405800 | 2791346 | Plus | 19271-19813 |
| | 405867 | 6758731 | Minus | 74553-75173 |
| | 405911 | 6758795 | Plus | 101008-101643 |
| | 405977 | 8247789 | Minus | 135548-136177 |

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|----|---|--|--|--|--|
| 40 | TABLE 11A: ABOUT 533 CNS-ENRICHED GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS TISSUES | | | | |
| | Table 11A lists about 533 CNS-enriched genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal CNS to "average" glioblastoma was greater than or equal to 2. The "average" normal CNS level was set to the 75th percentile amongst various normal CNS tissues. The "average" glioblastoma level was set to the 85th percentile amongst various tumor samples. To enrich for CNS specific genes, the ratio of "average" CNS to "average" non-CNS normal adult tissues was calculated to be greater than or equal to 2. The "average" CNS level was set to the 85th percentile amongst various CNS tissues. The "average" normal non-CNS adult tissue level was set to the 85th percentile amongst various non-CNS normal tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratios were evaluated. | | | | |
| 45 | Pkey: Unique Eos probeset identifier number | | | | |
| | ExAccn: Exemplar Accession number, Genbank accession number | | | | |
| 50 | UnigeneID: Unigene number | | | | |
| | Unigene Title: Unigene gene title | | | | |
| | R1: Ratio of 75th percentile normal central nervous system tissue to 85th percentile tumor | | | | |
| | R2: Ratio of 85th percentile central nervous system tissue to 85th percentile normal body tissue | | | | |

| | | | | | | |
|----|--------|-----------|-----------|--|------|------|
| 55 | Pkey | ExAccn | UnigeneID | Unigene Title | R1 | R2 |
| | 417275 | X63578 | Hs.295449 | parvalbumin | 29.0 | 30.0 |
| | 430829 | AW451999 | Hs.194024 | ESTs | 25.7 | 6.2 |
| | 410657 | AF063228 | Hs.65248 | dynein, cytoplasmic, intermediate polype | 22.6 | 25.8 |
| | 419954 | O14720 | Hs.93883 | myelin protein zero (Charcot-Marie-Tooth | 21.2 | 30.3 |
| 60 | 416133 | NM_001683 | Hs.89512 | ATPase, Ca++ transporting, plasma membra | 15.5 | 16.8 |
| | 416018 | AW138239 | Hs.78977 | proprotein convertase subtilisin/kexin t | 15.2 | 18.0 |
| | 417167 | AW206437 | Hs.4290 | ESTs | 14.8 | 17.7 |
| | 433940 | H05129 | Hs.7459 | cyclic AMP-regulated phosphoprotein, 21 | 13.4 | 18.1 |
| | 413324 | V00571 | Hs.75294 | corticotropin releasing hormone | 13.1 | 18.0 |
| 65 | 439830 | AA846666 | Hs.151489 | ESTs, Weakly similar to XE7_HUMAN PROTEI | 12.6 | 16.5 |
| | 408068 | AW148652 | Hs.167398 | ESTs | 12.6 | 16.9 |
| | 429096 | AB011106 | Hs.196012 | KIAA0534 protein | 12.2 | 21.1 |
| | 412638 | AA910199 | Hs.203838 | ESTs | 12.2 | 16.0 |
| | 442593 | R39804 | Hs.31961 | ESTs | 10.8 | 15.0 |
| 70 | 446353 | AI290919 | Hs.153661 | ESTs | 10.4 | 13.2 |
| | 426365 | AA376667 | Hs.10283 | RNA binding motif protein 88 | 10.0 | 5.9 |
| | 414937 | R38698 | Hs.12382 | ESTs | 10.0 | 10.8 |
| | 419643 | F06066 | Hs.91791 | chromosome 11 open reading frame 25 | 9.5 | 10.9 |
| | 412454 | R55745 | Hs.167330 | ESTs | 9.5 | 14.1 |
| 75 | 439366 | AF100143 | Hs.6540 | fibroblast growth factor 13 | 9.4 | 12.3 |
| | 441790 | AW294909 | Hs.132208 | ESTs | 9.2 | 3.2 |
| | 448117 | H49129 | Hs.172982 | ESTs | 9.1 | 12.8 |
| | 433558 | AA833757 | Hs.201769 | ESTs, Weakly similar to T24435 hypotheti | 9.0 | 14.7 |
| 80 | 412453 | R20205 | Hs.167330 | ESTs | 9.0 | 13.7 |
| | 408920 | AL120071 | Hs.48998 | fibronectin leucine rich transmembrane p | 8.9 | 17.3 |
| | 409031 | AA376836 | Hs.76728 | ESTs | 8.7 | 8.6 |
| | 446544 | AI631932 | Hs.7047 | ESTs, Weakly similar to Unknown [H.sapie | 8.2 | 20.0 |
| | 439480 | AL038511 | Hs.125316 | ESTs, Weakly similar to S33990 finger pr | 8.2 | 8.3 |

| | | | | | | |
|----|--------|-----------|-----------|--|-----|------|
| | 410200 | AA082557 | Hs.101915 | Stargardt disease 3 (autosomal dominant) | | |
| | 408428 | NM_014787 | Hs.44896 | DnaJ (Hsp40) homolog, subfamily B, membe | 8.0 | 8.9 |
| | 437073 | AJ885608 | Hs.94122 | ESTs | 7.9 | 9.6 |
| 5 | 408434 | AW195317 | Hs.107716 | hypothetical protein FLJ22344 | 7.9 | 11.3 |
| | 440209 | H05049 | Hs.22269 | neurixin 3 | 7.9 | 16.4 |
| | 408119 | W26213 | Hs.101672 | ESTs, Weakly similar to T00331 hypotheti | 7.8 | 34.3 |
| | 429611 | AJ889077 | Hs.211388 | Homo sapiens BAC clone CTB-60N22 from 7q | 7.8 | 9.0 |
| | 423440 | R25234 | Hs.143434 | contactin 1 | 7.7 | 5.0 |
| 10 | 445148 | AI214510 | Hs.145304 | ESTs | 7.7 | 9.9 |
| | 416294 | D86980 | Hs.79170 | KIAA0227 protein | 7.6 | 9.1 |
| | 424087 | N69333 | Hs.143434 | contactin 1 | 7.6 | 7.6 |
| | 437479 | R61866 | Hs.101277 | ESTs | 7.6 | 10.3 |
| | 430573 | AA744550 | Hs.136345 | ESTs | 7.5 | 9.3 |
| 15 | 448958 | AB020651 | Hs.22653 | KIAA0844 protein | 7.1 | 2.8 |
| | 419474 | AW968619 | Hs.155849 | ESTs | 7.1 | 10.4 |
| | 423605 | AF047826 | Hs.129887 | cadherin 19, type 2 | 7.1 | 3.0 |
| | 433098 | AW190593 | Hs.151143 | ESTs | 7.0 | 6.9 |
| | 449511 | AI436187 | Hs.296261 | guanine nucleotide binding protein (G pr | 7.0 | 9.2 |
| 20 | 428414 | AL049980 | Hs.184216 | DKFZP564C152 protein | 6.9 | 3.1 |
| | 443155 | R54485 | Hs.23772 | ESTs | 6.8 | 5.0 |
| | 450561 | R49674 | Hs.25909 | ESTs | 6.8 | 3.5 |
| | 433068 | NM_006456 | Hs.288215 | sialyltransferase | 6.8 | 8.1 |
| | 423589 | AA328082 | Hs.209569 | ESTs | 6.8 | 2.0 |
| 25 | 415681 | AI379882 | Hs.72630 | ESTs | 6.6 | 10.5 |
| | 413510 | F13044 | | gb:HSC3HH101 normalized infant brain cDN | 6.5 | 9.0 |
| | 427992 | Y15014 | Hs.181353 | UDP-Gal:betaGlcNAc beta 1,3-galactosyltr | 6.4 | 7.1 |
| | 450642 | R39773 | Hs.7130 | copine IV | 6.4 | 9.5 |
| | 429322 | D86984 | Hs.199243 | KIAA0231 protein | 6.4 | 5.7 |
| 30 | 447482 | AB033059 | Hs.18705 | KIAA1233 protein | 6.4 | 8.2 |
| | 446129 | AW244073 | Hs.145946 | ESTs | 6.4 | 2.3 |
| | 421913 | AI934365 | Hs.109439 | osteoglycin (osteoinductive factor, mime | 6.3 | 8.3 |
| | 434273 | AA913143 | Hs.26303 | ESTs | 6.3 | 2.1 |
| | 408480 | AI350337 | Hs.164568 | fibroblast growth factor 7 (keratinocyte | 6.2 | 10.3 |
| 35 | 451301 | AI769514 | Hs.209890 | EST | 6.2 | 3.5 |
| | 438356 | AA805530 | Hs.48527 | ESTs | 6.2 | 12.4 |
| | 426388 | AW081394 | Hs.97103 | ESTs | 6.2 | 8.1 |
| | 452502 | AI904296 | | gb:PM-BT046-220199-286_1 BT046 Homo sapi | 6.2 | 8.6 |
| 40 | 408165 | AL137573 | Hs.43143 | Homo sapiens mRNA; cDNA DKFZp564A2463 (I | 6.1 | 2.8 |
| | 442979 | AW440782 | Hs.174743 | ESTs | 6.1 | 6.3 |
| | 408713 | NM_001248 | Hs.47042 | ectonucleoside triphosphate diphosphohyd | 6.1 | 6.3 |
| | 430004 | U27768 | Hs.227571 | regulator of G-protein signalling 4 | 6.0 | 3.8 |
| | 425087 | R62424 | Hs.126059 | ESTs | 5.9 | 21.4 |
| | 441695 | T12411 | Hs.183745 | hypothetical protein FLJ13456 | 5.9 | 8.1 |
| 45 | 417175 | R44558 | Hs.94002 | ESTs | 5.9 | 3.1 |
| | 437483 | AL390174 | | gb:Homo sapiens mRNA; cDNA DKFZp547J184 | 5.8 | 12.5 |
| | 436427 | AI344378 | Hs.143399 | ESTs | 5.8 | 2.2 |
| | 450382 | AA397658 | Hs.60257 | Homo sapiens cDNA FLJ13598 fis, clone PL | 5.8 | 13.8 |
| 50 | 408478 | NM_000806 | Hs.45740 | gamma-aminobutyric acid (GABA) A recepto | 5.7 | 4.4 |
| | 442676 | AI733585 | Hs.130897 | ESTs | 5.7 | 12.5 |
| | 446443 | AV659082 | Hs.134228 | ESTs | 5.7 | 6.8 |
| | 459080 | AW192083 | Hs.290855 | ESTs | 5.7 | 6.4 |
| | 431984 | AL080239 | Hs.272284 | Human DNA sequence from clone GS1-256O22 | 5.6 | 15.6 |
| 55 | 428356 | AL046991 | Hs.10338 | ESTs | 5.6 | 8.2 |
| | 417877 | AI025829 | Hs.86320 | ESTs | 5.6 | 6.2 |
| | 429290 | AF203032 | Hs.198760 | neurofilament, heavy polypeptide (200kD) | 5.4 | 4.9 |
| | 408556 | U49516 | Hs.46362 | 5-hydroxytryptamine (serotonin) receptor | 5.3 | 13.1 |
| | 431930 | AB035301 | Hs.272211 | cadherin 7, type 2 | 5.3 | 6.6 |
| 60 | 438285 | AA782845 | Hs.22790 | ESTs | 5.2 | 6.0 |
| | 439901 | N73885 | Hs.124169 | ESTs | 5.2 | 7.3 |
| | 449222 | AW293984 | Hs.197621 | ESTs | 5.2 | 2.7 |
| | 408016 | AW136827 | Hs.256096 | ESTs | 5.2 | 8.1 |
| | 436953 | AW959074 | Hs.23648 | Homo sapiens cDNA FLJ13097 fis, clone NT | 5.1 | 2.5 |
| 65 | 436773 | AW078629 | Hs.82110 | PC4 and SFRS1 interacting protein 1 | 5.1 | 3.0 |
| | 409263 | AA069573 | Hs.50319 | ESTs | 5.1 | 7.3 |
| | 453830 | AA534296 | Hs.20953 | ESTs | 5.1 | 12.9 |
| | 441535 | AL135735 | Hs.7885 | phosphatidylinositol binding clathrin as | 5.1 | 3.4 |
| | 416490 | AF090116 | Hs.79348 | regulator of G-protein signalling 7 | 5.0 | 4.8 |
| 70 | 417284 | N62889 | Hs.107242 | Homo sapiens cDNA FLJ12965 fis, clone NT | 5.0 | 20.1 |
| | 448605 | AL109678 | Hs.21597 | Homo sapiens mRNA full length insert cDN | 5.0 | 3.9 |
| | 442240 | AI791883 | Hs.292719 | ESTs | 5.0 | 6.1 |
| | 427972 | AA864870 | Hs.181304 | putative gene product | 4.9 | 6.7 |
| | 416040 | AW819158 | Hs.289044 | Homo sapiens cDNA FLJ12048 fis, clone HE | 4.9 | 5.2 |
| | 444922 | AI921750 | Hs.144871 | Homo sapiens cDNA FLJ13752 fis, clone PL | 4.9 | 2.8 |
| 75 | 408936 | AL138043 | Hs.293549 | ESTs | 4.8 | 3.7 |
| | 414943 | D80647 | Hs.124193 | ESTs | 4.8 | 6.6 |
| | 429254 | H10133 | Hs.91846 | hypothetical protein DKFZp761C121 | 4.8 | 3.1 |
| | 407906 | AA369665 | Hs.41185 | Homo sapiens mRNA; cDNA DKFZp564O1262 (I | 4.8 | 2.3 |
| | 416577 | BE063207 | Hs.79381 | grancalcin | 4.8 | 9.1 |
| 80 | 420480 | AL137361 | Hs.98173 | hypothetical protein | 4.7 | 2.2 |
| | 404793 | | | | 4.7 | 2.8 |
| | 430895 | U66581 | Hs.248121 | G protein-coupled receptor 22 | 4.6 | 2.2 |
| | 438571 | AW020775 | Hs.56022 | ESTs | 4.6 | 7.4 |
| | 444585 | AW170015 | Hs.6594 | ESTs | 4.6 | 5.4 |
| | | | | | 4.6 | 6.0 |

| | | | | | | |
|----|--------|-----------|-----------|---|-----|------|
| 5 | 414272 | AI651603 | Hs.46988 | ESTs | 4.5 | 2.2 |
| | 414699 | AI815523 | Hs.76930 | synuclein, alpha (non A4 component of am | 4.5 | 30.9 |
| | 423449 | AI497900 | Hs.33067 | ESTs | 4.5 | 20.8 |
| | 433521 | T66087 | Hs.112482 | Homo sapiens unknown mRNA sequence | 4.4 | 2.0 |
| | 429876 | AB028977 | Hs.225974 | KIAA1054 protein | 4.4 | 19.2 |
| 10 | 429726 | AW628326 | Hs.27151 | ESTs | 4.4 | 10.2 |
| | 449093 | AB035356 | Hs.22998 | neurexin 1 | 4.4 | 9.4 |
| | 415716 | N59294 | Hs.179662 | nucleosome assembly protein 1-like 1 | 4.4 | 15.1 |
| | 419656 | AB002314 | Hs.92025 | KIAA0316 gene product | 4.4 | 8.2 |
| | 425864 | U56420 | Hs.159903 | olfactory receptor, family 5, subfamily | 4.4 | 2.4 |
| 15 | 435078 | AIW518888 | Hs.40937 | ESTs | 4.4 | 5.7 |
| | 432712 | AB016247 | Hs.288031 | sterol-C5-desaturase (fungal ERG3, delta | 4.3 | 5.9 |
| | 426867 | AA460967 | Hs.22668 | ESTs | 4.3 | 6.0 |
| | 412112 | BE180342 | | gb:RC3-HT0622-130400-012-s07 HT0622 Homo | 4.3 | 3.2 |
| | 410171 | H07892 | Hs.12431 | ESTs | 4.3 | 5.3 |
| 20 | 442339 | BE299668 | Hs.227591 | ESTs, Weakly similar to 1901303A Leu zip | 4.2 | 5.0 |
| | 421249 | AA285362 | | gb:HTH277 HTCDL1 Homo sapiens cDNA 5/3 | 4.2 | 3.5 |
| | 422528 | AB011182 | Hs.118087 | KIAA0610 protein | 4.2 | 3.9 |
| | 434460 | AA478486 | Hs.3852 | KIAA0368 protein | 4.1 | 8.3 |
| | 410362 | H04811 | Hs.93164 | proprotein convertase subtilisin/kexin 1 | 4.1 | 7.0 |
| 25 | 449754 | H00820 | Hs.30977 | ESTs, Weakly similar to B34087 hypothesi | 4.1 | 3.9 |
| | 408496 | AI683802 | Hs.136182 | ESTs | 4.1 | 4.7 |
| | 434101 | AA625205 | Hs.259599 | KIAA1622 protein | 4.1 | 6.3 |
| | 430212 | AA469153 | | gb:nc6704.s1 NCL_CGAP_Pr1 Homo sapiens | 4.0 | 2.5 |
| | 453165 | S74727 | Hs.32042 | aspartoacylase (aminoacylase 2, Canavan | 4.0 | 7.4 |
| 30 | 456407 | AW968614 | | gb:EST380690 MAGE resequences, MAGJ Homo | 4.0 | 5.1 |
| | 441869 | NM_003947 | Hs.8004 | huntingtin-associated protein interactin | 4.0 | 32.3 |
| | 429628 | H09604 | Hs.13268 | ESTs | 4.0 | 4.5 |
| | 410087 | F12079 | Hs.332579 | ESTs | 4.0 | 6.9 |
| | 419910 | AA662913 | Hs.190173 | ESTs, Weakly similar to A46010 X-linked | 4.0 | 2.6 |
| 35 | 441005 | Z41305 | Hs.303172 | Homo sapiens mRNA; cDNA DKFZp547G133 (fr | 3.9 | 21.7 |
| | 412677 | AW029608 | Hs.17384 | ESTs | 3.9 | 2.2 |
| | 453341 | AI758912 | Hs.296341 | adenylyl cyclase-associated protein 2 | 3.9 | 7.2 |
| | 416854 | H40164 | Hs.80296 | Purkinje cell protein 4 | 3.9 | 2.2 |
| | 414666 | NM_004466 | Hs.76828 | glypican 5 | 3.8 | 6.2 |
| 40 | 418217 | AI910647 | Hs.13442 | ESTs | 3.8 | 3.2 |
| | 421855 | F06504 | Hs.27384 | ESTs, Moderately similar to ALU4_HUMAN A | 3.8 | 2.2 |
| | 414764 | AW013887 | Hs.72047 | ESTs | 3.8 | 10.7 |
| | 433629 | R13140 | Hs.13359 | ESTs | 3.7 | 2.7 |
| | 424738 | AI963740 | Hs.46826 | ESTs | 3.7 | 2.1 |
| 45 | 407706 | AA191085 | Hs.26612 | ESTs, Moderately similar to S23650 retro | 3.7 | 5.3 |
| | 437268 | AI754847 | Hs.227571 | regulator of G-protein signalling 4 | 3.7 | 53.7 |
| | 423135 | N67655 | Hs.26411 | ESTs | 3.7 | 21.7 |
| | 446818 | AI342668 | Hs.279765 | ESTs | 3.7 | 2.6 |
| | 427562 | R56424 | Hs.26534 | ESTs | 3.6 | 3.6 |
| 50 | 439274 | AF086092 | Hs.48372 | ESTs | 3.6 | 34.5 |
| | 452381 | H23329 | Hs.290880 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.6 | 6.0 |
| | 422897 | AA679784 | Hs.4290 | ESTs | 3.6 | 5.1 |
| | 429656 | X05608 | Hs.211584 | neurofilament, light polypeptide (68kD) | 3.6 | 24.6 |
| | 417154 | AI674701 | Hs.21388 | ESTs | 3.6 | 5.8 |
| 55 | 447176 | Z42549 | Hs.160893 | ESTs | 3.6 | 6.4 |
| | 405977 | | | | 3.6 | 3.9 |
| | 423568 | NM_005256 | Hs.129818 | growth arrest-specific 2 | 3.6 | 2.5 |
| | 441235 | AI884586 | Hs.135570 | Homo sapiens cDNA: FLJ21268 fs, clone C | 3.6 | 5.4 |
| | 426775 | AA384564 | Hs.108829 | ESTs | 3.6 | 3.4 |
| 60 | 414831 | M31158 | Hs.77439 | protein kinase, cAMP-dependent, regulato | 3.6 | 2.8 |
| | 425153 | AW023193 | Hs.27046 | ESTs | 3.6 | 4.9 |
| | 446495 | D60923 | Hs.153460 | ESTs | 3.5 | 9.8 |
| | 445898 | AF070623 | Hs.13423 | Homo sapiens clone 24468 mRNA sequence | 3.5 | 16.6 |
| | 416421 | AA134006 | Hs.79306 | eukaryotic translation initiation factor | 3.5 | 5.0 |
| 65 | 418207 | C14685 | Hs.34772 | ESTs | 3.5 | 16.0 |
| | 425383 | D83407 | Hs.156007 | Down syndrome critical region gene 1-lik | 3.5 | 6.2 |
| | 417027 | AA192306 | Hs.23926 | triadin | 3.5 | 2.5 |
| | 408367 | AK001178 | Hs.44424 | homolog of rat orphan transporter v7-3 | 3.5 | 5.3 |
| | 408776 | AA057365 | Hs.63356 | ESTs, Weakly similar to I38022 hypothesi | 3.5 | 5.5 |
| 70 | 453220 | AB033089 | Hs.32452 | Homo sapiens mRNA for KIAA1263 protein, | 3.5 | 23.6 |
| | 419347 | C15944 | Hs.90005 | superior cervical ganglia, neural specifi | 3.5 | 42.3 |
| | 433803 | AI823593 | Hs.27688 | ESTs | 3.4 | 3.6 |
| | 450715 | AI266484 | Hs.31570 | ESTs, Weakly similar to KIAA1324 protein | 3.4 | 4.1 |
| | 415076 | NM_000857 | Hs.77890 | guanylate cyclase 1, soluble, beta 3 | 3.4 | 9.8 |
| 75 | 423826 | U20325 | Hs.1707 | cocaine- and amphetamine-regulated trans | 3.4 | 4.7 |
| | 427173 | BE255017 | Hs.97540 | ESTs | 3.4 | 2.4 |
| | 446092 | N33522 | Hs.145894 | ESTs | 3.4 | 3.5 |
| | 416868 | AI656856 | Hs.292597 | ESTs | 3.4 | 4.5 |
| | 458234 | BE551408 | Hs.127196 | ESTs | 3.4 | 4.5 |
| 80 | 434053 | AW445136 | Hs.134946 | ESTs | 3.4 | 3.9 |
| | 428536 | AI143139 | Hs.2288 | visinin-like 1 | 3.3 | 42.3 |
| | 410366 | AI267589 | Hs.302689 | hypothetical protein | 3.3 | 14.4 |
| | 425785 | T27017 | Hs.159528 | Homo sapiens clone 24400 mRNA sequence | 3.3 | 4.6 |
| | 434998 | AW975157 | Hs.26037 | ESTs | 3.3 | 4.7 |
| | 456359 | AI967991 | Hs.93574 | homeo box D3 | 3.3 | 4.4 |
| | 426527 | NM_001037 | Hs.170238 | sodium channel, voltage-gated, type 1, b | 3.3 | 5.2 |
| | 400302 | N48056 | Hs.1915 | folate hydrolase (prostate-specific memb | 3.3 | 9.0 |

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|----|--------|-----------|-----------|---|-----|------|
| 5 | 419875 | AA853410 | Hs.93557 | proenkephalin | | |
| | 444612 | AW138111 | Hs.22902 | ESTs | 3.3 | 3.6 |
| | 415242 | R45985 | Hs.295014 | ESTs | 3.3 | 3.0 |
| | 421640 | AW96652 | | gb:EST378726 MAGE resequences, MAGI Homo | 3.2 | 2.2 |
| | 408806 | AW847814 | Hs.289005 | Homo sapiens cDNA: FLJ21532 fis, clone C | 3.2 | 3.8 |
| 10 | 445015 | T30968 | Hs.13531 | hypothetical protein FLJ10971 | 3.2 | 2.4 |
| | 425495 | AA358454 | Hs.78026 | ESTs, Weakly similar to similar to ankyr | 3.2 | 3.2 |
| | 403092 | | | | 3.2 | 2.2 |
| | 452971 | AI873878 | Hs.91789 | ESTs | 3.2 | 2.9 |
| | 454100 | AI693231 | Hs.126043 | chromosome 21 open reading frame 51 | 3.2 | 4.5 |
| 15 | 448440 | AA173467 | Hs.62402 | p21/Cdc42/Rac1-activated kinase 1 (yeast | 3.2 | 2.7 |
| | 421200 | AA284811 | Hs.264433 | ESTs | 3.2 | 2.8 |
| | 440827 | AI733110 | Hs.128128 | ESTs | 3.2 | 2.7 |
| | 429809 | AL162010 | Hs.223603 | Homo sapiens mRNA; cDNA DKFZp761D09121 (| 3.2 | 2.1 |
| | 420156 | AW449258 | Hs.6187 | ESTs | 3.2 | 4.3 |
| 20 | 457535 | AA609685 | Hs.278672 | membrane component, chromosome 11, surfa | 3.2 | 19.0 |
| | 419956 | AL137939 | Hs.40096 | ESTs | 3.2 | 2.0 |
| | 423930 | AA332697 | Hs.42721 | ESTs | 3.1 | 8.7 |
| | 417858 | AI078534 | Hs.122592 | ESTs | 3.1 | 2.7 |
| | 423346 | AI267677 | Hs.127416 | synaptojanin 1 | 3.1 | 12.6 |
| 25 | 441921 | AI733376 | Hs.164478 | hypothetical protein FLJ21939 similar to | 3.1 | 12.0 |
| | 429470 | AI878901 | Hs.203862 | guanine nucleotide binding protein (G pr | 3.1 | 4.3 |
| | 408217 | AI433201 | Hs.279860 | tumor protein, translationally-controlled | 3.1 | 5.3 |
| | 427322 | AK002017 | Hs.176227 | hypothetical protein FLJ11155 | 3.1 | 7.1 |
| | 449078 | AK001256 | Hs.22975 | KIAA1576 protein | 3.1 | 6.3 |
| 30 | 429608 | U49250 | Hs.210862 | T-box, brain, 1 | 3.1 | 30.1 |
| | 442308 | AA989402 | Hs.111 | fibroblast growth factor 9 (glia-activat | 3.1 | 2.2 |
| | 411666 | AF106564 | Hs.71346 | neurofilament 3 (150kD medium) | 3.1 | 3.0 |
| | 427865 | AA416931 | Hs.126065 | ESTs | 3.1 | 10.9 |
| | 430708 | U78308 | Hs.278485 | olfactory receptor, family 1, subfamily | 3.1 | 7.5 |
| 35 | 451829 | AW964081 | Hs.247377 | ESTs | 3.1 | 3.4 |
| | 405911 | | | | 3.0 | 6.2 |
| | 418808 | AI821836 | Hs.10359 | ESTs | 3.0 | 2.4 |
| | 452893 | H18017 | Hs.22869 | ESTs, Moderately similar to KIAA1395 pro | 3.0 | 6.2 |
| | 423952 | AW877787 | Hs.136102 | KIAA0853 protein | 3.0 | 5.1 |
| 40 | 412000 | AW576555 | Hs.15780 | ATP-binding cassette, sub-family A (ABC1 | 3.0 | 2.1 |
| | 405793 | | | | 3.0 | 2.1 |
| | 410711 | AB002316 | Hs.65746 | KIAA0318 protein | 3.0 | 2.7 |
| | 427071 | AA397958 | Hs.192719 | ESTs | 3.0 | 14.3 |
| | 453534 | NM_014796 | Hs.33187 | KIAA0748 gene product | 3.0 | 2.1 |
| 45 | 413903 | AA496493 | Hs.23136 | ESTs | 3.0 | 14.5 |
| | 426866 | U02330 | Hs.172816 | neuregulin 1 | 3.0 | 2.2 |
| | 434945 | AB033065 | Hs.4280 | KIAA1239 protein | 3.0 | 11.3 |
| | 412639 | AW961284 | Hs.296235 | ESTs | 3.0 | 3.5 |
| | 453590 | AF150278 | Hs.33578 | KIAA0820 protein | 2.9 | 4.9 |
| 50 | 414502 | AL133721 | Hs.224680 | ESTs | 2.9 | 33.1 |
| | 434367 | AB020700 | Hs.3830 | KIAA0893 protein | 2.9 | 2.3 |
| | 425121 | AI797511 | Hs.154679 | synaptotagmin I | 2.9 | 23.1 |
| | 412494 | AL133900 | Hs.792 | ADP-ribosylation factor domain protein 1 | 2.9 | 8.1 |
| | 401213 | | | | 2.9 | 20.8 |
| 55 | 401028 | AW673312 | Hs.50848 | hypothetical protein FLJ20331 | 2.9 | 3.2 |
| | 415191 | AA190381 | Hs.120810 | ESTs | 2.9 | 3.4 |
| | 449275 | AW450848 | Hs.205457 | periaxin | 2.9 | 3.0 |
| | 419863 | AW952691 | Hs.93485 | Homo sapiens mRNA; cDNA DKFZp761D191 (fr | 2.9 | 5.6 |
| | 411421 | BE272110 | Hs.21177 | ESTs | 2.9 | 35.0 |
| 60 | 430865 | AI073424 | Hs.5232 | HSPC125 protein | 2.9 | 2.0 |
| | 437486 | AW952089 | Hs.5636 | RABGA, member RAS oncogene family | 2.9 | 11.4 |
| | 442357 | AI458586 | Hs.135706 | ESTs | 2.9 | 2.2 |
| | 408274 | R17315 | | gb:yg12g11.1.1 Soares infant brain 1N1B H | 2.9 | 6.0 |
| | 444185 | AW298350 | Hs.66020 | ESTs | 2.9 | 2.2 |
| 65 | 420173 | AA256151 | Hs.22999 | ESTs | 2.8 | 5.0 |
| | 428358 | AA993222 | Hs.101915 | Stargardt disease 3 (autosomal dominant) | 2.8 | 5.1 |
| | 447252 | R90916 | Hs.12449 | Homo sapiens transmembrane protein HTMP1 | 2.8 | 7.0 |
| | 440260 | AI972867 | Hs.7130 | copine IV | 2.8 | 4.4 |
| | 417084 | H08370 | Hs.33067 | ESTs | 2.8 | 10.6 |
| 70 | 438257 | AW474419 | Hs.224794 | ESTs | 2.8 | 8.4 |
| | 441934 | T23939 | Hs.7344 | ESTs | 2.8 | 2.8 |
| | 447885 | F11528 | Hs.303172 | Homo sapiens mRNA; cDNA DKFZp547G133 (fr | 2.8 | 6.2 |
| | 423552 | AF107028 | Hs.129783 | sodium channel, voltage-gated, type II, | 2.8 | 3.5 |
| | 450940 | AI744943 | Hs.143209 | ESTs, Weakly similar to I38022 hypothesi | 2.8 | 3.4 |
| 75 | 410011 | AB020641 | Hs.57856 | PFTAIIE protein kinase 1 | 2.8 | 14.4 |
| | 445887 | AI263105 | Hs.145597 | ESTs | 2.8 | 21.7 |
| | 425494 | N55540 | Hs.78026 | ESTs, Weakly similar to similar to ankyr | 2.8 | 5.1 |
| | 438202 | AW169287 | Hs.22588 | ESTs | 2.8 | 2.4 |
| | 436199 | R38946 | Hs.127951 | hypothetical protein FLJ14503 | 2.8 | 11.9 |
| 80 | 434826 | AF155661 | Hs.22265 | pyruvate dehydrogenase phosphatase | 2.8 | 6.0 |
| | 415462 | R52692 | Hs.12698 | ESTs | 2.8 | 2.4 |
| | 418070 | NM_000844 | Hs.83407 | glutamate receptor, metabotropic 7 | 2.8 | 3.4 |
| | 432149 | AW614326 | Hs.157022 | ESTs, Weakly similar to T34549 probable | 2.8 | 4.5 |
| | 430371 | D87466 | Hs.240112 | KIAA0276 protein | 2.8 | 9.5 |
| | 437357 | AL359559 | Hs.331666 | Homo sapiens mRNA; cDNA DKFZp762O2215 (f | 2.8 | 7.0 |
| | 415838 | R44336 | Hs.7093 | ESTs | 2.7 | 2.5 |
| | 438675 | AA813725 | Hs.213568 | ESTs | 2.7 | 3.6 |
| | | | | | 2.7 | 2.5 |

| | | | | | | |
|----|--------|-----------|-----------|--|-----|------|
| | 419558 | AW953679 | | gb:EST365749 MAGE resequences, MAGC Homo | 2.7 | 3.1 |
| | 446318 | AI949389 | Hs.18067 | ESTs | 2.7 | 4.1 |
| | 445183 | AB007877 | Hs.12385 | KIAA0417 gene product | 2.7 | 5.3 |
| | 457012 | R41480 | Hs.127630 | ESTs | 2.7 | 19.0 |
| 5 | 431988 | AC002302 | Hs.77202 | protein kinase C, beta 1 | 2.7 | 7.2 |
| | 430223 | NM_002514 | Hs.235935 | nephroblastoma overexpressed gene | 2.7 | 2.8 |
| | 447932 | AA837474 | Hs.20021 | vesicle-associated membrane protein 1 (s | 2.7 | 3.8 |
| | 450214 | BE439763 | Hs.227571 | regulator of G-protein signalling 4 | 2.7 | 6.9 |
| | 434731 | AA648049 | Hs.121518 | ESTs | 2.7 | 5.0 |
| 10 | 428839 | AI767756 | Hs.82302 | Homo sapiens cDNA FLJ14814 fis, clone NT | 2.7 | 5.2 |
| | 407709 | AA456135 | Hs.23023 | ESTs | 2.7 | 2.5 |
| | 422420 | U03398 | Hs.1524 | tumor necrosis factor (ligand) superfamily | 2.7 | 3.3 |
| | 443305 | AI050693 | Hs.133318 | ESTs | 2.7 | 5.9 |
| | 435648 | H24347 | Hs.27524 | ESTs | 2.7 | 15.0 |
| 15 | 418407 | AL044818 | Hs.84928 | nuclear transcription factor Y, beta | 2.7 | 2.7 |
| | 436771 | AW975687 | Hs.292979 | ESTs | 2.7 | 6.0 |
| | 428689 | NM_014351 | Hs.189810 | suffortranferase family 4A, member 1 | 2.7 | 4.8 |
| | 440503 | NM_006539 | Hs.7235 | calcium channel, voltage-dependent, gamma | 2.7 | 4.4 |
| | 441006 | AW605267 | Hs.7627 | CGI-60 protein | 2.7 | 3.1 |
| 20 | 410330 | AW023630 | Hs.46786 | ESTs | 2.6 | 29.5 |
| | 434398 | AA121098 | Hs.3838 | serum-inducible kinase | 2.6 | 2.6 |
| | 438831 | BE263273 | Hs.6439 | synapsin II | 2.6 | 7.8 |
| | 419066 | Z98492 | Hs.6975 | PRO1073 protein | 2.6 | 3.4 |
| | 412643 | AW971239 | Hs.293982 | ESTs | 2.6 | 2.2 |
| 25 | 430456 | AA314998 | Hs.241503 | hypothetical protein | 2.6 | 17.9 |
| | 416498 | U33632 | Hs.79351 | potassium channel, subfamily K, member 1 | 2.6 | 2.9 |
| | 401421 | | | | 2.6 | 2.0 |
| | 419530 | X98330 | Hs.90821 | ryanodine receptor 2 (cardiac) | 2.6 | 4.2 |
| | 441817 | AW969706 | Hs.293332 | ESTs | 2.6 | 3.8 |
| 30 | 439203 | AA448930 | Hs.8453 | KIAA1587 protein | 2.6 | 4.2 |
| | 426054 | U12431 | Hs.166109 | ELAV (embryonic lethal, abnormal vision, | 2.6 | 5.1 |
| | 444583 | AW994403 | Hs.100861 | hypothetical protein FLJ14600 | 2.6 | 3.7 |
| | 417919 | AI928203 | Hs.86379 | ESTs | 2.6 | 3.0 |
| | 434293 | NM_004445 | Hs.3796 | EphB6 | 2.6 | 3.2 |
| 35 | 431716 | D89053 | Hs.268012 | fatty-acid-Coenzyme A ligase, long-chain | 2.6 | 6.4 |
| | 443037 | AW500305 | Hs.299166 | syntaxin 7 | 2.6 | 2.2 |
| | 440736 | D56919 | Hs.265848 | myomegalin | 2.6 | 7.1 |
| | 404548 | | | | 2.6 | 3.0 |
| | 429995 | AA463571 | | gb:zx72e09.r1 Soares_total_fetus_Nb2HF8_ | 2.6 | 3.5 |
| 40 | 436508 | AW604381 | Hs.121121 | ESTs, Weakly similar to S00755 pleckstri | 2.6 | 3.9 |
| | 441190 | H09073 | Hs.25046 | ESTs | 2.6 | 3.1 |
| | 432278 | AL137506 | Hs.274256 | hypothetical protein FLJ23563 | 2.6 | 2.9 |
| | 442731 | AI868167 | Hs.131044 | ESTs | 2.6 | 4.1 |
| | 416836 | D54745 | Hs.80247 | cholecystokinin | 2.6 | 14.9 |
| 45 | 449071 | NM_005872 | Hs.22960 | breast carcinoma amplified sequence 2 | 2.5 | 2.4 |
| | 436321 | AA709133 | Hs.180144 | ESTs | 2.5 | 2.8 |
| | 439693 | AI741816 | Hs.125897 | ESTs | 2.5 | 3.6 |
| | 443212 | AW269515 | Hs.102500 | hypothetical protein FLJ20481 | 2.5 | 2.8 |
| | 423981 | AL122104 | Hs.136664 | Homo sapiens mRNA; cDNA DKFZp434A1627 (f | 2.5 | 3.8 |
| 50 | 407868 | NM_000950 | Hs.40637 | proline-rich Gla (G-carboxyglutamic acid | 2.5 | 3.1 |
| | 443992 | AW022228 | Hs.322922 | ESTs | 2.5 | 27.9 |
| | 444124 | R43097 | Hs.6818 | ESTs | 2.5 | 5.3 |
| | 411379 | AI816344 | Hs.12554 | ESTs, Weakly similar to NPL4_HUMAN NUCLE | 2.5 | 38.0 |
| | 440474 | AI207936 | Hs.7195 | gamma-aminobutyric acid (GABA) A recepto | 2.5 | 3.8 |
| 55 | 446277 | AI284218 | Hs.159204 | ESTs | 2.5 | 2.2 |
| | 410111 | AI620206 | Hs.189647 | ESTs | 2.5 | 3.5 |
| | 445162 | AB011131 | Hs.12376 | piccolo (presynaptic cytomatrix protein) | 2.5 | 4.8 |
| | 410718 | AI920783 | Hs.191435 | ESTs | 2.5 | 4.5 |
| | 417201 | T60432 | Hs.269084 | ESTs, Moderately similar to AF097994 1 L | 2.5 | 2.9 |
| 60 | 420274 | AW968000 | Hs.143389 | ESTs, Weakly similar to T14318 ubiquitin | 2.5 | 2.8 |
| | 433496 | AF064254 | Hs.49765 | VLCS-H1 protein | 2.5 | 4.7 |
| | 437331 | AL353933 | Hs.21710 | hypothetical protein DKFZp761G0313 | 2.5 | 3.3 |
| | 437368 | AI471969 | Hs.182606 | ESTs | 2.5 | 3.0 |
| 65 | 441985 | BE047625 | Hs.169815 | ESTs | 2.5 | 3.6 |
| | 410025 | BE220489 | Hs.113592 | ESTs, Moderately similar to I54374 gene | 2.5 | 9.2 |
| | 414680 | AA743331 | Hs.272572 | hemoglobin, alpha 2 | 2.5 | 3.6 |
| | 429956 | AI374651 | Hs.22542 | ESTs | 2.5 | 23.9 |
| | 429028 | AA443439 | Hs.48797 | ESTs | 2.5 | 2.8 |
| | 438109 | AI076621 | Hs.71367 | ESTs, Moderately similar to ALU7_HUMAN A | 2.5 | 3.1 |
| 70 | 439780 | AL109688 | | gb:Homo sapiens mRNA full length insert | 2.5 | 2.3 |
| | 440888 | N45600 | Hs.326880 | ESTs | 2.5 | 3.9 |
| | 445246 | AI217713 | Hs.147586 | ESTs | 2.5 | 2.6 |
| | 440152 | AB002376 | Hs.7006 | KIAA0378 protein | 2.4 | 23.6 |
| | 432740 | AF061034 | Hs.278898 | tumor necrosis factor alpha-inducible ce | 2.4 | 2.1 |
| 75 | 415122 | D60708 | Hs.22245 | ESTs | 2.4 | 3.9 |
| | 432298 | AL118812 | Hs.274293 | Homo sapiens mRNA; cDNA DKFZp761G1111 (f | 2.4 | 9.8 |
| | 437948 | AA772920 | Hs.303527 | ESTs | 2.4 | 9.8 |
| | 421360 | AA297012 | Hs.103839 | erythrocyte membrane protein band 4.1-b | 2.4 | 2.8 |
| | 427115 | AW972853 | Hs.112237 | ESTs | 2.4 | 2.2 |
| 80 | 452074 | BE299035 | Hs.27747 | G protein-coupled receptor 37 (endotheli | 2.4 | 10.0 |
| | 436639 | D14838 | Hs.111 | fibroblast growth factor 9 (glia-activat | 2.4 | 3.5 |
| | 434520 | AA205273 | Hs.177011 | hypothetical protein | 2.4 | 3.1 |
| | 411529 | AA430348 | Hs.317596 | Homo sapiens cDNA FLJ12927 fis, clone NT | 2.4 | 3.0 |

| | | | | | | |
|----|--------|-----------|-----------|--|-----|------|
| 5 | 442272 | AA988302 | Hs.129172 | ESTs | | |
| | 422927 | AW247388 | Hs.301423 | calcium binding protein 1 (calbrain) | 2.4 | 2.1 |
| | 444647 | H14718 | Hs.11506 | Human clone 23589 mRNA sequence | 2.4 | 2.7 |
| | 415827 | H17462 | Hs.23079 | ESTs | 2.4 | 2.8 |
| | 451397 | AA017432 | Hs.84529 | ESTs, Weakly similar to Z202_HUMAN ZINC | 2.4 | 15.0 |
| 10 | 445200 | AA084460 | Hs.12409 | somatostatin | 2.4 | 3.9 |
| | 451062 | AL110125 | Hs.25910 | Homo sapiens mRNA; cDNA DKFZp564C1416 (f | 2.4 | 3.7 |
| | 420328 | Y19062 | Hs.96870 | staurin (Drosophila, RNA-binding protein | 2.4 | 2.4 |
| | 432122 | AA526514 | | gb:n160f02.s1 NCL_CGAP_Ov2 Homo sapiens | 2.4 | 4.3 |
| | 444125 | AI124882 | Hs.118121 | ESTs | 2.4 | 4.3 |
| 15 | 430538 | AB032435 | Hs.242821 | differentiation-associated Na-dependent | 2.4 | 3.5 |
| | 457519 | X69438 | Hs.3052 | early growth response 4 | 2.4 | 10.8 |
| | 409371 | R51736 | Hs.12381 | ESTs | 2.4 | 2.4 |
| | 456303 | AA224872 | Hs.115088 | ESTs | 2.4 | 2.1 |
| | 440105 | AA694010 | Hs.6932 | Homo sapiens clone 23809 mRNA sequence | 2.4 | 3.2 |
| 20 | 400979 | | | | 2.4 | 23.4 |
| | 435296 | R49685 | Hs.24980 | ESTs | 2.4 | 4.1 |
| | 408950 | AA707814 | Hs.14945 | long fatty acyl-CoA synthetase 2 gene | 2.4 | 6.5 |
| | 452032 | BE244005 | Hs.27610 | retinoic acid- and interferon-inducible | 2.4 | 18.5 |
| | 432098 | AF252297 | Hs.91546 | cytochrome P450 retinoid metabolizing pr | 2.4 | 2.2 |
| 25 | 408974 | AW015458 | Hs.297017 | ESTs | 2.4 | 2.7 |
| | 412177 | Z23091 | Hs.73734 | glycoprotein V (platelet) | 2.4 | 2.5 |
| | 413153 | N94205 | | gb:za27a08.r1 Soares fetal liver spleen | 2.4 | 2.8 |
| | 417583 | AA668782 | Hs.191284 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.4 | 2.5 |
| | 452034 | F12234 | Hs.75893 | ankyrin 3, node of Ranvier (ankyrin G) | 2.4 | 2.6 |
| 30 | 424940 | AA985308 | Hs.194327 | ESTs | 2.3 | 3.0 |
| | 431706 | AI816086 | Hs.296341 | adenylyl cyclase-associated protein 2 | 2.3 | 6.3 |
| | 419125 | AA642452 | Hs.130881 | B-cell CLL/lymphoma 11A (zinc finger pro | 2.3 | 4.1 |
| | 423641 | AL137256 | Hs.130489 | ATPase, aminophospholipid transporter-li | 2.3 | 2.9 |
| | 436407 | T88803 | Hs.271507 | ESTs, Weakly similar to TIM_HUMAN PROBAB | 2.3 | 8.7 |
| 35 | 448681 | AL109781 | Hs.21754 | Homo sapiens mRNA full length insert cDN | 2.3 | 3.2 |
| | 415669 | NM_005025 | Hs.78589 | serine (or cysteine) proteinase inhibito | 2.3 | 5.2 |
| | 410765 | AI694972 | Hs.66180 | nucleosome assembly protein 1-like 2 | 2.3 | 54.7 |
| | 422386 | AF105374 | Hs.115830 | heparan sulfate (glucosamine) 3-O-sulfot | 2.3 | 9.1 |
| | 414828 | AA156651 | | gb:z105h05.r1 Soares_pregnant_uterus_NbH | 2.3 | 5.0 |
| 40 | 445556 | AI910241 | Hs.12887 | actin-related protein 3-beta | 2.3 | 2.4 |
| | 426968 | U07616 | Hs.173034 | amphiphysin (Stiff-Mann syndrome with br | 2.3 | 8.5 |
| | 444562 | AA186715 | Hs.336429 | RIKEN cDNA 9130422N19 gene | 2.3 | 26.3 |
| | 423420 | AI571364 | Hs.128382 | Homo sapiens mRNA; cDNA DKFZp76111224 (f | 2.3 | 2.5 |
| | 439450 | R51613 | Hs.125304 | ESTs | 2.3 | 7.6 |
| 45 | 427127 | AW802282 | Hs.22265 | pyruvate dehydrogenase phosphatase | 2.3 | 26.3 |
| | 447179 | AW015633 | Hs.157299 | ESTs | 2.3 | 2.2 |
| | 414711 | AI310440 | Hs.288735 | Homo sapiens cDNA FLJ13522 fis, clone PL | 2.3 | 3.8 |
| | 433449 | AW772282 | | gb:hn71b05.x1 NCL_CGAP_Kid11 Homo sapien | 2.3 | 2.3 |
| | 414320 | U13616 | Hs.75893 | ankyrin 3, node of Ranvier (ankyrin G) | 2.3 | 3.8 |
| 50 | 416778 | M16505 | Hs.79876 | steroid sulfatase (microsomal), arylsulf | 2.3 | 2.5 |
| | 425130 | AA448208 | Hs.99163 | ESTs | 2.3 | 7.8 |
| | 456664 | AW963354 | Hs.334409 | metallothionein 1G | 2.3 | 4.1 |
| | 438283 | AA58931 | Hs.37282 | ESTs | 2.3 | 2.5 |
| | 417455 | AW007066 | Hs.18949 | ESTs, Weakly similar to CA2B_HUMAN COLLA | 2.3 | 4.2 |
| 55 | 412100 | AW892731 | | gb:CMO-NN0005-100300-279-c02 NN0005 Homo | 2.3 | 3.0 |
| | 448981 | AI968719 | Hs.195387 | ESTs | 2.3 | 3.7 |
| | 416101 | R24854 | Hs.268806 | ESTs | 2.3 | 3.2 |
| | 439731 | AI953135 | Hs.45140 | hypothetical protein FLJ14084 | 2.3 | 6.5 |
| | 415734 | NM_014747 | Hs.78748 | KIAA0237 gene product | 2.3 | 17.8 |
| 60 | 424596 | AB020639 | Hs.151017 | estrogen-related receptor gamma | 2.3 | 40.1 |
| | 420230 | AL034344 | Hs.284186 | forkhead box C1 | 2.3 | 2.9 |
| | 451559 | AL119980 | Hs.20935 | hypothetical protein DKFZp761D221 | 2.3 | 2.4 |
| | 404835 | | | | 2.3 | 5.7 |
| | 456765 | AI497900 | Hs.33067 | ESTs | 2.3 | 2.1 |
| 65 | 455517 | AW984068 | | gb:RCO-HN0006-160300-011-e06 HN0006 Homo | 2.3 | 4.1 |
| | 408206 | AF041853 | Hs.43670 | kinesin family member 3A | 2.3 | 2.4 |
| | 411770 | NM_014278 | Hs.71992 | heat shock protein (hsp110 family) | 2.2 | 18.5 |
| | 430105 | X70297 | Hs.2540 | cholinergic receptor, nicotinic, alpha p | 2.2 | 3.9 |
| | 458694 | F12832 | Hs.13298 | ESTs | 2.2 | 2.6 |
| 70 | 415091 | AL044872 | Hs.77910 | 3-hydroxy-3-methylglutaryl-Coenzyme A sy | 2.2 | 4.9 |
| | 439642 | W81441 | Hs.153967 | ESTs | 2.2 | 4.4 |
| | 450138 | AW152104 | Hs.200879 | ESTs | 2.2 | 2.4 |
| | 454222 | BE144344 | Hs.7589 | ESTs, Weakly similar to A46010 X-linked | 2.2 | 4.9 |
| | 405326 | | | | 2.2 | 3.7 |
| 75 | 431342 | AW971018 | Hs.21659 | ESTs | 2.2 | 2.7 |
| | 453101 | AW952776 | Hs.94943 | ESTs | 2.2 | 5.2 |
| | 408897 | N50204 | Hs.283709 | lipopolysaccharide specific response-7 p | 2.2 | 3.3 |
| | 451398 | AI793124 | Hs.144479 | ESTs | 2.2 | 2.8 |
| | 438208 | AL041224 | Hs.65379 | ESTs | 2.2 | 4.6 |
| 80 | 408449 | NM_004408 | Hs.166161 | dynamitin 1 | 2.2 | 10.4 |
| | 414130 | AI670831 | Hs.71592 | Homo sapiens cDNA: FLJ21893 fis, clone H | 2.2 | 6.1 |
| | 445016 | U79716 | Hs.12246 | retin | 2.2 | 3.1 |
| | 424375 | AF070547 | Hs.146312 | Homo sapiens clone 24820 mRNA sequence | 2.2 | 3.9 |
| | 424645 | NM_014682 | Hs.151449 | KIAA0535 gene product | 2.2 | 2.3 |
| | 409729 | D51315 | Hs.106289 | ESTs | 2.2 | 11.7 |
| | 432809 | AA565509 | Hs.131703 | ESTs | 2.2 | 4.9 |
| | 422890 | Z43784 | Hs.75893 | ankyrin 3, node of Ranvier (ankyrin G) | 2.2 | 19.9 |
| | | | | | 2.2 | 10.4 |

| | | | | | | |
|----|--------|-----------|-----------|--|-----|------|
| | 428532 | AF157326 | Hs.184786 | TBP-interacting protein | 2.2 | 6.5 |
| | 413074 | AI871368 | Hs.8417 | hypothetical protein DKFZp761M0423 | 2.2 | 3.4 |
| | 414442 | AA156238 | Hs.32501 | ESTs | 2.2 | 3.2 |
| | 452768 | AW069459 | Hs.61539 | ESTs | 2.2 | 2.0 |
| 5 | 450440 | AB024334 | Hs.25001 | tyrosine 3-monooxygenase/tryptophan 5-mo | 2.2 | 3.2 |
| | 426281 | AK000987 | Hs.169111 | oxidation resistance 1 | 2.2 | 2.3 |
| | 428411 | AW291464 | Hs.10338 | ESTs | 2.2 | 2.3 |
| | 413787 | AI352558 | Hs.75544 | tyrosine 3-monooxygenase/tryptophan 5-mo | 2.2 | 3.1 |
| 10 | 451734 | NM_006176 | Hs.26944 | neurogranin (protein kinase C substrate, | 2.2 | 8.5 |
| | 439108 | AW163034 | Hs.6467 | synaptogyrin 3 | 2.2 | 7.9 |
| | 405385 | | | | 2.2 | 2.4 |
| | 447285 | AI371849 | Hs.200696 | ATPase, Class VI, type 11C | 2.2 | 2.2 |
| | 452667 | T87219 | Hs.13219 | ESTs | 2.2 | 3.1 |
| 15 | 422234 | AF119818 | Hs.113287 | discs, large (Drosophila) homolog-associ | 2.1 | 8.3 |
| | 410339 | AI916499 | Hs.298258 | ESTs | 2.1 | 3.2 |
| | 413231 | D87461 | Hs.75244 | BCL2-like 2 | 2.1 | 4.5 |
| | 447104 | R19085 | Hs.210706 | Homo sapiens cDNA FLJ13182 fis, clone NT | 2.1 | 2.2 |
| | 451952 | AL120173 | Hs.301663 | ESTs | 2.1 | 36.5 |
| 20 | 415841 | Z45637 | Hs.7093 | ESTs | 2.1 | 2.4 |
| | 441086 | AI928489 | Hs.213490 | ESTs, Weakly similar to N33_HUMAN N33 PR | 2.1 | 2.2 |
| | 450407 | NM_000810 | Hs.24969 | gamma-aminobutyric acid (GABA) A recepto | 2.1 | 6.6 |
| | 427627 | R87582 | Hs.179915 | guanine nucleotide binding protein (G pr | 2.1 | 5.3 |
| | 449712 | R56545 | Hs.6100 | ESTs | 2.1 | 4.5 |
| 25 | 409660 | AW452065 | Hs.258905 | ESTs | 2.1 | 2.1 |
| | 430434 | AL049548 | Hs.241420 | Homo sapiens mRNA for KIAA1756 protein, | 2.1 | 5.4 |
| | 434138 | AA625804 | | gbzu86h01.s1 Soares_testis_NHT Homo sap | 2.1 | 3.0 |
| | 448610 | NM_006157 | Hs.21602 | nel (chicken)-like 1 | 2.1 | 4.8 |
| | 418948 | AI217097 | | gb.qd43h07.x1 Soares_fetal_heart_NbHH19W | 2.1 | 2.9 |
| 30 | 414876 | AW950925 | Hs.924 | crystallin, mu | 2.1 | 3.4 |
| | 440426 | AI159800 | Hs.7181 | Homo sapiens cDNA FLJ13663 fis, clone PL | 2.1 | 3.7 |
| | 451249 | AA016227 | Hs.27280 | ESTs | 2.1 | 4.1 |
| | 451475 | T19093 | Hs.26450 | KIAA0725 protein | 2.1 | 2.1 |
| | 448743 | AB032962 | Hs.21896 | KIAA1136 protein | 2.1 | 29.7 |
| | 430814 | U89336 | Hs.247993 | NGS protein | 2.1 | 2.7 |
| 35 | 426990 | AL044315 | Hs.173094 | Homo sapiens mRNA for KIAA1750 protein, | 2.1 | 2.3 |
| | 426642 | AW068223 | Hs.171581 | ubiquitin C-terminal hydrolase UCH37 | 2.1 | 4.5 |
| | 427335 | AA448542 | Hs.251677 | G antigen 7B | 2.1 | 2.2 |
| | 459089 | F13036 | Hs.27373 | Homo sapiens mRNA; cDNA DKFZp564O1763 (f | 2.1 | 2.3 |
| 40 | 435832 | AA425688 | Hs.41641 | Bruno (Drosophila) -like 4, RNA binding | 2.1 | 5.9 |
| | 446383 | T05816 | Hs.92511 | ESTs | 2.1 | 2.9 |
| | 412768 | AW996044 | Hs.26239 | Human DNA sequence from clone RP11-43882 | 2.1 | 2.1 |
| | 453976 | BE463830 | Hs.163714 | ESTs | 2.1 | 4.2 |
| | 415111 | R39039 | Hs.328455 | EST | 2.1 | 3.3 |
| 45 | 452238 | F01811 | Hs.187931 | ESTs | 2.1 | 4.9 |
| | 445279 | R41900 | Hs.22245 | ESTs | 2.1 | 9.8 |
| | 448799 | AI937094 | Hs.179080 | ESTs | 2.1 | 3.1 |
| | 418338 | NM_002522 | Hs.84154 | neuronal pentraxin I | 2.1 | 8.3 |
| | 445725 | AK000956 | Hs.13209 | hypothetical protein FLJ10094 | 2.1 | 5.4 |
| 50 | 443537 | D13305 | Hs.203 | cholecystokinin B receptor | 2.1 | 4.1 |
| | 454066 | X00356 | Hs.37058 | calcitonin/calcitonin-related polypeptid | 2.1 | 6.4 |
| | 429954 | AI918130 | Hs.21374 | ESTs | 2.1 | 7.2 |
| | 415292 | H29016 | Hs.200576 | ESTs | 2.1 | 3.9 |
| | 423563 | R34734 | Hs.75209 | protein kinase (cAMP-dependent, catalyti | 2.1 | 3.1 |
| 55 | 424906 | AI566086 | Hs.153716 | Homo sapiens mRNA for Hmob33 protein, 3' | 2.1 | 4.7 |
| | 459309 | AA040620 | Hs.5672 | hypothetical protein AF140225 | 2.1 | 2.2 |
| | 439340 | AB032436 | Hs.6535 | brain-specific Na-dependent inorganic ph | 2.1 | 4.7 |
| | 402598 | BE314624 | Hs.3128 | polymerase (RNA) II (DNA directed) polyp | 2.1 | 5.4 |
| | 435406 | F26698 | Hs.4884 | calcium/calmodulin-dependent protein kin | 2.1 | 6.6 |
| 60 | 448792 | R42550 | Hs.12826 | ESTs | 2.1 | 4.1 |
| | 449500 | AW956345 | Hs.12926 | ESTs | 2.1 | 2.4 |
| | 441134 | W29092 | Hs.7678 | cellular retinoic acid-binding protein 1 | 2.1 | 5.8 |
| | 433361 | AW469373 | Hs.300141 | ribosomal protein L39 | 2.1 | 2.7 |
| | 452946 | X95425 | Hs.31092 | EphA5 | 2.1 | 5.0 |
| 65 | 426167 | AF039023 | Hs.167496 | RAN binding protein 6 | 2.0 | 2.2 |
| | 453666 | AW015681 | Hs.135229 | ESTs, Weakly similar to A2BP_HUMAN ATAXI | 2.0 | 3.1 |
| | 424632 | AB014523 | Hs.151406 | KIAA0623 gene product | 2.0 | 3.5 |
| | 448589 | AF017090 | Hs.21554 | KIAA1107 protein | 2.0 | 4.1 |
| | 430416 | AC005531 | Hs.57806 | Homo sapiens PAC clone RP4-701016 from 7 | 2.0 | 2.3 |
| 70 | 445627 | AW618475 | Hs.7363 | ESTs | 2.0 | 2.1 |
| | 417092 | H97508 | Hs.181165 | eukaryotic translation elongation factor | 2.0 | 2.5 |
| | 453653 | AW505554 | Hs.144559 | ESTs | 2.0 | 4.7 |
| | 435850 | AF250847 | Hs.283514 | mitochondrial ceramidase | 2.0 | 3.7 |
| | 435086 | AW975243 | Hs.122596 | ESTs | 2.0 | 2.1 |
| 75 | 423191 | D61506 | Hs.8417 | hypothetical protein DKFZp761M0423 | 2.0 | 2.1 |
| | 411562 | AL050201 | Hs.70769 | hypothetical protein DKFZp586E1923 | 2.0 | 2.8 |
| | 431645 | AF078849 | Hs.266483 | dynein light chain-A | 2.0 | 2.5 |
| | 429834 | AI929545 | Hs.225936 | synapsin I | 2.0 | 3.6 |
| | 439607 | BE540565 | Hs.159460 | ESTs | 2.0 | 17.5 |
| 80 | 408033 | AW138045 | Hs.242256 | ESTs | 2.0 | 4.0 |
| | 430317 | AB020645 | Hs.239189 | glutaminase | 2.0 | 2.7 |
| | 419631 | AW188117 | Hs.303154 | popeye protein 3 | 2.0 | 2.6 |
| | 432660 | AI288430 | Hs.54004 | ESTs | 2.0 | 2.3 |
| | 454048 | H05626 | Hs.6921 | ESTs | 2.0 | 15.9 |

| | | | | | | |
|---|--------|----------|-----------|--|-----|------|
| 5 | 426917 | AA913814 | Hs.172854 | DKFZP586B0923 protein | 2.0 | 3.1 |
| | 423246 | AL119114 | Hs.77196 | spectrin, alpha, non-erythrocytic 1 (alp | 2.0 | 2.9 |
| | 415989 | AI267700 | Hs.317584 | ESTs | 2.0 | 4.8 |
| | 420276 | AA290938 | Hs.190561 | ESTs, Highly similar to SORL_HUMAN SORTI | 2.0 | 5.1 |
| | 424983 | AI742434 | Hs.169911 | ESTs | 2.0 | 15.9 |
| | 446296 | AA985662 | Hs.53131 | Homo sapiens cDNA FLJ13155 fis, clone NT | 2.0 | 2.7 |
| | 450006 | AI241555 | Hs.60171 | ESTs | 2.0 | 3.5 |

TABLE 11B:

| | |
|-------------|---------------------------------------|
| Pkey: | Unique Eos probeset identifier number |
| CAT number: | Gene cluster number |
| Accession: | Genbank accession numbers |

| | | | |
|----|--------|------------|--|
| 15 | Pkey | CAT Number | Accession |
| | 408274 | 104999_1 | R17315 Z43964 AA053547 |
| | 412100 | 1277224_1 | AW892731 H08502 Z45826 |
| 20 | 412112 | 1277883_1 | BE180342 BE180347 AW901900 BE180222 BE180218 BE180226 BE180413 BE180416 AW901899 BE180228 AW901897 BE180224 AW901898 BE180223 BE180219 BE180346 BE180343 BE180418 BE180225 BE180221 BE180341 AW901894 BE180217 BE180227 AW901891 BE180345 AW893614 AW893615 H85799 H83501 BE180220 |
| | 413153 | 1350849_1 | N94205 BE067565 BE067556 |
| | 413510 | 1374377_1 | F13044 T77009 BE145525 BE145493 |
| 25 | 414828 | 149563_1 | AA156651 AA156622 R14472 |
| | 418948 | 180808_1 | AI217097 AW886090 W38035 W38792 AA232835 AW936043 |
| | 419558 | 185904_1 | AW953679 AW953680 AA244436 H82527 AA361046 AA244483 H82526 |
| 30 | 421249 | 200649_1 | AA285362 AW752386 AW847156 AA285373 AW879575 AW879558 |
| | 421640 | 204833_1 | AW966652 AW966653 AA294989 AA385977 |
| | 429995 | 311738_1 | AA463571 AI277645 AL118763 |
| 35 | 430212 | 314437_1 | AA469153 AI718503 AA469225 |
| | 432122 | 341756_1 | AA526514 AW973343 AA554293 |
| | 433449 | 366532_1 | AW772282 AA592974 |
| 40 | 434138 | 380572_1 | AA625804 AW418787 AW074833 AI675642 AI393368 |
| | 437483 | 43756_1 | AL390174 AW898817 |
| | 439780 | 47673_1 | AL109688 R23665 R26578 |
| 45 | 452502 | 919733_1 | AI904296 BE007223 R30687 |
| | 455517 | 1321782_1 | AW984068 AW984072 AW984077 |
| | 456407 | 184986_1 | AW986514 AA243209 AA281411 |

TABLE 11C:

| | |
|--------------|---|
| Pkey: | Unique number corresponding to an Eos probeset |
| Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. |
| Strand: | Indicates DNA strand from which exons were predicted. |
| Nt_position: | Indicates nucleotide positions of predicted exons. |

| | | | | |
|----|--------|---------|--------|---|
| 45 | Pkey | Ref | Strand | Nt_position |
| | 400979 | 8072554 | Plus | 160842-161028 |
| | 401213 | 9858408 | Plus | 98243-98380,98489-98619 |
| 50 | 401421 | 7452889 | Minus | 142291-142461 |
| | 403092 | 8954241 | Plus | 174720-175016,175104-175406,175508-175813 |
| | 404648 | 9796894 | Minus | 115334-116020 |
| 55 | 404793 | 7232206 | Minus | 61087-61590 |
| | 404835 | 6970743 | Plus | 85462-85684,88139-88287,90338-91018,94827-94990 |
| | 405326 | 4375975 | Plus | 10633-10709,30805-30893,38078-38253,55112-55327,57718-57818,66696-66841 |
| 60 | 405385 | 6552772 | Plus | 48332-48454 |
| | 405793 | 1405887 | Minus | 89197-89453 |
| | 405911 | 6758795 | Plus | 101008-101643 |
| 65 | 405977 | 8247789 | Minus | 135548-136177 |

TABLE 12A: ABOUT 678 GENES UP-REGULATED IN LOWER GRADE GLIOBLASTOMA COMPARED TO NORMAL CENTRAL NERVOUS SYSTEM

Table 12A lists about 678 genes up-regulated in lower grade glioblastoma (LGG) compared to normal central nervous system (CNS). These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" LGG to "average" CNS tissues was greater than or equal to 2.5. The "average" LGG level was set to the 85th percentile amongst various LGG tumors. The "average" normal CNS tissue level was set to the 85th percentile amongst various CNS tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

| | |
|----------------|---|
| Pkey: | Unique Eos probeset identifier number |
| ExAccn: | Exemplar Accession number, Genbank accession number |
| UnigeneID: | Unigene number |
| Unigene Title: | Unigene gene title |
| R1: | Ratio of LOWER GRADE GLIOBLASTOMA to normal CNS |

| | | | | | |
|----|--------|----------|-----------|--|------|
| 75 | Pkey | ExAccn | UnigeneID | Unigene Title | R1 |
| | 412420 | AL035668 | Hs.73853 | bone morphogenetic protein 2 | 20.3 |
| | 424800 | AL035588 | Hs.153203 | MyoD family inhibitor | 19.5 |
| 80 | 453392 | U23752 | Hs.32964 | SRY (sex determining region Y)-box 11 | 18.5 |
| | 402604 | | | Target Exon | 16.9 |
| | 444190 | AI878918 | Hs.10526 | cysteine and glycine-rich protein 2 | 15.0 |
| 85 | 409638 | AW450420 | Hs.21335 | ESTs | 14.0 |
| | 443731 | AI083928 | Hs.145418 | ESTs | 14.0 |
| | 456759 | BE259150 | Hs.127792 | delta (Drosophila)-like 3 | 13.6 |
| 90 | 447342 | AI199268 | Hs.19322 | Homo sapiens, Similar to RIKEN cDNA 2010 | 12.2 |
| | 433001 | AF217513 | Hs.279905 | clone HQ0310 PRO0310p1 | 10.3 |
| | 427019 | AA001732 | Hs.173233 | hypothetical protein FLJ10970 | 9.5 |

| | | | | | |
|----|--------|-----------|--|---|-----|
| | 425187 | AW014486 | Hs.22509 | ESTs | 9.0 |
| | 440210 | AW674562 | Hs.125296 | ESTs | 8.8 |
| | 448769 | N68037 | Hs.38173 | ESTs | 8.4 |
| 5 | 437034 | AA742643 | gb:ny91c01.s1 NCI_CGAP_GCB1 Homo sapiens | | 8.2 |
| | 449539 | W80363 | Hs.58446 | ESTs | 8.1 |
| | 417061 | AI575944 | Hs.188691 | Homo sapiens cDNA FLJ12033 fis, clone HE | 8.0 |
| | 435020 | AW505076 | Hs.301855 | DiGeorge syndrome critical region gene 8 | 7.8 |
| | 414217 | AI309298 | Hs.279898 | Homo sapiens cDNA: FLJ23165 fis, clone L | 7.7 |
| 10 | 449300 | AI556359 | Hs.346514 | ESTs | 7.6 |
| | 449969 | AW295142 | Hs.180187 | Homo sapiens cDNA FLJ14337 fis, clone PL | 7.5 |
| | 452372 | AI885742 | Hs.228474 | ESTs | 7.2 |
| | 410102 | AW248508 | Hs.279727 | ESTs; homologue of PEM-3 (Ciona savignyi) | 7.2 |
| | 417308 | H60720 | Hs.81892 | KIAA101 gene product | 7.2 |
| | 447004 | AW296968 | Hs.157539 | ESTs | 7.1 |
| 15 | 418113 | AI272141 | Hs.83484 | SRY (sex determining region Y)-box 4 | 7.1 |
| | 424635 | AA420687 | Hs.115455 | Homo sapiens cDNA FLJ14259 fis, clone PL | 7.1 |
| | 406478 | | | Target Exon | 7.1 |
| | 428728 | NM_016625 | Hs.191381 | hypothetical protein | 6.9 |
| 20 | 414761 | AU077228 | Hs.77256 | enhancer of zeste (Drosophila) homolog 2 | 6.9 |
| | 428037 | N47474 | Hs.89230 | potassium intermediate/small conductance | 6.7 |
| | 423343 | AA324643 | Hs.246106 | ESTs | 6.7 |
| | 418097 | R45137 | Hs.21868 | ESTs | 6.7 |
| | 431553 | X78075 | Hs.2799 | cartilage linking protein 1 | 6.6 |
| 25 | 412326 | R07566 | Hs.73817 | small inducible cytokine A3 (homologous | 6.6 |
| | 425397 | J04088 | Hs.156346 | topoisomerase (DNA) II alpha (170kD) | 6.4 |
| | 419169 | AW851980 | Hs.262346 | ESTs, Weakly similar to S72482 hypothe | 6.4 |
| | 431117 | AF003522 | Hs.250500 | delta (Drosophila)-like 1 | 6.4 |
| | 445908 | R13580 | Hs.13436 | Homo sapiens clone 24425 mRNA sequence | 6.3 |
| 30 | 402855 | | | NM_001839: Homo sapiens calponin 3, acid | 6.2 |
| | 424009 | F11690 | | gb:HSC30D041 normalized infant brain cDN | 6.2 |
| | 400419 | AF084545 | | Target | 6.2 |
| | 446584 | U53445 | Hs.15432 | downregulated in ovarian cancer 1 | 6.0 |
| | 414020 | NM_002984 | Hs.75703 | small inducible cytokine A4 (homologous | 6.0 |
| 35 | 426140 | AF131798 | Hs.343768 | Homo sapiens clone 25119 mRNA sequence | 5.9 |
| | 427144 | X95097 | Hs.2126 | vasoactive intestinal peptide receptor 2 | 5.9 |
| | 416658 | U03272 | Hs.79432 | fibrillin 2 (congenital contractural ara | 5.8 |
| | 405238 | | | Target Exon | 5.7 |
| | 421977 | W94197 | Hs.110165 | ribosomal protein L26 homolog | 5.7 |
| 40 | 405348 | | | C7001664:gi12698061 dbj BAB21849.1 (AB | 5.6 |
| | 428795 | R45503 | Hs.97469 | ESTs, Highly similar to A39769 N-acetyl | 5.4 |
| | 422672 | X12784 | Hs.119129 | collagen, type IV, alpha 1 | 5.3 |
| | 403349 | NM_001406 | | ephrin-B3 | 5.3 |
| | 453941 | U39817 | Hs.36820 | Bloom syndrome | 5.2 |
| 45 | 429139 | F09092 | Hs.66087 | ESTs | 5.2 |
| | 454860 | AW835767 | | gb:OV4-LT0016-240200-110-b08 LT0016 Homo | 5.2 |
| | 452279 | AA286844 | Hs.61260 | hypothetical protein FLJ13164 | 5.1 |
| | 418030 | BE207573 | Hs.83321 | neuromedin B | 5.1 |
| | 429469 | M64590 | Hs.27 | glycine dehydrogenase (decarboxylating; | 5.1 |
| 50 | 450639 | AI703186 | Hs.277174 | ESTs | 5.1 |
| | 412811 | H06382 | | ESTs | 5.1 |
| | 442832 | AW206560 | Hs.253569 | ESTs | 5.1 |
| | 436608 | AA628980 | | down syndrome critical region protein DS | 5.1 |
| | 408161 | AW952912 | Hs.300383 | hypothetical protein MGC3032 | 5.1 |
| 55 | 443744 | AI084326 | Hs.271548 | ESTs, Weakly similar to I78885 serine/th | 5.1 |
| | 447497 | AW167254 | Hs.205722 | ESTs | 5.0 |
| | 450811 | AI739486 | Hs.245497 | ESTs | 5.0 |
| | 433244 | AB040943 | Hs.271285 | KIAA1510 protein | 4.9 |
| | 438458 | AW975186 | | gb:EST387294 MAGE resequences, MAGN Homo | 4.9 |
| 60 | 438456 | AA913381 | Hs.20594 | ESTs | 4.9 |
| | 411048 | AK001742 | Hs.67991 | hypothetical protein DKFZp434G0522 | 4.9 |
| | 456304 | AI820973 | | gb:nc21c02.y5 NCI_CGAP_Pr1 Homo sapiens | 4.9 |
| | 442547 | AA306997 | Hs.217484 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 4.9 |
| | 419991 | AJ000098 | Hs.94210 | eyes absent (Drosophila) homolog 1 | 4.8 |
| 65 | 402274 | | | C19000498:gi14567179 gb AAD23607.1 AC00 | 4.8 |
| | 420092 | AA814043 | Hs.88045 | ESTs | 4.8 |
| | 436282 | R91913 | Hs.272104 | ESTs, Moderately similar to ALU1_HUMAN A | 4.8 |
| | 430809 | AI791150 | Hs.262009 | ESTs, Moderately similar to I38022 hypot | 4.8 |
| | 455104 | BE064863 | | gb:RC1-BT0313-110300-015-f06 BT0313 Homo | 4.8 |
| 70 | 403961 | | | Target Exon | 4.8 |
| | 424954 | NM_000546 | Hs.1846 | tumor protein p53 (Li-Fraumeni syndrome) | 4.8 |
| | 414825 | X06370 | Hs.77432 | epidermal growth factor receptor (avian | 4.8 |
| | 447891 | R41754 | Hs.6496 | ESTs | 4.7 |
| | 423529 | T87318 | Hs.120411 | ESTs | 4.7 |
| 75 | 422737 | M26939 | Hs.119571 | collagen, type III, alpha 1 (Ehlers-Danl | 4.7 |
| | 428722 | U76456 | Hs.190787 | tissue inhibitor of metalloproteinase 4 | 4.6 |
| | 437698 | R61837 | Hs.7990 | ESTs, Moderately similar to I84505 calci | 4.6 |
| | 403481 | | | Target Exon | 4.6 |
| | 426075 | AW513691 | Hs.270149 | ESTs, Weakly similar to 2109260A B cell | 4.6 |
| 80 | 422170 | AI791949 | Hs.112432 | anti-Müllerian hormone | 4.6 |
| | 416379 | N38857 | Hs.203933 | ESTs | 4.6 |
| | 406481 | | | Target Exon | 4.5 |
| | 456052 | BE311901 | Hs.28935 | gb:601142614F1 NIH_MGC_14 Homo sapiens c | 4.5 |
| | 423178 | AI033140 | Hs.124983 | Homo sapiens mRNA; cDNA DKFZp564C142 (tr | 4.5 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| 5 | 411642 | NM_014932 | Hs.71132 | neurofigin 1 | 4.5 |
| | 428282 | N34905 | Hs.44653 | Homo sapiens cDNA: FLJ22669 fis, clone H | 4.5 |
| | 432625 | AI243596 | Hs.94830 | ESTs, Moderately similar to T03094 A-kin | 4.5 |
| | 452994 | AW962597 | Hs.31305 | KIAA1547 protein | 4.5 |
| | 449961 | AW265634 | Hs.133100 | ESTs | 4.4 |
| 10 | 401454 | | | NM_014226*:Homo sapiens renal tumor anti | 4.4 |
| | 406395 | | | Target Exon | 4.4 |
| | 432281 | AK001239 | Hs.274263 | hypothetical protein FLJ10377 | 4.4 |
| | 453792 | AL134539 | Hs.254129 | KIAA1678 | 4.4 |
| | 415131 | D61119 | | gb:HUM158C11B Clontech human fetal brain | 4.4 |
| 15 | 437695 | AA769202 | Hs.192142 | ESTs | 4.4 |
| | 422081 | AW136820 | Hs.196011 | ESTs | 4.4 |
| | 437748 | AF234882 | Hs.5814 | suppression of tumorigenicity 7 | 4.3 |
| | 433323 | AA805132 | Hs.159142 | ESTs | 4.3 |
| | 420352 | BE258835 | | gb:601117374F1 NIH_MGC_16 Homo sapiens c | 4.3 |
| 20 | 444218 | AF070641 | Hs.10684 | Homo sapiens clone 24421 mRNA sequence | 4.3 |
| | 441035 | AI694309 | Hs.126458 | ESTs | 4.3 |
| | 443836 | BE221613 | Hs.140553 | ESTs | 4.3 |
| | 425292 | NM_005824 | Hs.155545 | 37 kDa leucine-rich repeat (LRR) protein | 4.3 |
| | 450166 | AA429504 | | ESTs | 4.3 |
| 25 | 429149 | AW193360 | Hs.197962 | ESTs, Weakly similar to I38022 hypotheti | 4.2 |
| | 422798 | R92347 | Hs.34574 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 4.2 |
| | 451254 | AI571016 | Hs.172967 | ESTs | 4.2 |
| | 409189 | AA125984 | | gb:zn27h06.r1 Stratagene neuroepithelium | 4.2 |
| | 445118 | AI208762 | Hs.345572 | ESTs | 4.2 |
| 30 | 444326 | AI939357 | Hs.270710 | ESTs | 4.2 |
| | 456060 | C14904 | Hs.45184 | Homo sapiens cDNA FLJ12284 fis, clone MA | 4.2 |
| | 404120 | | | C5000537*:gi3298595(gb)AAC41376.1} (AF0 | 4.2 |
| | 436899 | AA764852 | Hs.291567 | ESTs | 4.1 |
| | 407624 | AW157431 | Hs.248941 | ESTs | 4.1 |
| 35 | 453361 | AA035197 | Hs.107375 | ESTs | 4.1 |
| | 447439 | AA313565 | Hs.145020 | ESTs, Weakly similar to KIAA1205 protein | 4.1 |
| | 438372 | AI140189 | Hs.123191 | ESTs | 4.1 |
| | 438624 | AA889055 | Hs.123468 | ESTs | 4.1 |
| | 422493 | AW474183 | Hs.250173 | hypothetical protein FLJ13158 | 4.1 |
| 40 | 406872 | AI760903 | | gb:wi09h08.x1 NCI_CGAP_CLL1 Homo sapiens | 4.1 |
| | 425295 | AA431366 | Hs.37251 | ESTs | 4.1 |
| | 425849 | AJ000512 | Hs.296323 | serum/glucocorticoid regulated kinase | 4.1 |
| | 434206 | AW136973 | Hs.180479 | ESTs, Weakly similar to S69890 mitogen i | 4.0 |
| | 420602 | AF060877 | Hs.99236 | regulator of G-protein signalling 20 | 4.0 |
| 45 | 400645 | | | Target Exon | 4.0 |
| | 456306 | AA225313 | Hs.222886 | ESTs, Weakly similar to TRHY_HUMAN TRICH | 4.0 |
| | 419326 | W94915 | Hs.42419 | ESTs | 4.0 |
| | 414948 | C15240 | Hs.182155 | ESTs | 4.0 |
| | 423198 | M81933 | Hs.1634 | cell division cycle 25A | 4.0 |
| 50 | 411537 | BE073250 | | gb:MR0-BT0551-060300-102-e05 BT0551 Homo | 4.0 |
| | 421637 | AF035290 | Hs.106300 | Homo sapiens clone 23556 mRNA sequence | 3.9 |
| | 439231 | AW581935 | Hs.141480 | Homo sapiens mRNA; cDNA DKFZp434N079 (fr | 3.9 |
| | 429433 | AA452899 | Hs.213586 | ESTs, Weakly similar to KIAA1353 protein | 3.9 |
| | 424186 | AI536021 | Hs.288706 | Homo sapiens cDNA FLJ10281 fis, clone HE | 3.9 |
| 55 | 449932 | AI675444 | Hs.263024 | ESTs | 3.9 |
| | 434072 | H70854 | Hs.283059 | Homo sapiens PRO1082 mRNA, complete cds | 3.9 |
| | 434784 | AA649051 | Hs.164007 | ESTs | 3.9 |
| | 425146 | AW954627 | | gb:EST366697 MAGE resequences, MAGC Homo | 3.9 |
| | 428538 | AA446440 | Hs.98643 | ESTs | 3.9 |
| 60 | 443318 | AI051603 | Hs.133141 | ESTs | 3.9 |
| | 416857 | AA188775 | Hs.292453 | ESTs | 3.9 |
| | 411688 | AW953440 | | gb:EST365510 MAGE resequences, MAGB Homo | 3.9 |
| | 447343 | AA256641 | Hs.236894 | ESTs, Highly similar to S02392 alpha-2-m | 3.9 |
| | 425905 | AB032959 | Hs.318584 | novel C3HC4 type Zinc finger (ring finger | 3.8 |
| 65 | 403696 | | | C4001100*:gi35852342(gb)AAD54015.1} (AF0 | 3.8 |
| | 415884 | H22966 | Hs.13471 | ESTs | 3.8 |
| | 432646 | AW753310 | | gb:RC3-C70254-031099-012-c05 C70254 Homo | 3.8 |
| | 447057 | AI423407 | Hs.157697 | ESTs | 3.8 |
| | 400814 | | | Target Exon | 3.8 |
| 70 | 441329 | AI203575 | Hs.46821 | hypothetical protein FLJ20086 | 3.8 |
| | 416664 | H72780 | Hs.20289 | ESTs | 3.8 |
| | 426044 | AA502490 | Hs.170290 | ESTs | 3.8 |
| | 455646 | BE064420 | | gb:RC4-BT0311-241199-012-c08 BT0311 Homo | 3.8 |
| | 419043 | T19167 | Hs.89566 | els variant gene 1 | 3.8 |
| 75 | 445075 | AI651827 | Hs.344767 | ESTs | 3.8 |
| | 457211 | AW972565 | Hs.32399 | ESTs, Weakly similar to S51797 vasodilat | 3.8 |
| | 420004 | AW975532 | Hs.164039 | ESTs, Moderately similar to I38022 hypoth | 3.8 |
| | 428060 | AA420616 | Hs.249483 | ESTs | 3.7 |
| | 416427 | BE244050 | Hs.79307 | Rac/Cdc42 guanine exchange factor (GEF) | 3.7 |
| 80 | 453038 | AW292415 | Hs.20509 | HBV pX associated protein-8 | 3.7 |
| | 404584 | | | Target Exon | 3.7 |
| | 447143 | AW292408 | Hs.152290 | ESTs, Highly similar to JC2463 vasoactiv | 3.7 |
| | 453438 | AI469935 | Hs.22792 | ESTs | 3.7 |
| | 429643 | AA455889 | Hs.167279 | FYVE-finger-containing Rab5 effector pro | 3.7 |
| | 458072 | AI890347 | Hs.271923 | Homo sapiens cDNA: FLJ22785 fis, clone K | 3.7 |
| | 459660 | M79082 | | ESTs | 3.7 |
| | 432188 | AI362952 | Hs.2928 | solute carrier family 7 (cationic amino | 3.7 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 430744 | AA485229 | Hs.105649 | ESTs | 3.7 |
| | 454392 | BE260893 | Hs.236131 | homeodomain-interacting protein kinase 2 | 3.7 |
| | 454457 | AW753456 | | gb:QV2-CT0261-261099-011-d11 CT0261 Homo | 3.7 |
| | 435095 | AA021160 | Hs.4750 | hypothetical protein DKFZp564K0822 | 3.7 |
| 5 | 438206 | AA780385 | Hs.187885 | ESTs | 3.7 |
| | 418967 | NM_001725 | Hs.89535 | bactericidal/permeability-increasing pro | 3.7 |
| | 427809 | M26380 | Hs.180878 | lipoprotein lipase | 3.7 |
| | 427722 | AK000123 | Hs.180479 | hypothetical protein FLJ20116 | 3.7 |
| | 413986 | Z43567 | | gb:HSC1FC021 normalized infant brain cDN | 3.7 |
| 10 | 438898 | AI819863 | Hs.106243 | ESTs | 3.7 |
| | 418483 | W26076 | Hs.221847 | ESTs | 3.7 |
| | 415849 | R20529 | Hs.6806 | ESTs | 3.6 |
| | 438380 | T06430 | Hs.6194 | chondroitin sulfate proteoglycan BEHAB/b | 3.6 |
| | 440296 | D30829 | Hs.180610 | splicing factor proline/glutamine rich (| 3.6 |
| 15 | 438025 | AW501360 | Hs.258910 | ESTs | 3.6 |
| | 458970 | AW246119 | Hs.25300 | phosphatidylinositol 4-kinase type II | 3.6 |
| | 448002 | Y15227 | Hs.20149 | deleted in lymphocytic leukemia, 1 | 3.6 |
| | 432058 | AW665996 | Hs.130729 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.6 |
| | 409557 | BE182896 | Hs.211193 | ESTs | 3.6 |
| 20 | 418049 | AA211467 | Hs.190488 | Homo sapiens, Similar to nuclear localiz | 3.6 |
| | 425331 | AW962128 | | gb:EST374201 MAGE resequences, MAGG Homo | 3.6 |
| | 424051 | AL110203 | Hs.138411 | Homo sapiens mRNA; cDNA DKFZp586J1922 (f | 3.6 |
| | 404185 | | | Target Exon | 3.6 |
| 25 | 427517 | AA644142 | Hs.7107 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 3.6 |
| | 421094 | AW978202 | Hs.289064 | hypothetical protein FLJ22251 | 3.6 |
| | 440388 | AI693520 | Hs.223000 | ESTs | 3.6 |
| | 415934 | NM_000928 | Hs.992 | phospholipase A2, group IB (pancreas) | 3.6 |
| | 408292 | AW178363 | | gb:RC3-HT0105-010999-002-H06 HT0105 Homo | 3.6 |
| 30 | 442432 | BE093589 | Hs.38178 | hypothetical protein FLJ23468 | 3.6 |
| | 451826 | AA020741 | Hs.171611 | ESTs | 3.6 |
| | 427375 | AL035460 | Hs.177536 | metallocarboxypeptidase CPX-1 | 3.6 |
| | 419485 | AA489023 | Hs.99807 | ESTs, Weakly similar to unnamed protein | 3.6 |
| | 416370 | N90470 | Hs.203697 | ESTs, Weakly similar to I38022 hypothe | 3.6 |
| 35 | 418400 | BE243026 | Hs.301989 | KIAA0246 protein | 3.6 |
| | 436674 | AA725002 | Hs.272018 | low molecular mass ubiquinone-binding pr | 3.5 |
| | 407013 | U35637 | | gb:Human nebulin mRNA, partial cds | 3.5 |
| | 403108 | | | ENSP00000241415: Hypothetical 67.7 kDa p | 3.5 |
| | 422564 | AI148006 | Hs.222120 | ESTs | 3.5 |
| 40 | 450297 | AW901347 | Hs.38592 | hypothetical protein FLJ23342 | 3.5 |
| | 436338 | W92147 | Hs.118394 | ESTs | 3.5 |
| | 447458 | AI741082 | Hs.158961 | ESTs | 3.5 |
| | 457364 | AW971037 | | gb:EST383123 MAGE resequences, MAGK Homo | 3.5 |
| | 458814 | AI498957 | Hs.170861 | ESTs, Weakly similar to Z195_HUMAN ZINC | 3.5 |
| 45 | 441701 | AW339828 | Hs.127497 | ESTs | 3.5 |
| | 405558 | | | Target Exon | 3.5 |
| | 452682 | AA456193 | Hs.9071 | progesterone membrane binding protein | 3.5 |
| | 434589 | AF147363 | | gb:Homo sapiens full length insert cDNA | 3.5 |
| | 443282 | T47764 | Hs.132917 | ESTs | 3.5 |
| 50 | 405183 | | | NM_016358: Homo sapiens iroquois homeobo | 3.5 |
| | 410064 | X53416 | Hs.195464 | filamin A, alpha (actin-binding protein- | 3.5 |
| | 425234 | AW152225 | Hs.165909 | ESTs, Weakly similar to I38022 hypothe | 3.5 |
| | 404272 | | | Target Exon | 3.5 |
| | 428808 | AA436007 | Hs.188780 | ESTs | 3.5 |
| | 447444 | AK000318 | Hs.18616 | hypothetical protein FLJ20311 | 3.5 |
| 55 | 450475 | AW805634 | Hs.205015 | ESTs | 3.4 |
| | 454451 | AW846706 | | gb:QV3-CT0192-211099-008-g02 CT0192 Homo | 3.4 |
| | 400379 | NM_018432 | | Homo sapiens ovarian cancer related prot | 3.4 |
| | 440948 | AW188311 | Hs.128619 | ESTs | 3.4 |
| 60 | 449611 | AI970394 | Hs.197075 | ESTs | 3.4 |
| | 445666 | R59960 | Hs.282386 | ESTs | 3.4 |
| | 445828 | F05802 | Hs.81907 | ESTs | 3.4 |
| | 437528 | N59646 | Hs.169745 | crumbs (Drosophila) homolog 1 | 3.4 |
| | 442927 | AI024347 | Hs.131519 | ESTs | 3.4 |
| | 451130 | AI762250 | Hs.345554 | ESTs | 3.4 |
| 65 | 454765 | AW819629 | | gb:RC5-ST0293-140200-014-H05 ST0293 Homo | 3.4 |
| | 459200 | Y09306 | Hs.30148 | homeodomain-interacting protein kinase 3 | 3.4 |
| | 433791 | AA719352 | Hs.112718 | ESTs | 3.4 |
| | 444911 | U06117 | Hs.250 | xanthine dehydrogenase | 3.4 |
| 70 | 439753 | BE262233 | Hs.7423 | hypothetical protein from EUROIMAGE 2168 | 3.4 |
| | 440933 | AI208217 | Hs.142879 | ESTs | 3.4 |
| | 447726 | AL137638 | Hs.19368 | matrilin 2 | 3.4 |
| | 403849 | | | Target Exon | 3.4 |
| | 422418 | AK001383 | Hs.116385 | hypothetical protein FLJ10521 | 3.3 |
| 75 | 439533 | W76021 | | gb:zd64cd04.r1 Soares_fetal_heart_NbHH19W | 3.3 |
| | 416422 | H60457 | | ESTs, Moderately similar to ZN91_HUMAN Z | 3.3 |
| | 441668 | AI611973 | Hs.136313 | ESTs | 3.3 |
| | 432890 | NM_014442 | Hs.279751 | sialic acid binding Ig-like lectin 8 | 3.3 |
| | 412135 | AW895309 | | gb:QV4-NN0038-300300-155-e07 NN0038 Homo | 3.3 |
| 80 | 417130 | AW276858 | Hs.81256 | S100 calcium-binding protein A4 (calcium | 3.3 |
| | 447854 | AW138454 | Hs.11594 | ESTs | 3.3 |
| | 448048 | BE281291 | Hs.170408 | ESTs, Moderately similar to A47582 B-cel | 3.3 |
| | 404632 | | | NM_022490: Homo sapiens hypothetical prot | 3.3 |
| | 411565 | AW851728 | | gb:MR2-CT0222-011199-007-d06 CT0222 Homo | 3.3 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 436267 | AW450938 | Hs.180115 | ESTs | 3.3 |
| | 426625 | T78300 | Hs.300642 | serologically defined colon cancer anti | 3.3 |
| | 401272 | | | C9000559:gi12314195 emb CAB99338.1 (A | 3.3 |
| 5 | 433128 | AB021923 | Hs.23367 | EST-YD1 protein | 3.3 |
| | 401702 | | | NM_001171*:Homo sapiens ATP-binding cass | 3.3 |
| | 454363 | AW816274 | Hs.250154 | hypothetical protein FLJ12973 | 3.3 |
| | 440332 | AI218517 | Hs.188051 | ESTs | 3.3 |
| | 454177 | AW807321 | | gb:MR4-ST0062-240300-003-g05 ST0062 Homo | 3.3 |
| 10 | 423784 | AK000039 | Hs.132826 | Homo sapiens cDNA FLJ14913 fis, clone PL | 3.3 |
| | 440688 | AW404591 | Hs.147440 | ESTs, Weakly similar to Z192_HUMAN ZINC | 3.3 |
| | 410267 | AW978005 | Hs.12600 | N-ethylmaleimide-sensitive factor attach | 3.3 |
| | 455778 | BE088746 | | gb:CM2-BT0693-210300-123-d09 BT0693 Homo | 3.3 |
| | 430183 | BE010038 | | gb:PM3-BN0176-100400-001-g04 BN0176 Homo | 3.2 |
| 15 | 451597 | AW295250 | Hs.207536 | ESTs | 3.2 |
| | 451446 | AI826288 | Hs.171637 | hypothetical protein MGC2628 | 3.2 |
| | 421353 | AW292857 | Hs.255130 | ESTs | 3.2 |
| | 442710 | AI015631 | Hs.23210 | ESTs | 3.2 |
| | 420560 | AW207748 | Hs.59115 | ESTs | 3.2 |
| 20 | 417404 | NM_007350 | Hs.82101 | pleckstrin homology-like domain, family | 3.2 |
| | 437834 | AA769294 | Hs.283854 | gb:nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens | 3.2 |
| | 430694 | AA810624 | Hs.30936 | ESTs, Weakly similar to H2BH_HUMAN HISTO | 3.2 |
| | 412021 | AW885592 | | gb:RC4-OT0071-090300-011-g11 OT0071 Homo | 3.2 |
| | 443431 | AI056847 | Hs.20654 | ESTs | 3.2 |
| 25 | 445774 | AI254165 | Hs.339968 | ESTs | 3.2 |
| | 413335 | AI613318 | Hs.48442 | ESTs | 3.2 |
| | 450692 | H50603 | Hs.94037 | hypothetical protein FLJ23053 | 3.2 |
| | 411671 | BE049094 | | ESTs | 3.2 |
| | 404592 | | | NM_022739*:Homo sapiens E3 ubiquitin lig | 3.2 |
| 30 | 402747 | | | Target Exon | 3.2 |
| | 428600 | AW863261 | Hs.242413 | hypothetical protein DKFZp434K1421 | 3.2 |
| | 420300 | AA258245 | Hs.127573 | Homo sapiens FKSG41 (FKSG41) mRNA, compl | 3.2 |
| | 445347 | AF035318 | Hs.12533 | Homo sapiens clone Z3705 mRNA sequence | 3.2 |
| | 458438 | AI141520 | Hs.151464 | ESTs, Weakly similar to ALUC_HUMAN !!!! | 3.2 |
| 35 | 442314 | AI311854 | Hs.129220 | ESTs | 3.2 |
| | 436291 | BE568452 | Hs.344037 | protein regulator of cytokinesis 1 | 3.2 |
| | 413249 | AF167160 | Hs.75251 | DEAD/H (Asp-Glu-Ala-Asp/His) box binding | 3.2 |
| | 448789 | BE539108 | Hs.22051 | hypothetical protein MGC15548 | 3.2 |
| | 403291 | | | Target Exon | 3.2 |
| 40 | 436210 | AI825420 | Hs.197824 | ESTs | 3.2 |
| | 418079 | R40058 | Hs.6911 | ESTs | 3.2 |
| | 413951 | AW051200 | Hs.75640 | natriuretic peptide precursor A | 3.2 |
| | 435828 | AA700705 | Hs.13852 | ESTs | 3.2 |
| | 437722 | AW292947 | Hs.122872 | ESTs, Weakly similar to JU0033 hypotheti | 3.2 |
| 45 | 451418 | BE387790 | Hs.26369 | hypothetical protein FLJ20287 | 3.2 |
| | 405046 | | | C3000978:gi9280045 dbj BAB01579.1 (AB0 | 3.1 |
| | 444315 | R07860 | Hs.20039 | ESTs | 3.1 |
| | 453096 | AW294631 | Hs.11325 | ESTs | 3.1 |
| 50 | 433835 | AI806185 | | gb:wf26a10.x1 Soares_NFL_T_GBC_S1 Homo s | 3.1 |
| | 430608 | R45584 | Hs.23025 | ESTs, Weakly similar to ALU5_HUMAN ALU S | 3.1 |
| | 453324 | W26592 | Hs.232089 | ESTs | 3.1 |
| | 414884 | R54418 | Hs.183745 | hypothetical protein FLJ13456 | 3.1 |
| | 446862 | AV660697 | Hs.282700 | ESTs | 3.1 |
| 55 | 427241 | AA399988 | Hs.112087 | Human DNA sequence from clone RP11-530N1 | 3.1 |
| | 416486 | H81336 | Hs.37560 | ESTs | 3.1 |
| | 429940 | W25215 | | gb:zb87a09.r1 Soares_senescent_fibroblas | 3.1 |
| | 430535 | AW968485 | | gb:EST380561 MAGE resequences, MAGJ Homo | 3.1 |
| | 439544 | W26354 | Hs.28891 | hypothetical protein FLJ11360; artemis p | 3.1 |
| 60 | 437083 | AW082597 | Hs.244862 | ESTs | 3.1 |
| | 435677 | AA694142 | Hs.293726 | ESTs, Weakly similar to TSGA RAT TESTIS | 3.1 |
| | 458810 | BE407125 | Hs.231510 | ESTs | 3.1 |
| | 443484 | AI091458 | Hs.134559 | ESTs | 3.1 |
| | 427581 | NM_014788 | Hs.179703 | KIAA0129 gene product | 3.1 |
| 65 | 444016 | AA448154 | | gb:zw82h09.r1 Soares_testis_NHT Homo sap | 3.1 |
| | 423337 | NM_004655 | Hs.127337 | axin 2 (conductin, axil) | 3.1 |
| | 403288 | | | C1001737:gi7511201 pir T27904 hypothe | 3.1 |
| | 450125 | AA005418 | Hs.158186 | ESTs | 3.1 |
| | 438138 | R98299 | Hs.177502 | ESTs | 3.1 |
| 70 | 436222 | AI208737 | Hs.122810 | Homo sapiens cDNA FLJ11489 fis, clone HE | 3.1 |
| | 443433 | R44743 | Hs.301667 | ESTs | 3.1 |
| | 443725 | AW245680 | Hs.9701 | growth arrest and DNA-damage-inducible, | 3.1 |
| | 432044 | AW972727 | | gb:EST384819 MAGE resequences, MAGL Homo | 3.1 |
| | 405760 | | | Target Exon | 3.1 |
| | 423789 | AK002084 | Hs.132851 | hypothetical protein FLJ11222 | 3.1 |
| 75 | 411605 | AW006831 | Hs.177530 | ESTs | 3.1 |
| | 417893 | AA290605 | Hs.190002 | ESTs | 3.1 |
| | 449246 | AW411209 | Hs.23363 | hypothetical protein FLJ10983 | 3.1 |
| | 429528 | AI985303 | Hs.99361 | ESTs | 3.1 |
| | 456645 | AF227156 | Hs.110103 | RNA polymerase I transcription factor RR | 3.1 |
| 80 | 412490 | AW803564 | Hs.288850 | Homo sapiens cDNA: FLJ22528 fis, clone H | 3.1 |
| | 421679 | AI475110 | Hs.203933 | ESTs | 3.1 |
| | 434503 | T96231 | Hs.17762 | ESTs | 3.1 |
| | 450756 | AI733488 | Hs.144062 | ESTs | 3.1 |
| | 415293 | R49462 | Hs.106541 | ESTs | 3.1 |

| | | | | |
|----|--------|-----------|--|-----|
| | 403212 | | NM_019595: Homo sapiens intersectin 2 (IT | 3.0 |
| | 422757 | AI909935 | Hs.65551 Homo sapiens. Similar to DNA segment, Ch | 3.0 |
| | 427624 | AA406245 | Hs.24895 ESTs | 3.0 |
| | 449256 | AA059050 | Hs.59847 ESTs | 3.0 |
| 5 | 411543 | AW851248 | gb:IL3-CT0220-160200-066-F01 CT0220 Homo | 3.0 |
| | 409112 | BE243971 | Hs.50649 quinone oxidoreductase homolog | 3.0 |
| | 414403 | AW969551 | Hs.76064 ribosomal protein L27a | 3.0 |
| | 427418 | AA402587 | Hs.325520 LAT1-3TM protein | 3.0 |
| | 455481 | AW948317 | gb:RC0-MT0015-280300-021-a09 MT0015 Homo | 3.0 |
| 10 | 444396 | T65213 | Hs.4257 ESTs | 3.0 |
| | 407235 | D20569 | Hs.169407 SAC2 (suppressor of actin mutations 2, y | 3.0 |
| | 431431 | AL096711 | Hs.252953 Human DNA sequence from clone RP3-403A15 | 3.0 |
| | 451391 | AA017410 | Hs.40568 ESTs | 3.0 |
| | 430251 | AA609246 | Hs.181451 ESTs | 3.0 |
| 15 | 420658 | AW965215 | Hs.130707 ESTs | 3.0 |
| | 442786 | H50733 | Hs.256261 ESTs, Moderately similar to ALU8_HUMAN A | 3.0 |
| | 440897 | AW104275 | Hs.148348 ESTs | 3.0 |
| | 444609 | AW571659 | Hs.278081 ESTs | 3.0 |
| | 433062 | AK001757 | Hs.281348 hypothetical protein FLJ10895 | 3.0 |
| 20 | 408523 | AW833259 | Hs.314287 ESTs | 3.0 |
| | 443477 | R32325 | Hs.221794 ESTs | 3.0 |
| | 423869 | BE409301 | Hs.134012 C1q-related factor | 3.0 |
| | 405488 | | ENSP00000220888*: ZINC FINGER TRANSCRIPT1 | 3.0 |
| | 414988 | C17535 | gb:C17535 Human placenta cDNA (TFujwara | 3.0 |
| 25 | 440471 | AA886146 | Hs.307944 ESTs | 3.0 |
| | 416355 | H49875 | Hs.268906 ESTs | 3.0 |
| | 408926 | AF217525 | Hs.49002 Down syndrome cell adhesion molecule | 3.0 |
| | 424028 | AF055084 | Hs.153692 Homo sapiens cDNA FLJ14354 fis, clone Y7 | 2.9 |
| | 438201 | AA780243 | Hs.54647 ESTs | 2.9 |
| 30 | 413851 | AW897510 | Hs.137387 ESTs | 2.9 |
| | 402229 | BE262804 | mitochondrial ribosomal protein S2 | 2.9 |
| | 444145 | BE153823 | Hs.282385 ESTs, Weakly similar to 2004399A chromos | 2.9 |
| | 423770 | AW976766 | Hs.132776 Homo sapiens cDNA FLJ10077 fis, clone HE | 2.9 |
| | 439627 | BE621702 | Hs.29076 hypothetical protein FLJ21841 | 2.9 |
| 35 | 414232 | W86946 | Hs.238246 hypothetical protein FLJ22479 | 2.9 |
| | 400533 | | ENSP00000209376*: PRED65 protein (Fragmen | 2.9 |
| | 440483 | AI200836 | Hs.150386 ESTs | 2.9 |
| | 443502 | AI074528 | Hs.133949 ESTs | 2.9 |
| | 449667 | AB023227 | Hs.23860 KIAA1010 protein | 2.9 |
| 40 | 446809 | AW590171 | Hs.101413 ESTs | 2.9 |
| | 408788 | AL134947 | Hs.213956 Homo sapiens BAC clone RP11-1020S from Y | 2.9 |
| | 413627 | BE182082 | Hs.246973 ESTs | 2.9 |
| | 449655 | AI021987 | Hs.59970 ESTs | 2.9 |
| | 407378 | AA299264 | Hs.57776 ESTs, Moderately similar to I38022 hypot | 2.9 |
| 45 | 400090 | | Eos Control | 2.9 |
| | 454968 | AW849046 | gb:IL3-CT0214-150300-085-H06 CT0214 Homo | 2.9 |
| | 423352 | AA324808 | Hs.193576 ESTs | 2.9 |
| | 426197 | AA004410 | Hs.100009 acyl-Coenzyme A oxidase 1, palmitoyl | 2.9 |
| | 452102 | U04343 | Hs.27954 CD86 antigen (CD28 antigen ligand 2, B7- | 2.9 |
| 50 | 415346 | Z43108 | gb:HSC13E071 normalized infant brain cDN | 2.9 |
| | 436726 | AA324975 | Hs.198689 ESTs, Weakly similar to T00079 hypothe | 2.9 |
| | 442513 | AF150207 | Hs.207949 ESTs | 2.9 |
| | 425012 | T77666 | Hs.92414 Homo sapiens cDNA: FLJ22030 fis, clone H | 2.9 |
| | 402322 | | Target Exon | 2.9 |
| 55 | 427235 | AI126288 | Hs.192232 ESTs | 2.9 |
| | 456412 | AW749617 | Hs.280776 tankyrase, TRF1-interacting ankyrin-rela | 2.9 |
| | 431196 | AW974436 | Hs.154929 ESTs | 2.9 |
| | 439379 | AA835002 | Hs.125611 ESTs | 2.9 |
| | 423757 | AL049337 | Hs.132571 Homo sapiens mRNA; cDNA DKFZp564P016 (fr | 2.9 |
| 60 | 445134 | AW161234 | Hs.13993 TBP-like 1 | 2.9 |
| | 435645 | AI052789 | Hs.133263 ESTs | 2.9 |
| | 449385 | AI650471 | Hs.347290 ESTs | 2.9 |
| | 444161 | N52543 | Hs.142940 ESTs | 2.9 |
| | 406635 | U07162 | gb:Human clone LNA11 autoantibody Ig hea | 2.9 |
| 65 | 419239 | AA468183 | Hs.184598 Homo sapiens cDNA: FLJ23241 fis, clone C | 2.9 |
| | 458760 | AI498531 | Hs.111334 ferritin, light polypeptide | 2.9 |
| | 427245 | AA421022 | Hs.97739 ESTs | 2.9 |
| | 400658 | | ENSP00000237081*: KIAA1217 PROTEIN (FRAGM | 2.9 |
| | 430701 | AI760833 | Hs.293971 ESTs | 2.9 |
| 70 | 435294 | T84084 | Hs.196008 Homo sapiens cDNA FLJ11723 fis, clone HE | 2.9 |
| | 429927 | NM_001115 | Hs.2522 adenylate cyclase 8 (brain) | 2.9 |
| | 446160 | AW392197 | Hs.218003 ESTs | 2.9 |
| | 420674 | NM_000055 | Hs.1327 butyrylcholinesterase | 2.9 |
| | 424330 | AW073953 | Hs.333396 Homo sapiens cDNA FLJ13596 fis, clone PL | 2.9 |
| 75 | 418915 | AI474778 | Hs.118977 ESTs | 2.9 |
| | 425922 | AL157466 | Hs.162751 Homo sapiens mRNA; cDNA DKFZp761E2423 (f | 2.9 |
| | 447512 | AW958148 | Hs.129454 ESTs | 2.9 |
| | 449990 | AI279010 | Hs.48821 ESTs | 2.8 |
| | 423779 | AW071837 | Hs.57971 ESTs | 2.8 |
| 80 | 427395 | AW298741 | Hs.97861 ESTs, Moderately similar to I38022 hypot | 2.8 |
| | 416188 | BE157260 | Hs.79070 v-myc avian myelocytomatosis viral oncog | 2.8 |
| | 426746 | J03626 | Hs.2057 uridine monophosphate synthetase (orolat | 2.8 |
| | 400362 | AF068294 | Hs.272414 Homo sapiens HDCMB45P mRNA, partial cds | 2.8 |

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|----|--------|-----------|-----------|--|-----|
| | 457579 | AB030816 | Hs.36761 | HRAS-like suppressor | 2.8 |
| | 451059 | AW297465 | Hs.267150 | KIAA1409 protein | 2.8 |
| | 403903 | | | C5001632*:gij10645308 gb AAG21430.1 AC00 | 2.8 |
| 5 | 444491 | AI151091 | Hs.270714 | ESTs | 2.8 |
| | 455899 | BE155112 | | gb:PM1-HT0350-151299-003-a03 HT0350 Homo | 2.8 |
| | 457292 | AI921270 | Hs.281462 | hypothetical protein FLJ14251 | 2.8 |
| | 428305 | AA446628 | Hs.2799 | cartilage linking protein 1 | 2.8 |
| | 435375 | AI733610 | Hs.187832 | ESTs | 2.8 |
| 10 | 409078 | AW327515 | Hs.346209 | ESTs | 2.8 |
| | 436109 | AA922153 | Hs.132760 | hypothetical protein MGC15729 | 2.8 |
| | 444656 | AI277924 | Hs.145199 | ESTs | 2.8 |
| | 426384 | AI472078 | Hs.303662 | hypothetical protein FLJ13189 (FLJ13189) | 2.8 |
| | 424200 | AA337221 | | gb:EST41944 Endometrial tumor Homo sapie | 2.8 |
| 15 | 438243 | AI581311 | | ESTs | 2.8 |
| | 434012 | AA621425 | Hs.186256 | ESTs | 2.8 |
| | 402711 | | | Target Exon | 2.8 |
| | 442955 | AI683534 | Hs.131583 | ESTs | 2.8 |
| 20 | 418319 | AW611703 | Hs.190173 | ESTs, Weakly similar to A46010 X-linked | 2.8 |
| | 438934 | BE220137 | Hs.124323 | ESTs | 2.8 |
| | 438689 | AW129261 | Hs.181672 | ESTs | 2.8 |
| | 420083 | AA478847 | Hs.42484 | hypothetical protein FLJ10618 | 2.8 |
| | 400315 | U46120 | Hs.193392 | Human expressed unknown mRNA | 2.8 |
| 25 | 433563 | AI732637 | Hs.277901 | ESTs | 2.8 |
| | 458093 | AI207788 | Hs.343628 | sialyltransferase 4B (beta-galactosidase | 2.8 |
| | 409157 | AA064631 | | gb:z772c03.s1 Soares_pineal_gland_N3HPG | 2.8 |
| | 450597 | AI701635 | Hs.207077 | ESTs | 2.8 |
| | 425300 | AW601773 | Hs.270259 | ESTs | 2.8 |
| | 458617 | Z25900 | Hs.18724 | Homo sapiens mRNA; cDNA DKFZp564F093 (fr | 2.8 |
| 30 | 418312 | AW972468 | Hs.170307 | Ral guanine nucleotide exchange factor R | 2.8 |
| | 430335 | D80007 | Hs.239499 | KIAA0185 protein | 2.8 |
| | 454581 | AW809189 | | gb:MR4-ST0118-261099-012-e10 ST0118 Homo | 2.8 |
| | 419735 | AW750056 | Hs.169577 | Homo sapiens cDNA FLJ14743 fis, clone NT | 2.8 |
| 35 | 436265 | AA731331 | Hs.190668 | ESTs | 2.8 |
| | 439481 | AF086294 | Hs.125844 | ESTs | 2.8 |
| | 441964 | AA972619 | Hs.20506 | ESTs, Weakly similar to I38022 hypothe | 2.8 |
| | 422648 | D86983 | Hs.118893 | Melanoma associated gene | 2.8 |
| | 430503 | AA533574 | Hs.152274 | ESTs | 2.8 |
| | 403942 | | | Target Exon | 2.8 |
| 40 | 420565 | AI806770 | Hs.30258 | ESTs | 2.8 |
| | 439069 | H63144 | Hs.184178 | ESTs, Weakly similar to ALUB_HUMAN !!! | 2.8 |
| | 436480 | AJ271643 | Hs.87469 | putative acid-sensing ion channel | 2.8 |
| | 408137 | AI694131 | Hs.29002 | KIAA1706 protein | 2.8 |
| 45 | 451692 | AL137422 | Hs.26849 | Homo sapiens mRNA; cDNA DKFZp761A1623 (f | 2.8 |
| | 419713 | AW968058 | Hs.92381 | nudix (nucleoside diphosphate linked moi | 2.8 |
| | 452526 | W38537 | Hs.280740 | hypothetical protein MGC3040 | 2.8 |
| | 414300 | AI304870 | Hs.188580 | ESTs | 2.8 |
| | 419741 | NM_007019 | Hs.93002 | ubiquitin carrier protein E2-C | 2.8 |
| | 437933 | AI276132 | Hs.146155 | ESTs | 2.7 |
| 50 | 405941 | | | Target Exon | 2.7 |
| | 443210 | AI692649 | Hs.9451 | hypothetical protein MGC13168 | 2.7 |
| | 450651 | W79000 | Hs.44545 | ESTs, Weakly similar to B34087 hypothe | 2.7 |
| | 426765 | AA743603 | Hs.172108 | nucleoporin 88kD | 2.7 |
| | 418886 | AA93982 | Hs.130858 | ESTs | 2.7 |
| 55 | 429483 | AA974832 | Hs.128708 | ESTs | 2.7 |
| | 430426 | AA478807 | Hs.125173 | ESTs | 2.7 |
| | 439019 | AF085902 | Hs.271737 | ESTs | 2.7 |
| | 400924 | | | Target Exon | 2.7 |
| 60 | 458070 | AW503578 | Hs.209406 | ESTs, Weakly similar to I38600 zinc fing | 2.7 |
| | 427299 | AA830210 | Hs.214263 | ESTs, Moderately similar to ALU1_HUMAN A | 2.7 |
| | 442621 | AI004333 | Hs.130553 | ESTs, Weakly similar to ALUA_HUMAN !!! | 2.7 |
| | 437643 | AL080280 | | gb:Homo sapiens mRNA full length insert | 2.7 |
| | 426925 | NM_001196 | Hs.315689 | Homo sapiens cDNA: FLJ22373 fis, clone H | 2.7 |
| 65 | 443392 | AI055821 | Hs.293420 | ESTs | 2.7 |
| | 429972 | AI700846 | Hs.234518 | ribosomal protein L23 | 2.7 |
| | 438875 | AA827640 | Hs.189059 | ESTs | 2.7 |
| | 422551 | AW967284 | | gb:EST379359 MAGE resequences, MAGJ Homo | 2.7 |
| | 446139 | H77395 | Hs.39749 | ESTs | 2.7 |
| 70 | 429115 | AA446728 | Hs.289020 | Homo sapiens cDNA FLJ14098 fis, clone MA | 2.7 |
| | 428612 | AA770001 | Hs.188778 | ESTs | 2.7 |
| | 439947 | AB006627 | Hs.6788 | astrotactin | 2.7 |
| | 439699 | AF086534 | Hs.187561 | ESTs, Moderately similar to ALU1_HUMAN A | 2.7 |
| | 438335 | AI498421 | Hs.243168 | ESTs | 2.7 |
| 75 | 456680 | AL137758 | Hs.116072 | Homo sapiens mRNA; cDNA DKFZp434H245 (fr | 2.7 |
| | 412074 | S74683 | Hs.73139 | ADP-ribosyltransferase 1 | 2.7 |
| | 412225 | AW902042 | | gb:QV0-NN1022-170400-193-c02 NN1022 Homo | 2.7 |
| | 438801 | AA825971 | Hs.124284 | ESTs | 2.7 |
| | 442892 | AI038379 | Hs.131865 | ESTs | 2.7 |
| 80 | 432964 | AF118395 | Hs.279865 | trans-prenyltransferase | 2.7 |
| | 403790 | | | NM_001334*:Homo sapiens cathepsin O (CTS | 2.7 |
| | 400335 | Y13187 | Hs.248068 | Homo sapiens dmd gene, intron 11 | 2.7 |
| | 415467 | RS0891 | Hs.260274 | ESTs | 2.7 |
| | 428715 | AW293716 | Hs.53126 | ESTs | 2.7 |
| | 457750 | AI651474 | Hs.163944 | ESTs | 2.7 |

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|----|--------|----------|-----------|---|-----|
| | 424480 | AA341442 | Hs.205299 | ESTs | 2.7 |
| | 444822 | BE164351 | Hs.292767 | hypothetical protein FLJ23109 | 2.7 |
| | 432651 | AW973744 | Hs.293100 | ESTs | 2.7 |
| | 439823 | AW665287 | Hs.124514 | ESTs | 2.7 |
| 5 | 457021 | AW968934 | Hs.173108 | Homo sapiens cDNA: FLJ21897 fs, clone H | 2.7 |
| | 440026 | AA861299 | Hs.160371 | ESTs | 2.7 |
| | 446960 | AW294936 | Hs.156762 | ESTs | 2.7 |
| | 435046 | AA662772 | Hs.174330 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.7 |
| 10 | 431999 | AL133573 | Hs.272312 | Homo sapiens mRNA; cDNA DKFZp434J2235 (I | 2.7 |
| | 458527 | AI950256 | Hs.224875 | ESTs | 2.7 |
| | 445899 | AI263736 | Hs.145626 | ESTs | 2.7 |
| | 404254 | | | ENSP00000082468::DJ45P21.3 (butyrophilin | 2.7 |
| | 402344 | | | Target Exon | 2.7 |
| 15 | 426503 | AA380153 | | gb:EST93093 Skin tumor 1 Homo sapiens cD | 2.7 |
| | 446420 | AW015693 | Hs.135614 | ESTs | 2.7 |
| | 426914 | AA393328 | Hs.194303 | ESTs | 2.7 |
| | 407903 | AI287341 | Hs.154029 | bHLH factor Hes4 | 2.7 |
| | 433009 | AA761668 | | gb:nz24c08.s1 NCI_CGAP_GCB1 Homo sapiens | 2.7 |
| 20 | 403431 | | | Target Exon | 2.7 |
| | 403290 | | | C10001011::gij4758212[ref]NP_004411.1] d | 2.7 |
| | 435143 | R12375 | Hs.194600 | ESTs | 2.7 |
| | 416569 | H64891 | | gb:yr68h03.r1 Soares fetal liver spleen | 2.7 |
| | 428690 | AI948490 | Hs.98765 | ESTs | 2.7 |
| 25 | 425128 | BE561929 | Hs.154718 | tumor protein D52-like 2 | 2.7 |
| | 443361 | AI792628 | Hs.133273 | ESTs | 2.7 |
| | 404053 | | | Target Exon | 2.7 |
| | 435113 | AA665469 | Hs.117136 | ESTs | 2.6 |
| | 405717 | | | CX000838:gil10092633[ref]NP_055314.1] pu | 2.6 |
| 30 | 413098 | BE065279 | | gb:RC1-BT0314-030500-016-b09 BT0314 Homo | 2.6 |
| | 444884 | AI201094 | Hs.148540 | ESTs | 2.6 |
| | 419015 | T79262 | Hs.14463 | ESTs | 2.6 |
| | 423234 | AA323534 | Hs.296162 | AD037 protein | 2.6 |
| | 406871 | AA993857 | Hs.180842 | ribosomal protein L13 | 2.6 |
| 35 | 426670 | AA431682 | Hs.134832 | ESTs | 2.6 |
| | 408371 | AF161545 | Hs.44439 | hypothetical protein | 2.6 |
| | 413929 | BE501689 | Hs.75617 | collagen, type IV, alpha 2 | 2.6 |
| | 408369 | R38438 | Hs.182575 | solute carrier family 15 (H???) transport | 2.6 |
| | 419817 | AA743434 | Hs.193778 | ESTs | 2.6 |
| 40 | 415788 | AW628686 | Hs.78851 | KIAA0217 protein | 2.6 |
| | 427388 | BE379610 | Hs.177592 | ribosomal protein, large, P1 | 2.6 |
| | 451018 | AW965599 | Hs.247324 | mitochondrial ribosomal protein S14 | 2.6 |
| | 405863 | | | Target Exon | 2.6 |
| | 454037 | AW998716 | | gb:PM4-BN0067-250300-002-f11 BN0067 Homo | 2.6 |
| 45 | 430147 | R60704 | Hs.234434 | hair/enhancer-of-split related with YRP | 2.6 |
| | 425480 | AB023198 | Hs.158135 | KIAA0981 protein | 2.6 |
| | 407182 | AA312551 | Hs.230157 | ESTs | 2.6 |
| | 439538 | AA837323 | Hs.56407 | ESTs | 2.6 |
| | 449249 | T52285 | Hs.193115 | Homo sapiens mRNA for KIAA1764 protein, | 2.6 |
| 50 | 429569 | AA454993 | Hs.138343 | ESTs, Weakly similar to I78885 serine/th | 2.6 |
| | 402936 | | | ENSP00000217246::DJ803K15.1 (novel prote | 2.6 |
| | 420670 | AW973577 | | ESTs | 2.6 |
| | 455409 | AW936832 | | gb:PM2-DT0023-050400-003-h03 DT0023 Homo | 2.6 |
| | 413151 | H47969 | Hs.141971 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.6 |
| 55 | 422484 | AA568770 | Hs.123158 | Homo sapiens cDNA FLJ12830 fs, clone NT | 2.6 |
| | 400780 | | | NM_007325::Homo sapiens glutamate recept | 2.6 |
| | 429258 | AA448765 | | gb:zx10e09.r1 Soares_total_fetus_Nb2HF8_ | 2.6 |
| | 448970 | AW138582 | | gb:UH-BI1-acw-a-06-0-UI.s1 NCI_CGAP_Su | 2.6 |
| | 402615 | | | C1003844::gij6912550[ref]NP_036483.1] ol | 2.6 |
| 60 | 417099 | BE537357 | Hs.306995 | hypothetical protein MGC5457 | 2.6 |
| | 428397 | AA428040 | | gb:zw50e02.r1 Soares_total_fetus_Nb2HF8_ | 2.6 |
| | 449164 | AI632772 | Hs.264165 | ESTs | 2.6 |
| | 412584 | X54870 | Hs.74085 | DNA segment on chromosome 12 (unique) 24 | 2.6 |
| | 443635 | AI080230 | Hs.134214 | ESTs | 2.6 |
| | 402981 | | | Target Exon | 2.6 |
| 65 | 433258 | AI806626 | Hs.207300 | ESTs, Weakly similar to ALUB_HUMAN !!!! | 2.6 |
| | 428917 | AA437337 | Hs.16689 | ESTs | 2.6 |
| | 418557 | BE140602 | Hs.246645 | ESTs | 2.6 |
| | 445211 | BE045601 | Hs.119248 | ESTs, Weakly similar to YC18_HUMAN HYPOT | 2.6 |
| 70 | 404423 | | | C800067::gij10432400[emb]CAC10290.1] (A | 2.6 |
| | 435953 | AI767087 | Hs.114142 | ESTs | 2.6 |
| | 435937 | AA830893 | Hs.119769 | ESTs | 2.6 |
| | 439220 | AW295340 | Hs.130417 | ESTs, Weakly similar to Z195_HUMAN ZINC | 2.6 |
| | 419597 | W73692 | | gb:zd50c01.s1 Soares_fetal_heart_NbHH19W | 2.6 |
| 75 | 436852 | AI814817 | Hs.269099 | ESTs | 2.6 |
| | 430569 | AF241254 | Hs.178098 | angiotensin I converting enzyme (peptidy | 2.6 |
| | 443845 | AI590084 | Hs.148485 | ESTs, Weakly similar to A47161 Mac-2-bin | 2.6 |
| | 414223 | AA954566 | Hs.238246 | hypothetical protein FLJ22479 | 2.6 |
| | 443770 | AW815924 | | gb:MR3-ST0218-191199-012-a10 ST0218 Homo | 2.6 |
| 80 | 450443 | AA009847 | Hs.120744 | ESTs | 2.6 |
| | 435523 | T62849 | Hs.110590 | membrane-spanning 4-domains, subfamily A | 2.6 |
| | 400492 | | | C10001573::gij7302749[gb]AAF57827.1] (AE | 2.6 |
| | 450202 | AW969756 | Hs.34145 | ESTs, Weakly similar to B49647 GTP-bindi | 2.6 |
| | 416845 | H95279 | Hs.293788 | gb:yu20h02.s1 Soares fetal liver spleen | 2.6 |

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|----|--------|-----------|-----------|---|-----|
| | 446423 | AW139655 | Hs.150120 | ESTs | |
| | 447587 | AW292139 | Hs.115789 | ESTs | 2.6 |
| | 437014 | AA808757 | Hs.222531 | ESTs, Weakly similar to S59501 interfero | 2.6 |
| 5 | 426411 | AK000708 | Hs.169764 | hypothetical protein FLJ20701 | 2.6 |
| | 432668 | AA558601 | Hs.43296 | ESTs | 2.6 |
| | 436682 | AI590055 | Hs.124110 | ESTs | 2.6 |
| | 426894 | AI204209 | Hs.143911 | ESTs | 2.6 |
| | 402605 | | | Target Exon | 2.6 |
| 10 | 457554 | AA570111 | Hs.155873 | ESTs, Weakly similar to ALUE_HUMAN !!! | 2.6 |
| | 438166 | N30158 | Hs.122645 | ESTs | 2.6 |
| | 443021 | AA368546 | Hs.8904 | Ig superfamily protein | 2.6 |
| | 427005 | AA394228 | Hs.97494 | ESTs | 2.6 |
| | 437085 | AA743935 | Hs.202329 | ESTs | 2.6 |
| 15 | 408603 | R25283 | Hs.326416 | Homo sapiens mRNA; cDNA DKFZp564H1916 (f | 2.6 |
| | 431019 | NM_005249 | Hs.2714 | forkhead box G1B | 2.6 |
| | 437287 | AA748180 | Hs.159346 | hypothetical protein FLJ21369 | 2.5 |
| | 458552 | AW136139 | Hs.245856 | ESTs | 2.5 |
| | 436350 | AA713661 | Hs.121091 | ESTs | 2.5 |
| 20 | 421988 | AW450481 | Hs.161333 | ESTs | 2.5 |
| | 416704 | H77795 | Hs.39785 | ESTs | 2.5 |
| | 447830 | R98920 | Hs.164314 | ESTs | 2.5 |
| | 413278 | BE563085 | Hs.833 | interferon-stimulated protein, 15 kDa | 2.5 |
| | 406789 | AI041403 | | ribosomal protein L29 | 2.5 |
| 25 | 433683 | AI817723 | Hs.22678 | hypothetical protein FLJ21832 | 2.5 |
| | 433523 | H29882 | | ESTs | 2.5 |
| | 452296 | T65535 | Hs.111539 | ESTs | 2.5 |
| | 428878 | AA436884 | Hs.48926 | ESTs | 2.5 |
| | 442476 | AF069475 | | gb:AF069475 Homo sapiens astrocytoma lib | 2.5 |
| 30 | 452785 | AL359942 | Hs.296434 | erythroid differentiation and denucleati | 2.5 |
| | 444422 | AI768623 | Hs.108264 | ESTs | 2.5 |
| | 420579 | AA278449 | Hs.137429 | ESTs | 2.5 |
| | 416505 | H66470 | Hs.16004 | ESTs | 2.5 |
| | 402595 | | | C1001578:gil6759903:gb:AAF28099.1 (AF1 | 2.5 |
| 35 | 447930 | R44574 | Hs.107510 | ESTs | 2.5 |
| | 459527 | AW977556 | Hs.291735 | ESTs, Weakly similar to I78885 serine/th | 2.5 |
| | 458421 | AI279978 | Hs.22547 | ESTs | 2.5 |
| | 427527 | AI809057 | Hs.293441 | immunoglobulin heavy constant mu | 2.5 |
| | 436035 | AA703679 | Hs.106999 | ESTs, Weakly similar to SYTS_HUMAN SYNAP | 2.5 |
| 40 | 453362 | H14988 | Hs.107375 | ESTs | 2.5 |
| | 423600 | AI633559 | Hs.310359 | ESTs | 2.5 |
| | 433325 | AW206986 | Hs.143905 | ESTs | 2.5 |
| | 415983 | AI436798 | Hs.117078 | Homo sapiens cDNA: FLJ23028 fis, clone L | 2.5 |
| | 431198 | AL047634 | Hs.231913 | ESTs | 2.5 |
| 45 | 430530 | AA480870 | Hs.47660 | ESTs | 2.5 |
| | 455276 | BE176479 | | gb:RC3-HT0585-160300-022-b09 HT0585 Homo | 2.5 |
| | 416665 | H72974 | | gb:yu28a10.s1 Soares fetal liver spleen | 2.5 |
| | 422352 | AA766296 | Hs.99200 | ESTs | 2.5 |
| | 427613 | AW273851 | Hs.98025 | ESTs | 2.5 |
| 50 | 453685 | AL110309 | | gb:DKFZp564L0278_r1 564 (synonym: hibr2) | 2.5 |
| | 450508 | R37408 | Hs.101654 | ESTs | 2.5 |
| | 436361 | AA825814 | Hs.149065 | ESTs | 2.5 |
| | 427709 | AI631811 | Hs.180403 | STRIN protein | 2.5 |
| | 432036 | AF224266 | Hs.272373 | interleukin 20 | 2.5 |
| 55 | 422752 | BE247253 | Hs.21263 | suppressor of potassium transport defect | 2.5 |
| | 413786 | AW613780 | Hs.13500 | ESTs | 2.5 |
| | 439706 | AW872527 | Hs.59761 | ESTs, Weakly similar to DAP1_HUMAN DEATH | 2.5 |
| | 451533 | NM_004657 | Hs.26530 | serum deprivation response (phosphatidyl | 2.5 |
| | 414959 | D59968 | Hs.45184 | Homo sapiens cDNA FLJ12284 fis, clone MA | 2.5 |
| 60 | 449919 | AI674685 | Hs.200141 | ESTs | 2.5 |
| | 458891 | AI659166 | Hs.207144 | ESTs | 2.5 |
| | 427140 | AA398487 | Hs.97642 | ESTs | 2.5 |
| | 405239 | U89281 | | oxidative 3 alpha hydroxysteroid dehydro | 2.5 |
| 65 | 428450 | NM_014791 | Hs.184339 | KIAA0175 gene product | 2.5 |
| | 443753 | AW367578 | Hs.134749 | ESTs | 2.5 |
| | 432888 | T85823 | | gb:yd81a08.s1 Soares fetal liver spleen | 2.5 |
| | 445065 | AI806657 | Hs.302024 | glycoprotein beta-Gal 3'-sulfoltransferas | 2.5 |
| | 431202 | AA495824 | Hs.188822 | ESTs, Weakly similar to A46010 X-linked | 2.5 |
| | 445658 | AI469062 | Hs.172660 | ESTs | 2.5 |
| 70 | 435330 | R16769 | Hs.173174 | Homo sapiens cDNA FLJ14429 fis, clone HE | 2.5 |
| | 435703 | AW630133 | Hs.83313 | GK003 protein | 2.5 |
| | 456232 | AL040357 | | gb:DKFZp434O0713_r1 434 (synonym: htes3) | 2.5 |
| | 421955 | AK000160 | Hs.121576 | Homo sapiens cDNA FLJ20153 fis, clone CO | 2.5 |
| | 420796 | L34355 | Hs.99931 | sarcoglycan, alpha (50kD dystrophin-asso | 2.5 |
| 75 | 425428 | AL110261 | Hs.157211 | DKFZP586B0621 protein | 2.5 |
| | 437627 | AW469925 | Hs.257837 | ESTs | 2.5 |
| | 408574 | AA328046 | Hs.46405 | polymerase (RNA) II (DNA directed) polyp | 2.5 |
| | 418733 | AA227714 | Hs.179703 | KIAA0129 gene product | 2.5 |
| | 440473 | BE562314 | Hs.98711 | Homo sapiens, clone IMAGE:3677165, mRNA, | 2.5 |
| 80 | 422106 | D84239 | Hs.111732 | Fc fragment of IgG binding protein | 2.5 |
| | 411480 | AW848022 | | gb:IL3-CT0214-231299-053-A09 CT0214 Homo | 2.5 |
| | 436391 | AJ227892 | Hs.146274 | ESTs | 2.5 |
| | 424947 | R77952 | | ESTs, Weakly similar to alternatively sp | 2.5 |
| | 450831 | R37974 | Hs.25255 | ESTs | 2.5 |

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|--------|----------|-----------|--|-----|
| 447527 | AI702896 | Hs.42091 | ESTs | 2.5 |
| 424686 | AA345504 | | gb:EST51529 Gall bladder II Homo sapiens | 2.5 |
| 453385 | AW296101 | Hs.252806 | ESTs | 2.5 |

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TABLE 12B:

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|-------------|---------------------------------------|
| Pkey: | Unique Eos probeset identifier number |
| CAT number: | Gene cluster number |
| Accession: | Genbank accession numbers |

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| Pkey | CAT Number | Accession |
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| 408292 | 1050507_1 | AW178363 AW846011 AW845964 AW845988 AW845977 AW846002 |
| 409157 | 110363_1 | AA064631 AA722000 AA064793 |
| 409189 | 110687_1 | AA125984 AA127189 AA065075 AA070377 AA100017 AA079891 AA113255 AA075168 AA082764 AA083380 N84829 AA084752 AA076512 AA085119 |

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| 411480 | 1247089_1 | AW848022 AW848704 AW848168 AW848959 AW848476 AW848699 AW848700 AW848761 |
| 411537 | 1248899_1 | BE073250 BE073378 BE073379 AW850533 AW850529 |
| 411543 | 1249127_1 | AW851248 AW851425 AW850805 AW851021 AW850905 |
| 411565 | 1249756_1 | AW851728 AW851607 AW851621 AW851702 AW851647 AW851727 AW851658 AW851617 AW851628 |

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| 411671 | 125369_1 | BE049094 AA700765 H86770 AA094646 R02483 C03868 N56170 |
| 411688 | 1254076_1 | AW953440 T08189 AW857085 |
| 412021 | 1272156_1 | AW885592 AW885594 AW885579 AW885651 |
| 412135 | 1279148_1 | AW895309 AW895290 AW895307 AW895397 AW895378 AW895402 AW895403 AW895311 AW895298 AW895390 AW895488 AW895468 AW895481 |

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| 412225 | 1284108_1 | AW902042 N77591 |
| 412811 | 132943_1 | H06382 AW957730 AA352014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 A1424991 A1693507 A1863108 AA599060 A1091148 AA598689 |

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|--------|-----------|---|
| 413098 | 1349115_1 | R39887 AAB13482 AW016452 H06383 R41807 A1364268 AA620528 A1241940 AW089149 AW090733 AW088875 Z38240 AA121202 R17734 |
| 413986 | 140720_1 | BE065279 BE065306 BE065164 BE065389 |
| 414988 | 1511316_1 | Z43567 H24159 AA134240 |
| 415131 | 1523680_1 | C17535 D59244 D58878 D79090 |

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| 415346 | 1534581_1 | D61119 D81508 D81734 |
| 416422 | 1593811_1 | Z43108 F06295 R13085 |
| 416569 | 1601567_1 | H60457 H68709 H73528 H54335 R87154 |
| 416665 | 1607797_1 | H64891 R93444 R93458 R05590 |
| 419597 | 1863413_1 | H72974 W28967 |

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| 420352 | 192979_1 | W73692 W73836 W95650 |
| 420670 | 195442_1 | BE258835 AW968316 AA258918 AW843305 R14744 A1580388 BE071923 R36280 |
| 422551 | 217767_1 | AW973577 AA553621 AA279187 |
| 424009 | 234177_1 | AW967284 AA312192 AA312203 |

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| 424200 | 236595_1 | F11690 AW965370 AA333585 D30830 |
| 424686 | 242486_1 | AA337221 AA336756 AW966196 |
| 424947 | 245247_1 | AA345504 AA345251 AW963243 |
| 425146 | 247244_1 | R77952 AA348809 AW959960 AW959962 A1565552 AW070702 AA973910 R85973 |

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|--------|----------|-----------------------------------|
| 425331 | 250199_1 | AW954627 AW954629 AA351258 R25935 |
| 426503 | 268283_1 | AW982128 AA355353 AA427363 |
| 428397 | 290994_1 | AA380153 AA380233 AW963529 |
| 429258 | 301917_1 | AA428040 AW889864 AA836434 |

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| 429940 | 310884_1 | AA448765 C04967 C03045 AA658293 |
| 430183 | 31412_2 | W25215 AA461079 AA461391 |
| 430535 | 319643_1 | BE010038 AA676833 A1311783 T86895 W68032 BE064393 BE064394 BE157228 BE183282 A1936370 AA552514 T67280 AA039909 |
| 432044 | 340773_1 | AW968485 AW968670 AA480922 BE350425 |

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| 432646 | 351909_1 | AW972727 AA524829 AW972733 |
| 432888 | 355780_1 | AW753310 AW974000 AA557840 AA558570 AW751539 |
| 433009 | 357371_1 | T86823 A1821425 A1732232 AA569589 AA570737 |
| 433523 | 368873_1 | AA761668 AA573621 R92814 R09670 |

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| 433835 | 374758_1 | H29882 AW665533 AW149901 A1572917 AA598500 A1686466 A1336390 AW864390 AW864320 |
| 434589 | 38929_1 | A1806185 AA610063 A1693089 A1693075 |
| 436608 | 42361_3 | AF147363 T47219 T47218 |
| 437034 | 431713_1 | AA628980 A126603 BE504035 |

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|--------|----------|---------------------------------|
| 437643 | 43998_1 | AA742643 AA808575 AW976668 |
| 438243 | 453072_1 | AL080280 T73124 H02689 AL080281 |
| 438458 | 457837_1 | A1581311 AA781682 AA781678 |
| 439533 | 47349_1 | AW975186 AA807807 D29548 |

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|--------|----------|----------------------------|
| 442476 | 543547_1 | W76021 AF088052 W72465 |
| 443770 | 579849_1 | AF069475 AF069477 AF069476 |
| 444016 | 58899_1 | AW815924 AW815926 A1085174 |
| 448970 | 791254_1 | AA448154 AV647571 |

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| | | |
|--------|-----------|--|
| 450166 | 82677_1 | AW138582 A1638298 A1631640 A1963868 A1611082 |
| 453685 | 977734_1 | AA429504 R41904 AA279467 H09648 AA007236 |
| 454037 | 996287_1 | AL110309 AW088119 H22881 |
| 454177 | 1049351_1 | AW998716 AW022148 N68020 |

| | | | |
|----|--------|-----------|---|
| | 455409 | 1288355_1 | AW936832 AW936609 AW936657 AW936611 AW936739 AW936734 AW936779 AW936688 AW936659 AW936738 AW936827 AW936737 AW936736 AW936740 AW936833 AW936777 AW936830 AW936834 AW936829 AW936772 AW936638 AW936658 AW936636 AW936774 AW936778 AW936766 AW936776 AW936831 AW9 |
| 5 | 455481 | 1293182_1 | AW948317 AW948322 AW948329 AW948316 AW948298 AW948330 AW948325 AW948324 |
| | 455646 | 1348557_1 | BE064420 BE064435 BE064429 BE064414 BE064400 BE064517 |
| | 455778 | 1364506_1 | BE088746 BE088802 BE088755 BE088876 BE088947 BE088881 BE088952 |
| | 455899 | 1381547_1 | BE155112 BE155154 BE155087 BE155247 BE155499 BE155367 BE155452 |
| | 456232 | 168294_1 | AL040357 AA883621 AA203230 |
| 10 | 456304 | 176820_1 | AI820973 AI734077 AI820984 AA225796 AA225060 AA225101 |
| | 457364 | 328154_1 | AW971037 AA508019 AA492345 |

TABLE 12C:

| | | |
|----|--------------|---|
| 15 | Key: | Unique Eos probeset identifier number |
| | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. |
| | Strand: | Indicates DNA strand from which exons were predicted. |
| | Nt_position: | Indicates nucleotide positions of predicted exons. |

| | Key | Ref | Strand | Nt_position |
|----|--------|---------|--------|---|
| 20 | 400492 | 9213749 | Minus | 123881-124090 |
| | 400533 | 6981826 | Minus | 277132-277595 |
| | 400645 | 8117693 | Minus | 58471-58716 |
| | 400658 | 8118459 | Minus | 73525-73644 |
| 25 | 400780 | 8131663 | Minus | 118372-118619 |
| | 400814 | 8569925 | Minus | 72840-72924,74761-74849 |
| | 400924 | 7107613 | Minus | 30309-30498 |
| | 401272 | 9797373 | Minus | 98374-98509 |
| | 401454 | 9186923 | Minus | 114659-114832 |
| 30 | 401702 | 1871197 | Minus | 68182-68325 |
| | 402229 | 9965022 | Minus | 15739-15951,16166-16779 |
| | 402274 | 2935596 | Plus | 5604-6527 |
| | 402322 | 7630359 | Minus | 75078-75203 |
| | 402344 | 8099256 | Minus | 76812-79040 |
| 35 | 402595 | 7705171 | Plus | 37870-37923,39664-39717,71711-71764 |
| | 402604 | 9909420 | Plus | 20393-20767 |
| | 402605 | 9909420 | Minus | 47680-47973 |
| | 402615 | 9926801 | Plus | 131390-132157 |
| | 402711 | 8901247 | Minus | 114306-115418 |
| 40 | 402747 | 9212492 | Minus | 7105-7357 |
| | 402855 | 9662953 | Minus | 59763-59909 |
| | 402936 | 8894303 | Plus | 51655-51771 |
| | 402981 | 9944246 | Minus | 45716-45889 |
| | 403108 | 8980955 | Plus | 93253-93667 |
| 45 | 403212 | 7630897 | Minus | 156037-156210 |
| | 403288 | 8081479 | Plus | 133763-133899,135813-135958 |
| | 403290 | 8083176 | Plus | 19288-20076 |
| | 403291 | 7230870 | Plus | 95177-95435 |
| | 403349 | 8569773 | Minus | 167815-168374 |
| 50 | 403431 | 7139839 | Plus | 56509-56860 |
| | 403481 | 9965004 | Plus | 93496-93633 |
| | 403696 | 3135242 | Minus | 143467-143634 |
| | 403790 | 8084957 | Minus | 87826-87947,89835-90002 |
| | 403849 | 7708855 | Plus | 95043-96519 |
| 55 | 403903 | 7710671 | Minus | 101165-102597 |
| | 403942 | 7711825 | Minus | 99606-99757 |
| | 403961 | 7596976 | Minus | 110393-110603 |
| | 404053 | 3548785 | Plus | 61797-64205 |
| | 404120 | 7342152 | Plus | 135775-136000 |
| 60 | 404185 | 4572584 | Minus | 129171-129327 |
| | 404254 | 9367203 | Plus | 129350-129873 |
| | 404272 | 9885189 | Plus | 83207-83355,84358-84496,90519-90720,91371-91447 |
| | 404423 | 7407959 | Plus | 34438-34618 |
| | 404584 | 9857511 | Plus | 138651-139153 |
| 65 | 404592 | 9943965 | Minus | 39067-39225 |
| | 404632 | 9796668 | Plus | 45096-45229 |
| | 405046 | 7596829 | Minus | 4373-4528 |
| | 405183 | 7209940 | Plus | 12335-12653 |
| | 405238 | 7249119 | Minus | 51728-51836 |
| 70 | 405239 | 7249119 | Plus | 144345-144464,144690-144836,151750-151883,152407-152484 |
| | 405348 | 2914717 | Minus | 43310-43462 |
| | 405488 | 7131455 | Minus | 75771-75883,105295-105398,134754-134875 |
| | 405558 | 1621110 | Plus | 4502-4644,5983-6083 |
| | 405717 | 9588573 | Plus | 11275-11973 |
| 75 | 405760 | 6066938 | Minus | 37424-38045 |
| | 405863 | 7657810 | Plus | 49410-49620 |
| | 405941 | 6758796 | Plus | 2798-3444 |
| | 406395 | 9256242 | Minus | 20805-20960 |
| | 406478 | 9857502 | Plus | 68314-68523,68853-68950 |
| 80 | 406481 | 9864741 | Minus | 91439-91579 |

TABLE 13A: 964 GENES UP-REGULATED IN LOWER GRADE GLIOBLASTOMA COMPARED TO NORMAL ADULT TISSUES

Table 13A lists about 678 genes up-regulated in lower grade glioblastoma (LGG) compared to normal normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" LGG to "average" normal tissues was greater than or equal to 3.0. The "average" LGG level was set to the 85th

percentile amongst various LGG tumors. The "average" normal tissue level was set to the 85th percentile amongst various non-malignant adult tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

| | Pkey: | Unique Eos probeset identifier number | | | |
|----|----------------|---|-----------|--|------|
| 5 | ExAccn: | Exemplar Accession number, Genbank accession number | | | |
| | UnigeneID: | Unigene number | | | |
| | Unigene Title: | Unigene gene title | | | |
| | R1: | Ratio of LOWER GRADE GLIOBLASTOMA to NORMAL ADULT TISSUES | | | |
| 10 | Pkey | ExAccn | UnigeneID | Unigene Title | R1 |
| | 427343 | AI880044 | Hs.176977 | protein kinase C binding protein 2 | 67.6 |
| | 409389 | AB007979 | Hs.301281 | Homo sapiens mRNA, chromosome 1 specific | 58.2 |
| | 418375 | NM_003081 | Hs.84389 | synaptosomal-associated protein, 25kD | 53.8 |
| 15 | 431917 | D16181 | Hs.2868 | peripheral myelin protein 2 | 50.6 |
| | 428321 | AI699994 | Hs.2868 | peripheral myelin protein 2 | 48.3 |
| | 426325 | D28114 | Hs.169309 | myelin-associated oligodendrocyte basic | 44.3 |
| | 435147 | AL133731 | Hs.4774 | Homo sapiens mRNA; cDNA DKFZp761C1712 (I | 44.2 |
| | 456759 | BE259150 | Hs.127792 | delta (Drosophila)-like 3 | 43.8 |
| 20 | 415817 | U88967 | Hs.78867 | protein tyrosine phosphatase, receptor-I | 40.8 |
| | 429007 | D80642 | | gb:HUM092E09B Human fetal brain (TFujiwa | 40.1 |
| | 417183 | R52089 | Hs.172717 | ESTs | 38.8 |
| | 430838 | N46664 | Hs.169395 | hypothetical protein FLJ12015 | 36.8 |
| | 413472 | BE242870 | Hs.75379 | solute carrier family 1 (glial high affi | 34.9 |
| 25 | 425088 | AA663372 | Hs.169395 | hypothetical protein FLJ12015 | 34.4 |
| | 429276 | AF056085 | Hs.198612 | G protein-coupled receptor 51 | 34.2 |
| | 424140 | Z48051 | Hs.141308 | myelin oligodendrocyte glycoprotein | 33.9 |
| | 450133 | AW969769 | Hs.105201 | ESTs | 33.8 |
| | 423849 | AL157425 | Hs.133315 | Homo sapiens mRNA; cDNA DKFZp761J1324 (I | 32.8 |
| | 413333 | M74028 | Hs.75297 | fibroblast growth factor 1 (acidic) | 32.8 |
| 30 | 449494 | AW237014 | Hs.315369 | Homo sapiens cDNA: FLJ23075 fis, clone L | 31.3 |
| | 402604 | | | Target Exon | 30.3 |
| | 412733 | AA984472 | Hs.74554 | KIAA0080 protein | 28.8 |
| | 416829 | AB013805 | Hs.80220 | catenin (cadherin-associated protein), d | 28.2 |
| 35 | 439239 | AI031540 | Hs.235331 | ESTs | 27.9 |
| | 444378 | R41339 | Hs.47860 | neurotrophic tyrosine kinase, receptor, | 27.1 |
| | 439415 | F05538 | Hs.4273 | ESTs | 26.2 |
| | 425048 | H05468 | Hs.164502 | ESTs | 25.5 |
| | 429903 | AL134197 | Hs.93597 | cyclin-dependent kinase 5, regulatory su | 25.3 |
| 40 | 425057 | AA826434 | Hs.1619 | achaete-scute complex (Drosophila) homol | 24.0 |
| | 425799 | T08133 | Hs.182906 | Homo sapiens mRNA for KIAA1872 protein, | 23.5 |
| | 447359 | NM_012093 | Hs.18268 | adenylate kinase 5 | 23.5 |
| | 425842 | AI587490 | Hs.159523 | NK-2 (Drosophila) homolog B | 23.2 |
| | 423853 | AB011537 | Hs.133466 | slit (Drosophila) homolog 1 | 23.2 |
| | 435708 | AI362949 | Hs.75169 | ESTs | 22.9 |
| 45 | 437268 | AI754847 | Hs.227571 | regulator of G-protein signalling 4 | 21.6 |
| | 409395 | U46745 | Hs.336678 | dystrobrevin, alpha | 21.1 |
| | 441285 | NM_002374 | Hs.167 | microtubule-associated protein 2 | 20.4 |
| | 422656 | AI870435 | Hs.1569 | LIM homeobox protein 2 | 20.0 |
| 50 | 425523 | AB007948 | Hs.158244 | KIAA0479 protein | 19.7 |
| | 437204 | AL110216 | Hs.22826 | ESTs, Weakly similar to I55214 salivary | 19.5 |
| | 416370 | N90470 | Hs.203697 | ESTs, Weakly similar to I38022 hypotheti | 19.4 |
| | 441497 | R51064 | Hs.23172 | ESTs | 19.3 |
| | 453392 | U23752 | Hs.32964 | SRY (sex determining region Y)-box 11 | 19.1 |
| 55 | 408604 | D51408 | Hs.21925 | ESTs | 18.9 |
| | 413597 | AW302885 | Hs.117183 | ESTs | 18.8 |
| | 422980 | N46569 | Hs.76722 | CCAAT/enhancer binding protein (C/EBP), | 18.8 |
| | 428392 | H10233 | Hs.2265 | secretory granule, neuroendocrine protei | 18.6 |
| | 429466 | M85835 | Hs.12827 | ESTs | 18.2 |
| 60 | 448302 | AI480208 | Hs.182906 | Homo sapiens mRNA for KIAA1872 protein, | 18.2 |
| | 439199 | R40373 | Hs.26299 | ESTs | 17.4 |
| | 448743 | AB032962 | Hs.21896 | KIAA1136 protein | 17.4 |
| | 418338 | NM_002522 | Hs.84154 | neuronal pentraxin I | 17.3 |
| | 444513 | AL120214 | Hs.7117 | glutamate receptor, ionotropic, AMPA 1 | 17.2 |
| 65 | 444783 | AK001468 | Hs.62180 | anillin (Drosophila Scraps homolog), act | 17.1 |
| | 447004 | AW296968 | Hs.157539 | ESTs | 16.8 |
| | 425984 | AW836277 | Hs.165636 | hypothetical protein DKFZp761C07121 | 16.5 |
| | 448672 | AI955511 | Hs.225106 | ESTs | 16.1 |
| | 452372 | AI885742 | Hs.228474 | ESTs | 15.8 |
| 70 | 424120 | T80579 | Hs.290270 | ESTs | 15.7 |
| | 424581 | M62062 | Hs.150917 | catenin (cadherin-associated protein), a | 15.6 |
| | 424790 | AL119344 | Hs.13326 | ESTs, Weakly similar to 2004399A chromos | 15.4 |
| | 426269 | H15302 | Hs.168950 | Homo sapiens mRNA; cDNA DKFZp566A1046 (I | 15.2 |
| | 446692 | Z44514 | | Homo sapiens mRNA for KIAA1763 protein, | 15.2 |
| 75 | 453642 | AI370936 | Hs.34074 | dipeptidylpeptidase VI | 14.9 |
| | 429037 | X81895 | Hs.194765 | H.sapiens GENX-5624 mRNA, 3' UTR | 14.7 |
| | 441440 | AI807981 | Hs.30495 | ESTs | 14.6 |
| | 429927 | NM_001115 | Hs.2522 | adenylate cyclase 8 (brain) | 14.6 |
| | 415849 | R20529 | Hs.6806 | ESTs | 14.4 |
| 80 | 418110 | R43523 | Hs.217754 | hypothetical protein FLJ22202 | 14.2 |
| | 434277 | X77748 | Hs.3786 | glutamate receptor, metabotropic 3 | 14.0 |
| | 409638 | AW450420 | Hs.21335 | ESTs | 14.0 |
| | 441350 | AB020690 | Hs.7782 | paraneoplastic antigen MA2 | 13.9 |
| | 415734 | NM_014747 | Hs.78748 | KIAA0237 gene product | 13.7 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 424945 | AI221919 | | hypothetical protein FLJ10582 | 13.6 |
| | 426344 | H41821 | Hs.322469 | transcriptional activator of the c-fos p | 13.4 |
| | 446372 | AB020644 | Hs.14945 | long fatty acyl-CoA synthetase 2 gene | 13.3 |
| 5 | 429946 | R49390 | Hs.254129 | KIAA1678 | 13.3 |
| | 444119 | R41231 | Hs.184261 | ESTs, Weakly similar to T26686 hypothe | 13.3 |
| | 438380 | T06430 | Hs.6194 | chondroitin sulfate proteoglycan BEHAB/b | 13.2 |
| | 415910 | U20350 | Hs.78913 | chemokine (C-X3-C) receptor 1 | 13.2 |
| | 412266 | N59006 | Hs.26133 | ESTs | 13.2 |
| 10 | 436878 | BE465204 | Hs.47448 | ESTs | 13.1 |
| | 428536 | AI143139 | Hs.2288 | visinin-like 1 | 13.1 |
| | 425649 | U30930 | Hs.158540 | UDP glycosyltransferase 8 (UDP-galactose | 13.1 |
| | 428982 | NM_005097 | Hs.194704 | leucine-rich, glioma inactivated 1 | 13.0 |
| | 437948 | AA772920 | Hs.303527 | ESTs | 13.0 |
| 15 | 444124 | R43097 | Hs.6818 | ESTs | 12.9 |
| | 428342 | AI739168 | | Homo sapiens cDNA FLJ13458 fis, clone PL | 12.7 |
| | 419249 | X14767 | Hs.89768 | gamma-aminobutyric acid (GABA) A recepto | 12.7 |
| | 412959 | D87458 | Hs.75090 | KIAA0282 protein | 12.6 |
| | 419863 | AW952691 | Hs.93485 | Homo sapiens mRNA; cDNA DKFZp761D191 (f | 12.6 |
| 20 | 431467 | N71831 | Hs.256398 | Homo sapiens mRNA; cDNA DKFZp434E0528 (f | 12.6 |
| | 431019 | NM_005249 | Hs.2714 | forkhead box G1B | 12.4 |
| | 420547 | AF155140 | Hs.98738 | gonadotropin-regulated testicular RNA he | 12.4 |
| | 430091 | AB032958 | Hs.233023 | KIAA1132 protein | 12.4 |
| | 448595 | AB014544 | Hs.21572 | KIAA0644 gene product | 12.2 |
| 25 | 447342 | AI199268 | Hs.19322 | Homo sapiens, Similar to RIKEN cDNA 2010 | 12.2 |
| | 409049 | AI423132 | Hs.146343 | ESTs | 12.0 |
| | 421264 | AL039123 | Hs.103042 | microtubule-associated protein 1B | 11.9 |
| | 451952 | AL120173 | Hs.301663 | ESTs | 11.9 |
| | 411305 | BE241596 | Hs.69547 | myelin basic protein | 11.8 |
| 30 | 433551 | AI985544 | Hs.12450 | protocadherin 9 | 11.6 |
| | 431988 | AC002302 | Hs.77202 | protein kinase C, beta 1 | 11.6 |
| | 415170 | R44386 | Hs.164578 | ESTs | 11.5 |
| | 408562 | AI436323 | Hs.31141 | Homo sapiens mRNA for KIAA1568 protein, | 11.4 |
| | 435501 | AW051819 | Hs.129908 | KIAA0591 protein | 11.4 |
| 35 | 429656 | X05608 | Hs.211584 | neurofilament, light polypeptide (68kD) | 11.1 |
| | 423419 | R55336 | Hs.23539 | ESTs | 11.1 |
| | 424432 | AB037821 | Hs.146858 | protocadherin 10 | 10.9 |
| | 433896 | AW294729 | Hs.274461 | ESTs | 10.9 |
| | 415293 | R49462 | Hs.106541 | ESTs | 10.9 |
| 40 | 447101 | N72185 | Hs.44189 | ESTs | 10.9 |
| | 440105 | AA694010 | Hs.6932 | Homo sapiens clone 23809 mRNA sequence | 10.9 |
| | 438054 | AA776626 | Hs.169309 | ESTs | 10.8 |
| | 433597 | AA708205 | Hs.100343 | ESTs | 10.7 |
| | 421659 | NM_014459 | Hs.106511 | protocadherin 17 | 10.6 |
| 45 | 445102 | AW204610 | Hs.22270 | ESTs | 10.6 |
| | 425154 | NM_001851 | Hs.154850 | collagen, type IX, alpha 1 | 10.6 |
| | 451625 | R56793 | Hs.106576 | alanine-glyoxylate aminotransferase 2-li | 10.6 |
| | 435191 | R15912 | Hs.4817 | Homo sapiens clone 24461 mRNA sequence | 10.6 |
| | 450154 | R15891 | Hs.281587 | Human (clone CTG-A4) mRNA sequence | 10.5 |
| 50 | 407886 | AW969688 | Hs.100826 | ESTs | 10.4 |
| | 420345 | AW295230 | Hs.25231 | ESTs | 10.4 |
| | 426728 | NM_016625 | Hs.191381 | hypothetical protein | 10.3 |
| | 424997 | AL138167 | Hs.96920 | ESTs | 10.3 |
| | 440184 | AB002297 | Hs.7022 | dedicator of cyto-kinesis 3 | 10.2 |
| 55 | 419078 | M93119 | Hs.89584 | insulinoma-associated 1 | 10.2 |
| | 445495 | BE622641 | Hs.38489 | ESTs, Weakly similar to I38022 hypothe | 10.1 |
| | 416857 | AA188775 | Hs.292453 | ESTs | 10.0 |
| | 445041 | T64183 | Hs.282982 | solute carrier | 10.0 |
| | 419271 | N34901 | Hs.238532 | ESTs | 9.8 |
| 60 | 446711 | AF169692 | Hs.12450 | protocadherin 9 | 9.8 |
| | 426847 | S78723 | Hs.298623 | 5-hydroxytryptamine (serotonin) receptor | 9.7 |
| | 427304 | AA761526 | Hs.163853 | ESTs | 9.7 |
| | 418097 | R45137 | Hs.21868 | ESTs | 9.7 |
| | 449300 | AI656959 | Hs.346514 | ESTs | 9.7 |
| 65 | 419985 | H66373 | Hs.5856 | ESTs, Highly similar to bA393J16.3 [H.s.a | 9.7 |
| | 443785 | AW449952 | Hs.190125 | basic-helix-loop-helix-PAS protein | 9.5 |
| | 415486 | H12214 | Hs.13284 | ESTs, Weakly similar to 2109260A B cell | 9.5 |
| | 453220 | AB033089 | Hs.32452 | Homo sapiens mRNA for KIAA1263 protein, | 9.5 |
| | 438209 | AL120659 | Hs.6111 | aryl-hydrocarbon receptor nuclear transl | 9.4 |
| 70 | 424028 | AF055084 | Hs.153692 | Homo sapiens cDNA FLJ14354 fis, clone Y7 | 9.4 |
| | 419683 | AA248897 | Hs.48784 | ESTs | 9.4 |
| | 414175 | AI308876 | Hs.103849 | hypothetical protein DKFZp761D112 | 9.2 |
| | 400292 | AA250737 | Hs.72472 | BMP-R1B | 9.2 |
| | 408947 | AL080093 | Hs.49117 | Homo sapiens mRNA; cDNA DKFZp564N1662 (f | 9.2 |
| 75 | 454048 | H05626 | Hs.6921 | ESTs | 9.2 |
| | 454027 | R40192 | Hs.21527 | Human DNA sequence from clone GS1-115M3 | 9.1 |
| | 441016 | AW138653 | Hs.25845 | ESTs | 9.0 |
| | 425187 | AW014486 | Hs.22509 | ESTs | 9.0 |
| | 445568 | H00918 | Hs.268744 | KIAA1796 protein | 8.9 |
| 80 | 453941 | U39817 | Hs.36820 | Bloom syndrome | 8.9 |
| | 422411 | AW749443 | Hs.22511 | ESTs | 8.8 |
| | 447350 | AI375572 | Hs.172634 | ESTs | 8.8 |
| | 424481 | R19453 | Hs.1787 | proteolipid protein 1 (Pefizeus-Merzbac | 8.7 |
| | 448902 | Z45998 | Hs.22543 | Homo sapiens mRNA; cDNA DKFZp76111912 (f | 8.7 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 448986 | H42169 | Hs.347310 | hypothetical protein FLJ14627 | 8.6 |
| | 423135 | N67655 | Hs.26411 | ESTs | 8.5 |
| | 418030 | BE207573 | Hs.83321 | neuromedin B | 8.4 |
| 5 | 448769 | N66037 | Hs.38173 | ESTs | 8.4 |
| | 407748 | AL079409 | Hs.38176 | KIAA0606 protein; SCN Circadian Oscillat | 8.3 |
| | 400293 | N51002 | Hs.306480 | Homo sapiens mRNA; cDNA DKFZp761E2112 (f | 8.3 |
| | 415279 | F04237 | Hs.1447 | glial fibrillary acidic protein | 8.2 |
| | 451516 | AI800515 | Hs.12024 | ESTs | 8.2 |
| 10 | 419629 | AB020695 | Hs.91662 | KIAA0888 protein | 8.2 |
| | 437034 | AA742643 | | gb:ny91c01.s1 NCJ_CGAP_GCB1 Homo sapiens | 8.2 |
| | 456965 | AW131888 | Hs.172792 | ESTs, Weakly similar to hypothetical pro | 8.1 |
| | 417417 | F05745 | Hs.89512 | ATPase, Ca transporting, plasma membrane | 8.1 |
| | 452279 | AA286844 | Hs.61260 | hypothetical protein FLJ13164 | 8.1 |
| 15 | 422864 | AA318323 | Hs.12627 | gb:EST20390 Retina II Homo sapiens cDNA | 8.1 |
| | 452526 | W38537 | Hs.280740 | hypothetical protein MGC3040 | 8.0 |
| | 435793 | AB037734 | Hs.4993 | KIAA1313 protein | 7.9 |
| | 415669 | NM_005025 | Hs.78589 | serine (or cysteine) proteinase inhibitor | 7.9 |
| | 407168 | R45175 | Hs.117183 | ESTs | 7.9 |
| 20 | 447414 | D82343 | Hs.74376 | neuroblastoma (nerve tissue) protein | 7.8 |
| | 442710 | AI015631 | Hs.23210 | ESTs | 7.8 |
| | 416836 | D54745 | Hs.80247 | cholecystokinin | 7.8 |
| | 419721 | NM_001650 | Hs.288650 | aquaporin 4 | 7.7 |
| | 438080 | AA777381 | Hs.291530 | ESTs, Weakly similar to ALUC_HUMAN !!!! | 7.7 |
| 25 | 436109 | AA922153 | Hs.132760 | hypothetical protein MGC15729 | 7.7 |
| | 428845 | AL157579 | Hs.153610 | KIAA0751 gene product | 7.7 |
| | 448321 | NM_005883 | Hs.20912 | adenomatous polyposis coli like | 7.7 |
| | 410305 | AF030409 | Hs.62185 | solute carrier family 9 (sodium/hydrogen | 7.6 |
| | 443392 | AI055821 | Hs.293420 | ESTs | 7.6 |
| 30 | 429038 | AL023513 | Hs.194766 | seizure related gene 6 (mouse)-like | 7.5 |
| | 418738 | AW388633 | Hs.6682 | solute carrier family 7, (cationic amino | 7.5 |
| | 423361 | AW170055 | Hs.47628 | ESTs | 7.5 |
| | 447198 | D61523 | Hs.283435 | ESTs | 7.5 |
| | 448555 | AI536697 | Hs.159863 | ESTs | 7.5 |
| 35 | 458332 | AI000341 | Hs.220491 | ESTs | 7.4 |
| | 407034 | U84540 | | gb:Human dystrobrevin isoform DTN-3 (DTN | 7.4 |
| | 425354 | U62027 | Hs.155935 | complement component 3a receptor 1 | 7.4 |
| | 426814 | AF036943 | Hs.172619 | myelin transcription factor 1-like | 7.4 |
| | 448507 | AL133109 | Hs.21333 | Homo sapiens mRNA; cDNA DKFZp566N1047 (f | 7.4 |
| 40 | 439845 | AL355743 | Hs.56663 | Homo sapiens EST from clone 41214, full | 7.4 |
| | 449078 | AK001256 | Hs.22975 | KIAA1576 protein | 7.3 |
| | 410102 | AW248508 | Hs.279727 | ESTs; homologue of PEM-3 [Ciona savignyi | 7.2 |
| | 425741 | AF052152 | Hs.159412 | Homo sapiens clone 24528 mRNA sequence | 7.2 |
| | 440210 | AW674562 | Hs.125296 | ESTs | 7.2 |
| 45 | 415651 | AI207162 | Hs.3815 | slathmin-like-protein RB3 | 7.2 |
| | 428409 | AW117207 | Hs.98523 | ESTs | 7.1 |
| | 413409 | AI638418 | Hs.1440 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypep | 7.1 |
| | 443992 | AW022228 | Hs.322922 | ESTs | 7.1 |
| | 455601 | AI368680 | Hs.816 | SRY (sex determining region Y)-box 2 | 7.1 |
| 50 | 427540 | R12014 | Hs.20976 | ESTs | 7.0 |
| | 439979 | AW600291 | Hs.6823 | hypothetical protein FLJ10430 | 7.0 |
| | 424893 | AW295112 | Hs.153548 | Homo sapiens cDNA FLJ13303 fis, clone OV | 7.0 |
| | 452355 | N54926 | Hs.29202 | G protein-coupled receptor 34 | 7.0 |
| | 414696 | AF002020 | Hs.76918 | Niemann-Pick disease, type C1 | 7.0 |
| 55 | 440152 | AB002376 | Hs.7006 | KIAA0378 protein | 7.0 |
| | 454293 | H49739 | Hs.134013 | ESTs, Moderately similar to HK61_HUMAN H | 7.0 |
| | 425782 | U66468 | Hs.159525 | cell growth regulatory with EF-hand doma | 7.0 |
| | 416805 | F13271 | Hs.79981 | Human clone 23560 mRNA sequence | 7.0 |
| | 419991 | AJ000098 | Hs.94210 | eyes absent (Drosophila) homolog 1 | 7.0 |
| 60 | 424343 | AW956360 | Hs.4748 | adenylate cyclase activating polypeptide | 6.9 |
| | 408369 | R38438 | Hs.182575 | solute carrier family 15 (H777) transport | 6.9 |
| | 449605 | AW138581 | Hs.198416 | ESTs | 6.9 |
| | 444396 | T65213 | Hs.4257 | ESTs | 6.9 |
| | 444165 | AL137443 | Hs.10441 | hypothetical protein FLJ11236 | 6.9 |
| 65 | 414245 | BE148072 | Hs.75850 | WAS protein family, member 1 | 6.9 |
| | 412155 | R38167 | Hs.12449 | Homo sapiens transmembrane protein HTMP1 | 6.9 |
| | 424624 | AB032947 | Hs.151301 | Ca2+-dependent activator protein for secr | 6.9 |
| | 448681 | AL109781 | Hs.21754 | Homo sapiens mRNA full length insert cDN | 6.9 |
| | 411379 | AI816344 | Hs.12554 | ESTs, Weakly similar to NPL4_HUMAN NUCLE | 6.9 |
| 70 | 446782 | AI653048 | Hs.144006 | ESTs | 6.8 |
| | 426919 | AL041228 | | ELAV (embryonic lethal, abnormal vision, | 6.8 |
| | 423346 | AI267677 | Hs.127416 | synaptotagmin 1 | 6.8 |
| | 436643 | AA575626 | Hs.10941 | ESTs, Weakly similar to IPP1_HUMAN PROTE | 6.8 |
| | 414922 | D00723 | Hs.77631 | glycine cleavage system protein H (amino | 6.8 |
| 75 | 410037 | AB020725 | Hs.58009 | KIAA0918 protein | 6.8 |
| | 442613 | AI004002 | Hs.130522 | Kv channel-interacting protein 1 | 6.8 |
| | 413589 | AW452631 | Hs.313803 | ESTs, Highly similar to AF157833 1 noncl | 6.8 |
| | 422175 | N79885 | Hs.6382 | ESTs, Highly similar to T00391 hypotheti | 6.8 |
| | 421141 | AW117261 | Hs.125914 | ESTs | 6.7 |
| 80 | 452786 | R61362 | Hs.106642 | ESTs, Weakly similar to T09052 hypotheti | 6.7 |
| | 441916 | AA993571 | Hs.129075 | ESTs | 6.7 |
| | 448533 | AL119710 | Hs.21365 | nucleosome assembly protein 1-like 3 | 6.7 |
| | 428037 | N47474 | Hs.89230 | potassium intermediate/small conductance | 6.7 |
| | 423343 | AA324643 | Hs.246106 | ESTs | 6.7 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 456723 | Z43902 | Hs.4748 | adenylate cyclase activating polypeptide | 6.7 |
| | 414214 | D49958 | Hs.75819 | glycoprotein M5A | 6.7 |
| | 434811 | AW971205 | Hs.114280 | ESTs | 6.7 |
| 5 | 424922 | BE386547 | Hs.217112 | hypothetical protein MGC10825 | 6.7 |
| | 449328 | AI962493 | Hs.345303 | ESTs | 6.6 |
| | 431553 | X78075 | Hs.2799 | cartilage linking protein 1 | 6.6 |
| | 420156 | AW449258 | Hs.6187 | ESTs | 6.6 |
| | 431117 | AF003522 | Hs.250500 | delta (Drosophila)-like 1 | 6.6 |
| 10 | 422960 | AW890487 | Hs.63984 | cadherin 13, H-cadherin (heart) | 6.6 |
| | 429239 | AA448419 | Hs.45209 | ESTs | 6.5 |
| | 453924 | R49295 | Hs.24886 | ESTs | 6.5 |
| | 433929 | AI375499 | Hs.27379 | ESTs | 6.5 |
| | 426529 | AF090100 | Hs.170241 | Homo sapiens clone IMAGE 23915 | 6.5 |
| 15 | 414683 | S78296 | Hs.76888 | hypothetical protein MGC12702 | 6.4 |
| | 409746 | NM_004794 | Hs.56294 | RAB33A, member RAS oncogene family | 6.4 |
| | 419169 | AW851980 | Hs.262346 | ESTs, Weakly similar to S72482 hypothesi | 6.4 |
| | 453590 | AF150278 | Hs.33578 | KIAA0820 protein | 6.4 |
| | 422263 | AA307639 | Hs.129908 | KIAA0591 protein | 6.4 |
| 20 | 421688 | AK000307 | Hs.106825 | hypothetical protein FLJ20300 | 6.4 |
| | 447197 | R36075 | | gb:yt88b01.s1 Soares placenta Nb2HP Homo | 6.3 |
| | 425588 | F07396 | Hs.46627 | ESTs | 6.3 |
| | 410366 | AI267589 | Hs.302689 | hypothetical protein | 6.3 |
| | 419498 | AL036591 | Hs.20887 | hypothetical protein FLJ10392 | 6.3 |
| 25 | 446997 | AA383439 | Hs.16758 | Spir-1 protein | 6.3 |
| | 427958 | AA418000 | Hs.98280 | potassium intermediate/small conductance | 6.3 |
| | 445908 | R13580 | Hs.13436 | Homo sapiens clone 24425 mRNA sequence | 6.3 |
| | 412068 | S72043 | Hs.73133 | metallothionein 3 (growth inhibitory fac | 6.3 |
| | 452834 | AI638627 | Hs.105685 | KIAA1688 protein | 6.3 |
| 30 | 408790 | AW580227 | Hs.47860 | neurotrophic tyrosine kinase, receptor, | 6.3 |
| | 418512 | AW489874 | | diacylglycerol kinase, zeta (104kD) | 6.2 |
| | 410099 | AA081630 | | KIAA0036 gene product | 6.2 |
| | 452744 | AI267652 | Hs.246107 | Homo sapiens mRNA; cDNA DKFZp434E082 (fr | 6.2 |
| | 427897 | NM_017413 | Hs.303084 | apelin; peptide ligand for APJ receptor | 6.2 |
| 35 | 416427 | BE244050 | Hs.79307 | Rac/Cdc42 guanine exchange factor (GEF) | 6.2 |
| | 439274 | AF086092 | Hs.48372 | ESTs | 6.2 |
| | 431552 | AI815863 | Hs.259873 | axonal transport of synaptic vesicles | 6.2 |
| | 439607 | BE540565 | Hs.159460 | ESTs | 6.2 |
| | 408950 | AA707814 | Hs.14945 | long fatty acyl-CoA synthetase 2 gene | 6.2 |
| 40 | 412709 | AL022327 | Hs.74518 | KIAA0027 protein | 6.2 |
| | 435624 | AF218942 | Hs.24889 | formin 2 | 6.1 |
| | 425977 | R15138 | Hs.165570 | Homo sapiens clone 25052 mRNA sequence | 6.1 |
| | 420077 | AW512260 | Hs.87767 | ESTs | 6.1 |
| | 457005 | AJ007421 | Hs.172597 | sal (Drosophila)-like 3 | 6.1 |
| 45 | 440471 | AA886146 | Hs.307944 | ESTs | 6.1 |
| | 423770 | AW976766 | Hs.132776 | Homo sapiens cDNA FLJ10077 fis, clone HE | 6.1 |
| | 438624 | AA889055 | Hs.123468 | ESTs | 6.1 |
| | 452752 | AW044058 | Hs.33578 | KIAA0820 protein | 6.1 |
| | 438208 | AL041224 | Hs.65379 | ESTs | 6.1 |
| 50 | 416072 | AL110370 | Hs.79000 | growth associated protein 43 | 6.1 |
| | 407808 | AA663559 | Hs.279789 | histone deacetylase 3 | 6.1 |
| | 433701 | AW445023 | Hs.15155 | ESTs | 6.1 |
| | 419704 | AA429104 | Hs.45067 | ESTs | 6.1 |
| | 429250 | H56585 | Hs.198308 | tryptophan rich basic protein | 6.1 |
| 55 | 433244 | AB040943 | Hs.271285 | KIAA1510 protein | 6.0 |
| | 422544 | AB018259 | Hs.118140 | KIAA0716 gene product | 6.0 |
| | 420133 | AA426117 | Hs.155543 | ESTs | 6.0 |
| | 440491 | R35252 | Hs.130558 | ESTs, Weakly similar to 2109260A B cell | 6.0 |
| | 422728 | AW937826 | Hs.103262 | ESTs, Weakly similar to ZN91_HUMAN ZINC | 6.0 |
| 60 | 415257 | F03016 | Hs.27513 | ESTs | 5.9 |
| | 417160 | N76497 | Hs.1787 | proteolipid protein 1 (Pelizaeus-Merzbac | 5.9 |
| | 430188 | AL049242 | Hs.234794 | Homo sapiens mRNA; cDNA DKFZp564B083 (fr | 5.9 |
| | 437372 | AA323968 | Hs.283631 | hypothetical protein DKFZp547G183 | 5.9 |
| | 430471 | AF064845 | Hs.241523 | hypothetical protein FLJ10142 | 5.9 |
| 65 | 433523 | H29882 | | ESTs | 5.9 |
| | 408926 | AF217525 | Hs.49002 | Down syndrome cell adhesion molecule | 5.9 |
| | 427317 | AB028955 | Hs.175780 | KIAA1032 protein | 5.9 |
| | 426140 | AF131798 | Hs.343768 | Homo sapiens clone 25119 mRNA sequence | 5.9 |
| | 409892 | AW956113 | Hs.7149 | gb:EST368183 MAGE resequences, MAGD Homo | 5.8 |
| 70 | 459516 | AI049662 | Hs.246858 | EST | 5.8 |
| | 442910 | AI365130 | Hs.11307 | ESTs, Weakly similar to T15326 hypothesi | 5.8 |
| | 414737 | AI160386 | Hs.125087 | ESTs | 5.8 |
| | 424332 | AA338919 | Hs.101615 | ESTs | 5.8 |
| | 403142 | | | NM_002706; Homo sapiens protein phosphat | 5.8 |
| 75 | 420111 | AA255652 | | gb:zs21h11.1 NCI_CGAP_GCB1 Homo sapiens | 5.8 |
| | 450813 | AI739625 | Hs.203376 | ESTs | 5.8 |
| | 402145 | | | Target Exon | 5.8 |
| | 434792 | AA649253 | Hs.132458 | ESTs | 5.8 |
| | 422421 | AA325138 | Hs.235873 | hypothetical protein FLJ22672 | 5.8 |
| 80 | 445745 | AB007924 | Hs.13245 | KIAA0455 gene product | 5.8 |
| | 420608 | BE548277 | Hs.103104 | ESTs | 5.8 |
| | 451407 | AA131376 | Hs.343809 | fibroblast growth factor 12B | 5.7 |
| | 441102 | AA973905 | | intermediate filament protein syncofin | 5.7 |
| | 424560 | AA158727 | Hs.150555 | protein predicted by clone 23733 | 5.7 |

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|----|--------|-----------|-----------|--|-----|
| | 430287 | AW182459 | Hs.125759 | ESTs, Weakly similar to LEU5_HUMAN LEUKE | 5.7 |
| | 405238 | | | Target Exon | 5.7 |
| | 432890 | NM_014442 | Hs.279751 | sialic acid binding Ig-like lectin 8 | 5.7 |
| | 440492 | R39127 | Hs.21433 | hypothetical protein DKFZp547J036 | 5.7 |
| 5 | 413492 | D87470 | Hs.75400 | KIAA0280 protein | 5.7 |
| | 427624 | AA406245 | Hs.24895 | ESTs | 5.7 |
| | 418079 | R40058 | Hs.6911 | ESTs | 5.6 |
| | 424458 | M29273 | Hs.1780 | myelin associated glycoprotein | 5.6 |
| | 448299 | AA497044 | Hs.20887 | hypothetical protein FLJ10392 | 5.6 |
| 10 | 429698 | AI685086 | Hs.26339 | ESTs, Weakly similar to S21348 probable | 5.6 |
| | 430228 | AW950939 | Hs.6382 | ESTs, Highly similar to T00391 hypotheti | 5.6 |
| | 445255 | NM_014841 | Hs.12477 | synaptosomal-associated protein, 91 kDa | 5.6 |
| | 436887 | AW953157 | Hs.193235 | hypothetical protein DKFZp547D155 | 5.6 |
| | 452898 | AA814497 | Hs.78792 | ESTs | 5.6 |
| 15 | 435538 | AB011540 | Hs.4930 | low density lipoprotein receptor-related | 5.6 |
| | 436035 | AA703679 | Hs.106999 | ESTs, Weakly similar to SYT5_HUMAN SYNAP | 5.5 |
| | 412190 | R16180 | Hs.274461 | ESTs | 5.5 |
| | 459278 | AW294659 | Hs.34054 | Homo sapiens cDNA: FLJ22488 fis, clone H | 5.5 |
| | 416490 | AF090116 | Hs.79348 | regulator of G-protein signalling 7 | 5.5 |
| 20 | 423449 | AI497900 | Hs.33067 | ESTs | 5.5 |
| | 440866 | AI703103 | Hs.271360 | hypothetical protein MGC16275 | 5.5 |
| | 432154 | AI701523 | Hs.112577 | ESTs | 5.4 |
| | 423476 | AL035633 | | Human DNA sequence from clone RPS-1046G1 | 5.4 |
| 25 | 428588 | F12101 | Hs.185701 | Homo sapiens mRNA full length insert cDN | 5.4 |
| | 447773 | AI423930 | Hs.36790 | ESTs, Weakly similar to putative p150 [H | 5.4 |
| | 436936 | AL134451 | Hs.197478 | ESTs | 5.4 |
| | 427250 | R35941 | Hs.25418 | ESTs | 5.4 |
| | 427302 | AA400540 | Hs.135282 | Homo sapiens cDNA FLJ11554 fis, clone HE | 5.4 |
| 30 | 452856 | AF034799 | Hs.30881 | protein tyrosine phosphatase, receptor t | 5.4 |
| | 428795 | R45503 | Hs.97469 | ESTs, Highly similar to A39769 N-acetyl | 5.4 |
| | 407385 | AA610150 | Hs.272072 | ESTs, Weakly similar to I38022 hypotheti | 5.4 |
| | 405348 | | | C7001664:gi12698061 dbj BAB21849.1 (AB | 5.4 |
| | 438330 | AW450572 | Hs.257316 | ESTs | 5.3 |
| 35 | 426503 | AA380153 | | gb:EST93093 Skin tumor I Homo sapiens cD | 5.3 |
| | 448148 | NM_016578 | Hs.20509 | HBV pX associated protein-8 | 5.3 |
| | 410386 | W26187 | Hs.3327 | Homo sapiens cDNA: FLJ22219 fis, clone H | 5.3 |
| | 445225 | AI216555 | Hs.202398 | ESTs | 5.3 |
| | 428784 | Y12851 | Hs.193470 | purinergic receptor P2X, ligand-gated io | 5.3 |
| 40 | 418759 | AA227879 | Hs.187621 | ESTs | 5.3 |
| | 402605 | | | Target Exon | 5.3 |
| | 412046 | Y07847 | Hs.73088 | RAS-related on chromosome 22 | 5.3 |
| | 423869 | BE409301 | Hs.134012 | C1q-related factor | 5.2 |
| | 430130 | AL137311 | Hs.234074 | Homo sapiens mRNA; cDNA DKFZp761G02121 (| 5.2 |
| 45 | 453096 | AW294631 | Hs.11325 | ESTs | 5.2 |
| | 450475 | AW805634 | Hs.205015 | ESTs | 5.2 |
| | 429139 | F09092 | Hs.66087 | ESTs | 5.2 |
| | 451783 | R42554 | Hs.210862 | T-box, brain, 1 | 5.2 |
| | 436568 | H12049 | Hs.91564 | ESTs | 5.2 |
| 50 | 424330 | AW073953 | Hs.333396 | Homo sapiens cDNA FLJ13596 fis, clone PL | 5.2 |
| | 408453 | AI369838 | Hs.45127 | chondroitin sulfate proteoglycan 5 (neur | 5.2 |
| | 447499 | AW262580 | Hs.147674 | protocadherin beta 16 | 5.2 |
| | 402855 | | | NM_001839: Homo sapiens calponin 3, acid | 5.2 |
| | 420805 | L10333 | Hs.99947 | reticulon 1 | 5.2 |
| 55 | 426457 | AW894667 | Hs.169965 | chimerin (chimaerin) 1 | 5.2 |
| | 417355 | D13168 | Hs.82002 | endothelin receptor type B | 5.1 |
| | 429469 | M64590 | Hs.27 | glycine dehydrogenase (decarboxylating; | 5.1 |
| | 450639 | AI703186 | Hs.277174 | ESTs | 5.1 |
| | 412811 | H06382 | | ESTs | 5.1 |
| 60 | 400379 | NM_018432 | | Homo sapiens ovarian cancer related prot | 5.1 |
| | 441869 | NM_003947 | Hs.8004 | huntingtin-associated protein interactin | 5.1 |
| | 442832 | AW206560 | Hs.253569 | ESTs | 5.1 |
| | 422709 | AA315331 | Hs.153485 | ESTs | 5.1 |
| | 411555 | AF113537 | Hs.70669 | HMP19 protein | 5.1 |
| 65 | 419043 | T19167 | Hs.89566 | ets variant gene 1 | 5.0 |
| | 430979 | AI479755 | Hs.129010 | ESTs | 5.0 |
| | 451320 | AW118072 | | diacylglycerol kinase, zeta (104kD) | 5.0 |
| | 423678 | AW963357 | Hs.7847 | ESTs | 5.0 |
| | 429918 | AW873986 | Hs.119383 | ESTs | 5.0 |
| 70 | 452785 | AL359942 | Hs.296434 | erythroid differentiation and denucleati | 5.0 |
| | 453128 | AW026516 | Hs.31791 | acytphosphatase 2, muscle type | 5.0 |
| | 428001 | H97428 | Hs.219907 | ESTs, Moderately similar to Transforming | 5.0 |
| | 430183 | BE010038 | | gb:PM3-BN0176-100400-001-g04 BN0176 Homo | 5.0 |
| | 449969 | AW295142 | Hs.180187 | Homo sapiens cDNA FLJ14337 fis, clone PL | 5.0 |
| | 439108 | AW163034 | Hs.6467 | synaptogyrin 3 | 5.0 |
| 75 | 426271 | AF026547 | Hs.169047 | chondroitin sulfate proteoglycan 3 (neur | 5.0 |
| | 451752 | AB032997 | Hs.26966 | KIAA1171 protein | 5.0 |
| | 420578 | AA813546 | Hs.99034 | GTP-binding protein Rho7 | 4.9 |
| | 427315 | AA179949 | Hs.175563 | Homo sapiens mRNA; cDNA DKFZp564N0763 (I | 4.9 |
| 80 | 428186 | AW504300 | Hs.295605 | mannosidase, alpha, class 2A, member 2 | 4.9 |
| | 445133 | AW157646 | Hs.198689 | ESTs | 4.9 |
| | 410359 | R38624 | Hs.106313 | ESTs | 4.9 |
| | 427144 | X95097 | Hs.2126 | vasoactive intestinal peptide receptor 2 | 4.9 |
| | 448548 | R13209 | Hs.21413 | solute carrier family 12, (potassium-chl | 4.9 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 457561 | AA331517 | Hs.286055 | chimerin (chimaerin) 2 | 4.9 |
| | 409100 | H98216 | Hs.42245 | ESTs, Moderately similar to I38022 hypol | 4.9 |
| | 437117 | AL049256 | Hs.122593 | ESTs | 4.9 |
| | 415101 | R45531 | Hs.144534 | ESTs | 4.9 |
| 5 | 438458 | AW975186 | | gb:EST387294 MAGE resequences, MAGN Homo | 4.9 |
| | 442026 | AJ243749 | Hs.8074 | brain-specific angiogenesis inhibitor 3 | 4.9 |
| | 438283 | AJ458931 | Hs.37282 | ESTs | 4.9 |
| | 449714 | AB033015 | Hs.23941 | KIAA1189 protein | 4.9 |
| 10 | 420871 | AA702972 | Hs.65300 | ESTs | 4.9 |
| | 425256 | BE297611 | Hs.155392 | collapsin response mediator protein 1 | 4.9 |
| | 424001 | W67883 | Hs.137476 | paternally expressed 10 | 4.9 |
| | 419103 | Z40229 | Hs.96423 | hypothetical protein FLJ23033 | 4.9 |
| | 446727 | AB011095 | Hs.16032 | KIAA0523 protein | 4.8 |
| 15 | 408670 | AF160967 | Hs.46784 | potassium large conductance calcium-acti | 4.8 |
| | 428189 | AA424030 | Hs.46627 | ESTs | 4.8 |
| | 420092 | AA814043 | Hs.88045 | ESTs | 4.8 |
| | 410631 | AA086469 | Hs.47171 | ESTs | 4.8 |
| | 449277 | AA001064 | Hs.43670 | ESTs | 4.8 |
| 20 | 436282 | R91913 | Hs.272104 | ESTs, Moderately similar to ALU1_HUMAN A | 4.8 |
| | 414705 | AW340125 | Hs.76989 | KIAA0097 gene product | 4.8 |
| | 438703 | AI803373 | Hs.31599 | ESTs | 4.8 |
| | 439340 | AB032436 | Hs.6535 | brain-specific Na-dependent inorganic ph | 4.8 |
| | 445890 | AF055019 | Hs.21906 | Homo sapiens clone 24670 mRNA sequence | 4.8 |
| 25 | 436734 | AI937612 | Hs.273758 | hypothetical protein FLJ23112 | 4.7 |
| | 408177 | AI241733 | Hs.43871 | ESTs | 4.7 |
| | 445740 | T78281 | Hs.13226 | Homo sapiens clone 25181 mRNA sequence | 4.7 |
| | 459527 | AW977556 | Hs.291735 | ESTs, Weakly similar to I78885 serine/th | 4.7 |
| | 445523 | Z30118 | Hs.293788 | ESTs, Moderately similar to unnamed prot | 4.7 |
| 30 | 409172 | Z99399 | Hs.122593 | ESTs | 4.7 |
| | 437748 | AF234882 | Hs.5814 | suppression of tumorigenicity 7 | 4.7 |
| | 421637 | AF035290 | Hs.106300 | Homo sapiens clone 23556 mRNA sequence | 4.7 |
| | 448044 | AK58682 | | gb:tk13e01.x1 NCI_CGAP_Lu24 Homo sapiens | 4.7 |
| | 459311 | R40192 | Hs.21527 | Human DNA sequence from clone GS1-115M3 | 4.7 |
| 35 | 447891 | R41754 | Hs.6496 | ESTs | 4.7 |
| | 426968 | U07616 | Hs.173034 | amphiphysin (Stiff-Mann syndrome with br | 4.7 |
| | 404819 | | | NM_002688: Homo sapiens peanut (Drosophi | 4.7 |
| | 409125 | R17268 | Hs.343567 | axonal transport of synaptic vesicles | 4.7 |
| 40 | 437762 | T78028 | Hs.154679 | synaptotagmin I | 4.7 |
| | 441668 | AI611973 | Hs.136313 | ESTs | 4.7 |
| | 444190 | AI878918 | Hs.10526 | cysteine and glycine-rich protein 2 | 4.7 |
| | 429269 | AA449013 | Hs.99203 | ESTs | 4.6 |
| | 433009 | AA761668 | | gb:nz24c08.s1 NCI_CGAP_GCB1 Homo sapiens | 4.6 |
| 45 | 416586 | D44643 | Hs.14144 | secreted modular calcium-binding protein | 4.6 |
| | 427701 | AA411101 | Hs.243886 | nuclear autoantigenic sperm protein (his | 4.6 |
| | 426925 | NM_001196 | Hs.315689 | Homo sapiens cDNA: FLJ22373 fis, clone H | 4.6 |
| | 410264 | AK001853 | Hs.61508 | Homo sapiens cDNA FLJ10991 fis, clone PL | 4.6 |
| | 437698 | R61837 | Hs.7990 | ESTs, Moderately similar to I84505 calci | 4.6 |
| 50 | 445813 | Z42023 | Hs.106576 | alanine-glyoxylate aminotransferase 2-li | 4.6 |
| | 424264 | D80400 | Hs.239388 | Human DNA sequence from clone RP1-304B14 | 4.6 |
| | 448765 | R15337 | Hs.21958 | Homo sapiens mRNA: cDNA DKFZp547D086 (fr | 4.6 |
| | 419723 | AL120193 | Hs.339810 | longevity assurance (LAG1, S. cerevisiae | 4.6 |
| | 424282 | R76421 | Hs.135694 | ESTs | 4.6 |
| | 429401 | AW296102 | Hs.99272 | ESTs, Weakly similar to S32567 A4 protei | 4.6 |
| 55 | 426413 | AA377823 | | gb:EST90805 Synovial sarcoma Homo sapien | 4.6 |
| | 407896 | D76435 | Hs.41154 | Zic family member 1 (odd-paired Drosophi | 4.5 |
| | 413248 | T64858 | Hs.21433 | hypothetical protein DKFZp547J036 | 4.5 |
| | 443731 | AI083928 | Hs.145418 | ESTs | 4.5 |
| | 449539 | W80363 | Hs.58446 | ESTs | 4.5 |
| 60 | 420362 | U79734 | Hs.97206 | huntingtin interacting protein 1 | 4.5 |
| | 443301 | AI733614 | Hs.220587 | ESTs, Moderately similar to ALU5_HUMAN A | 4.5 |
| | 423178 | AI033140 | Hs.124983 | Homo sapiens mRNA: cDNA DKFZp564C142 (fr | 4.5 |
| | 437933 | AI276132 | Hs.146155 | ESTs | 4.5 |
| | 446544 | AI631932 | Hs.7047 | ESTs, Weakly similar to Unknown [H.sapie | 4.5 |
| 65 | 411642 | NM_014932 | Hs.71132 | neuroigin 1 | 4.5 |
| | 428282 | N34905 | Hs.44653 | Homo sapiens cDNA: FLJ22669 fis, clone H | 4.5 |
| | 411498 | NM_014210 | Hs.70499 | ecotropic viral integration site 2A | 4.5 |
| | 408622 | AA056060 | Hs.202577 | Homo sapiens cDNA FLJ12166 fis, clone MA | 4.5 |
| | 436637 | AI783629 | Hs.26766 | ESTs | 4.5 |
| 70 | 438456 | AA913381 | Hs.20594 | ESTs | 4.5 |
| | 400533 | | | ENSP00000209376: PRED65 protein (Fragmen | 4.4 |
| | 413951 | AW051200 | Hs.75640 | natriuretic peptide precursor A | 4.4 |
| | 417632 | R20855 | Hs.5422 | glycoprotein M6B | 4.4 |
| | 425138 | H08849 | Hs.167464 | glutamate receptor, ionotropic, N-methyl | 4.4 |
| 75 | 457211 | AW972565 | Hs.32399 | ESTs, Weakly similar to S51797 vasodilat | 4.4 |
| | 413812 | AW188687 | Hs.44748 | ESTs | 4.4 |
| | 448451 | AW015994 | Hs.345433 | gb:U1-H-BI0p-abh-g-09-0-UI.s1 NCI_CGAP_S | 4.4 |
| | 432281 | AK001239 | Hs.274263 | hypothetical protein FLJ10377 | 4.4 |
| | 458760 | AI498631 | Hs.111334 | ferritin, light polypeptide | 4.4 |
| 80 | 405819 | | | NM_002578: Homo sapiens p21 (CDKN1A)-acti | 4.4 |
| | 447877 | AI435184 | Hs.164252 | ESTs | 4.4 |
| | 431342 | AW971018 | Hs.21659 | ESTs | 4.4 |
| | 408577 | H50572 | Hs.19515 | ESTs, Highly similar to NRG3_HUMAN PRO-N | 4.4 |
| | 445729 | H21066 | Hs.13223 | Homo sapiens mRNA full length insert cDN | 4.4 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 422253 | W81526 | Hs.118329 | ESTs, Moderately similar to GAD_HUMAN GA | 4.4 |
| | 419088 | AI538323 | Hs.52620 | integrin, beta 8 | 4.4 |
| | 428305 | AA446628 | Hs.2799 | cartilage linking protein 1 | 4.4 |
| 5 | 410768 | AF038185 | Hs.66187 | Homo sapiens clone 23700 mRNA sequence | 4.4 |
| | 428722 | U76456 | Hs.190787 | tissue inhibitor of metalloproteinase 4 | 4.4 |
| | 451621 | AI879148 | Hs.26770 | fatty acid binding protein 7, brain | 4.4 |
| | 424240 | AB023185 | Hs.143535 | calcium/calmodulin-dependent protein kin | 4.3 |
| | 433932 | AW954599 | Hs.169330 | neuronal protein | 4.3 |
| | 439935 | S75105 | Hs.8358 | glutamate receptor, ionotropic, kainate | 4.3 |
| 10 | 436039 | AW023323 | Hs.121070 | ESTs | 4.3 |
| | 416220 | N49776 | Hs.170994 | hypothetical protein MGC10946 | 4.3 |
| | 409953 | AA332277 | Hs.57691 | cadherin 18, type 2 | 4.3 |
| | 456497 | AW967956 | Hs.123648 | ESTs, Weakly similar to AF108460 1 ubinu | 4.3 |
| | 420352 | BE258835 | | gb:601117374F1 NIH_MGC_16 Homo sapiens c | 4.3 |
| 15 | 454032 | W31790 | Hs.194293 | ESTs, Weakly similar to I54374 gene NF2 | 4.3 |
| | 421790 | AW896201 | Hs.22654 | sodium channel, voltage-gated, type I, a | 4.3 |
| | 444218 | AF070641 | Hs.10684 | Homo sapiens clone 24421 mRNA sequence | 4.3 |
| | 436391 | AJ227892 | Hs.146274 | ESTs | 4.3 |
| | 452106 | AI141031 | Hs.21342 | ESTs | 4.3 |
| 20 | 422465 | AF073710 | Hs.117149 | regulator of G-protein signalling 9 | 4.3 |
| | 439285 | AL133916 | | hypothetical protein FLJ20093 | 4.3 |
| | 404541 | | | NM_030795:Homo sapiens stathmin-like 4 (| 4.3 |
| | 424572 | M19650 | | 2',3'-cyclic nucleotide 3' phosphodiester | 4.3 |
| 25 | 449048 | Z45051 | Hs.22920 | similar to S68401 (cattle) glucose induc | 4.3 |
| | 409182 | AA064970 | Hs.122593 | ESTs | 4.3 |
| | 444600 | R41398 | Hs.6996 | ESTs | 4.3 |
| | 408838 | AI669535 | Hs.40369 | ESTs | 4.3 |
| | 410592 | R94088 | Hs.43569 | ESTs | 4.3 |
| | 440168 | AA868507 | Hs.126141 | ESTs | 4.2 |
| 30 | 445078 | AI869975 | Hs.4775 | junctophilin 3 | 4.2 |
| | 428670 | AA431682 | Hs.134832 | ESTs | 4.2 |
| | 411666 | AF106564 | Hs.71346 | neurofilament 3 (150kD medium) | 4.2 |
| | 412505 | AA974491 | Hs.21734 | ESTs | 4.2 |
| | 418506 | AA084248 | Hs.85339 | G protein-coupled receptor 39 | 4.2 |
| 35 | 441707 | R42637 | Hs.21963 | hypothetical protein DKFZp761B0514 | 4.2 |
| | 449433 | AI672096 | Hs.9012 | ESTs, Weakly similar to S26650 DNA-bind | 4.2 |
| | 441523 | AW514263 | Hs.301771 | ESTs, Weakly similar to ALUF_HUMAN !!!! | 4.2 |
| | 448243 | AW369771 | Hs.52620 | integrin, beta 8 | 4.2 |
| | 429149 | AW193360 | Hs.197962 | ESTs, Weakly similar to I38022 hypotheti | 4.2 |
| 40 | 430676 | AF084866 | | gb:Homo sapiens envelope protein RIC-3 (| 4.2 |
| | 404584 | | | Target Exon | 4.2 |
| | 422798 | R92347 | Hs.34574 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 4.2 |
| | 451254 | AI571016 | Hs.172967 | ESTs | 4.2 |
| | 428585 | AB007863 | Hs.185140 | KIAA0403 protein | 4.2 |
| 45 | 439231 | AW581935 | Hs.141480 | Homo sapiens mRNA; cDNA DKFZp434N079 (fr | 4.2 |
| | 425287 | R88249 | Hs.155524 | peanut (Drosophila)-like 2 | 4.2 |
| | 425790 | AW136286 | Hs.288446 | ESTs | 4.2 |
| | 450407 | NM_000810 | Hs.24969 | gamma-aminobutyric acid (GABA) A recepto | 4.2 |
| | 425241 | AA324624 | Hs.155247 | aldolase C, fructose-bisphosphate | 4.2 |
| 50 | 445292 | AV653264 | Hs.13982 | Homo sapiens cDNA FLJ14666 fis, clone NT | 4.1 |
| | 400777 | | | NM_007325*:Homo sapiens glutamate recept | 4.1 |
| | 422170 | AI791949 | Hs.112432 | anti-Mullerian hormone | 4.1 |
| | 410765 | AI694972 | Hs.66180 | nucleosome assembly protein 1-like 2 | 4.1 |
| | 425402 | AI215881 | Hs.24970 | ESTs, Weakly similar to B34323 GTP-bindi | 4.1 |
| 55 | 438461 | AW075485 | Hs.286049 | phosphoserine aminotransferase | 4.1 |
| | 421268 | AI126821 | Hs.30514 | ESTs | 4.1 |
| | 416439 | AA180363 | Hs.118769 | ESTs | 4.1 |
| | 419687 | AI638859 | Hs.227699 | ESTs, Weakly similar to T2D3_HUMAN TRANS | 4.1 |
| | 435040 | AI932350 | Hs.152825 | ESTs | 4.1 |
| 60 | 439774 | AL360257 | Hs.213493 | Homo sapiens mRNA full length insert cDN | 4.1 |
| | 458435 | AI418718 | Hs.144121 | ESTs, Weakly similar to T46916 hypotheti | 4.1 |
| | 410320 | AA084071 | Hs.93816 | Homo sapiens mRNA; cDNA DKFZp547N093 (fr | 4.1 |
| | 436899 | AA764852 | Hs.291567 | ESTs | 4.1 |
| | 454171 | AW854832 | | gb:QV2-CT0261-201099-011-405 CT0261 Homo | 4.1 |
| 65 | 453118 | AW195849 | Hs.252757 | ESTs | 4.1 |
| | 428771 | AB028992 | Hs.193143 | KIAA1069 protein | 4.1 |
| | 444185 | AW298350 | Hs.66020 | ESTs | 4.1 |
| | 422374 | AW732869 | Hs.1519 | protein kinase, cAMP-dependent, regulato | 4.1 |
| 70 | 430147 | R60704 | Hs.234434 | hair/enhancer-of-split related with YRP | 4.1 |
| | 456060 | C14904 | Hs.45184 | Homo sapiens cDNA FLJ12284 fis, clone MA | 4.1 |
| | 433819 | AW511097 | Hs.112765 | ESTs | 4.1 |
| | 415827 | H17462 | Hs.23079 | ESTs | 4.1 |
| | 437397 | AA349847 | Hs.4221 | hypothetical protein DKFZp761H039 | 4.1 |
| | 441390 | AI692560 | Hs.131175 | ESTs | 4.1 |
| 75 | 440483 | AI200836 | Hs.150386 | ESTs | 4.0 |
| | 435294 | T84084 | Hs.196008 | Homo sapiens cDNA FLJ11723 fis, clone HE | 4.0 |
| | 447397 | BE247676 | Hs.18442 | E-1 enzyme | 4.0 |
| | 425390 | AI092634 | Hs.156114 | protein tyrosine phosphatase, non-recept | 4.0 |
| | 432022 | AL162042 | Hs.272348 | Homo sapiens mRNA; cDNA DKFZp761L1212 (f | 4.0 |
| 80 | 420602 | AF060877 | Hs.99236 | regulator of G-protein signalling 20 | 4.0 |
| | 408081 | AW451597 | Hs.167409 | ESTs | 4.0 |
| | 453313 | BE005771 | Hs.153746 | hypothetical protein FLJ22490 | 4.0 |
| | 436511 | AA721252 | Hs.291502 | ESTs | 4.0 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 448944 | AB014605 | Hs.22599 | atrophin-1 interacting protein 1; activi | 4.0 |
| | 419412 | AW161058 | Hs.90297 | synuclein, beta | 4.0 |
| | 409091 | AW970386 | Hs.269423 | ESTs | 4.0 |
| 5 | 453438 | AJ469935 | Hs.22792 | ESTs | 4.0 |
| | 450582 | AJ339732 | | G-rich RNA sequence binding factor 1 | 4.0 |
| | 440553 | AA889416 | Hs.344043 | Homo sapiens cDNA FLJ14459 fis, clone HE | 4.0 |
| | 437449 | AL390153 | Hs.208339 | Homo sapiens mRNA; cDNA DKFZp762G113 (fr | 4.0 |
| | 445888 | AF070564 | Hs.13415 | Homo sapiens clone 24571 mRNA sequence | 4.0 |
| 10 | 439450 | R51613 | Hs.125304 | ESTs | 4.0 |
| | 453792 | AL134539 | Hs.254129 | KIAA1678 | 4.0 |
| | 459080 | AW192083 | Hs.290855 | ESTs | 4.0 |
| | 438810 | AW897846 | Hs.6421 | hypothetical protein DKFZp761N09121 | 4.0 |
| | 446233 | AI282028 | Hs.25205 | ESTs | 4.0 |
| 15 | 412754 | AW160375 | Hs.74565 | amyloid beta (A4) precursor-like protein | 4.0 |
| | 412326 | R07566 | Hs.73817 | small inducible cytokine A3 (homologous | 4.0 |
| | 434859 | BE255080 | Hs.299315 | collapsin response mediator protein-5; C | 4.0 |
| | 423279 | AW959861 | Hs.290943 | ESTs | 4.0 |
| | 416340 | N31772 | Hs.79226 | fasciculation and elongation protein zet | 3.9 |
| 20 | 410126 | BE169274 | | KIAA0036 gene product | 3.9 |
| | 431173 | AW971198 | Hs.294068 | ESTs | 3.9 |
| | 446936 | H10207 | Hs.47314 | ESTs | 3.9 |
| | 424899 | AL119387 | Hs.119062 | ESTs | 3.9 |
| | 419038 | AW134924 | Hs.190325 | ESTs | 3.9 |
| 25 | 450530 | NM_006668 | Hs.25121 | cytochrome P450, subfamily 46 (cholester | 3.9 |
| | 438142 | T90309 | Hs.269651 | ESTs | 3.9 |
| | 412659 | AW753865 | Hs.74376 | otactomedin related ER localized protei | 3.9 |
| | 412788 | AA120960 | Hs.198416 | ESTs | 3.9 |
| | 410909 | AW898161 | Hs.53112 | ESTs, Moderately similar to ALU8_HUMAN A | 3.9 |
| 30 | 429433 | AA452899 | Hs.213586 | ESTs, Weakly similar to KIAA1353 protein | 3.9 |
| | 432809 | AA565509 | Hs.131703 | ESTs | 3.9 |
| | 424186 | AI536021 | Hs.288706 | Homo sapiens cDNA FLJ10281 fis, clone HE | 3.9 |
| | 425480 | AB023198 | Hs.158135 | KIAA0981 protein | 3.9 |
| | 449932 | AI675444 | Hs.263024 | ESTs | 3.9 |
| 35 | 434072 | H70854 | Hs.283059 | Homo sapiens PRO1082 mRNA, complete cds | 3.9 |
| | 450590 | AI701507 | Hs.273740 | ESTs | 3.9 |
| | 419586 | AI088485 | Hs.144759 | ESTs, Weakly similar to I38022 hypotheti | 3.9 |
| | 414040 | N58513 | Hs.32171 | ESTs | 3.9 |
| | 436480 | AJ271643 | Hs.87469 | putative acid-sensing ion channel | 3.9 |
| 40 | 443210 | AI692649 | Hs.9451 | hypothetical protein MGC13168 | 3.9 |
| | 448448 | NM_014954 | Hs.21239 | KIAA0985 protein | 3.9 |
| | 447067 | R42098 | Hs.21964 | ESTs | 3.9 |
| | 413199 | M62843 | Hs.75236 | ELAV (embryonic lethal, abnormal vision, | 3.9 |
| | 429421 | AL031658 | | Human DNA sequence from clone RP1-310Q13 | 3.9 |
| 45 | 415796 | R87548 | Hs.78854 | ATPase, Na ⁺ transporting, beta 2 polypep | 3.8 |
| | 417333 | AL157545 | Hs.173179 | bromodomain and PHD finger containing, 3 | 3.8 |
| | 418771 | AA807881 | Hs.25329 | ESTs | 3.8 |
| | 417565 | AI203405 | Hs.47831 | ESTs | 3.8 |
| | 412420 | AL035668 | Hs.73853 | bone morphogenetic protein 2 | 3.8 |
| 50 | 450202 | AW969756 | Hs.34145 | ESTs, Weakly similar to B49647 GTP-bindi | 3.8 |
| | 435312 | AJ243396 | Hs.4865 | voltage-gated sodium channel beta-3 subu | 3.8 |
| | 435832 | AA425688 | Hs.41641 | Bruno (Drosophila) -like 4, RNA binding | 3.8 |
| | 435854 | AJ278120 | Hs.4996 | putative ankyrin-repeat containing prote | 3.8 |
| | 459079 | AI821122 | | gb:ns91g10.y5 NCI_CGAP_Pr3 Homo sapiens | 3.8 |
| 55 | 425905 | AB032959 | Hs.318584 | novel C3HC4 type Zinc finger (ring finger | 3.8 |
| | 421977 | W94197 | Hs.110165 | ribosomal protein L26 homolog | 3.8 |
| | 437756 | AA767537 | Hs.197096 | ESTs | 3.8 |
| | 403696 | | | C4001100:gi5852342[gb]AAD54015.1[(AF0 | 3.8 |
| | 453033 | AA325869 | Hs.31463 | KIAA0281 gene product | 3.8 |
| 60 | 441732 | AW298818 | Hs.127341 | ESTs | 3.8 |
| | 415884 | H22966 | Hs.13471 | ESTs | 3.8 |
| | 432646 | AW753310 | | gb:RC3-CT0254-031099-012-c05 CT0254 Homo | 3.8 |
| | 451059 | AW297465 | Hs.267150 | KIAA1409 protein | 3.8 |
| | 447057 | AI423407 | Hs.157697 | ESTs | 3.8 |
| 65 | 418915 | AI474778 | Hs.118977 | ESTs | 3.8 |
| | 441111 | AI806867 | Hs.126594 | ESTs | 3.8 |
| | 447818 | W79940 | Hs.21906 | Homo sapiens clone 24670 mRNA sequence | 3.8 |
| | 457183 | H91882 | Hs.118569 | Dvl-binding protein IDAX (inhibition of | 3.8 |
| | 418358 | L02840 | Hs.84244 | potassium voltage-gated channel, Shab-re | 3.8 |
| 70 | 410711 | AB002316 | Hs.65746 | KIAA0318 protein | 3.8 |
| | 428878 | AA436884 | Hs.48926 | ESTs | 3.8 |
| | 438944 | AA302517 | Hs.92732 | KIAA1444 protein | 3.8 |
| | 420898 | AB002379 | Hs.100113 | KIAA0381 protein | 3.8 |
| | 418329 | AW247430 | Hs.84152 | cystathionine-beta-synthase | 3.8 |
| 75 | 427209 | H06509 | Hs.92423 | KIAA1566 protein | 3.7 |
| | 445319 | AF052108 | Hs.12513 | Homo sapiens clone 23687 mRNA sequence | 3.7 |
| | 428841 | AI418430 | Hs.104935 | ESTs | 3.7 |
| | 414821 | M63835 | Hs.77424 | Fc fragment of IgG, high affinity Ia, re | 3.7 |
| | 443310 | BE552018 | Hs.133152 | ESTs | 3.7 |
| 80 | 407728 | AW071502 | Hs.175931 | ESTs | 3.7 |
| | 429643 | AA455889 | Hs.167279 | FYVE-finger-containing Rab5 effector pro | 3.7 |
| | 444127 | N53620 | Hs.13281 | ESTs | 3.7 |
| | 425652 | AB021742 | Hs.322431 | neurogenic differentiation 2 | 3.7 |
| | 458072 | AI890347 | Hs.271923 | Homo sapiens cDNA: FLJ22785 fis, clone K | 3.7 |

| | | | | |
|----|--------|-----------|--|-----|
| | 459660 | M79082 | ESTs | 3.7 |
| | 432188 | AI362952 | Hs.2928 | 3.7 |
| | 437627 | AW469925 | Hs.257837 | 3.7 |
| | 408508 | AI806109 | Hs.135736 | 3.7 |
| 5 | 448999 | AF179274 | Hs.22791 | 3.7 |
| | 410623 | AW958932 | Hs.293833 | 3.7 |
| | 430744 | AA485229 | Hs.105649 | 3.7 |
| | 454392 | BE260893 | Hs.236131 | 3.7 |
| | 453739 | AL120266 | ESTs | 3.7 |
| 10 | 407198 | H91679 | gb:yyv04a07.s1 Soares fetal liver spleen | 3.7 |
| | 405239 | U89281 | oxidative 3 alpha hydroxysteroid dehydro | 3.7 |
| | 433615 | AA732982 | Hs.269607 | 3.7 |
| | 424800 | AL035588 | Hs.153203 | 3.7 |
| | 451027 | AW519204 | Hs.40808 | 3.7 |
| 15 | 415131 | D61119 | gb:HUM158C118 Clontech human fetal brain | 3.7 |
| | 443454 | AI057494 | Hs.133421 | 3.7 |
| | 423779 | AW071837 | Hs.57971 | 3.7 |
| | 452092 | BE245374 | Hs.27842 | 3.7 |
| | 435910 | AI084152 | Hs.21782 | 3.6 |
| 20 | 447028 | AI973128 | Hs.167257 | 3.6 |
| | 452997 | N64777 | Hs.44656 | 3.6 |
| | 408601 | U47928 | Hs.86122 | 3.6 |
| | 407332 | AI801565 | Hs.200113 | 3.6 |
| | 455646 | BE064420 | Hs.8124 | 3.6 |
| 25 | 433657 | AI244368 | Hs.203933 | 3.6 |
| | 421679 | AI475110 | Hs.22777 | 3.6 |
| | 448985 | AA324885 | Hs.77031 | 3.6 |
| | 414709 | AA704703 | Hs.11775 | 3.6 |
| 30 | 439099 | AB037800 | Hs.6462 | 3.6 |
| | 436315 | BE390513 | Hs.27935 | 3.6 |
| | 423611 | AB011163 | Hs.129908 | 3.6 |
| | 453169 | AB037815 | Hs.130425 | 3.6 |
| | 436954 | AA740151 | Hs.170053 | 3.6 |
| 35 | 439249 | AF086060 | Hs.130729 | 3.6 |
| | 432058 | AW665996 | Hs.90207 | 3.6 |
| | 419390 | AI701162 | Hs.184592 | 3.6 |
| | 428483 | AI908539 | Hs.211193 | 3.6 |
| | 409557 | BE182896 | Hs.190488 | 3.6 |
| 40 | 418049 | AA211467 | Hs.9740 | 3.6 |
| | 443774 | AL117428 | Hs.283955 | 3.6 |
| | 425331 | AW962128 | Hs.138411 | 3.6 |
| | 445105 | AF238869 | Hs.135614 | 3.6 |
| | 424051 | AL110203 | Hs.293799 | 3.6 |
| 45 | 446420 | AW015693 | Target Exon | 3.6 |
| | 428138 | AA773842 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 3.6 |
| | 404185 | AA644142 | ESTs | 3.6 |
| | 427517 | AI034467 | ESTs | 3.6 |
| 50 | 443150 | AW954272 | gb:EST366342 MAGE resequences, MAGC Homo | 3.6 |
| | 408065 | AL137310 | Hs.4749 | 3.6 |
| | 435092 | BE387287 | Hs.83384 | 3.6 |
| | 418064 | AI925195 | Hs.130891 | 3.6 |
| | 433560 | NM_013257 | Hs.279696 | 3.6 |
| 55 | 432882 | AI659306 | Hs.73826 | 3.6 |
| | 412350 | BE262233 | Hs.7423 | 3.6 |
| | 439753 | NM_006176 | Hs.26944 | 3.6 |
| | 451734 | AI147061 | Hs.32450 | 3.6 |
| | 437056 | AI492261 | Hs.26468 | 3.6 |
| 60 | 438328 | NM_005503 | Hs.130489 | 3.6 |
| | 451489 | AL137256 | Hs.164007 | 3.5 |
| | 423641 | AA649051 | Hs.7979 | 3.5 |
| | 434784 | AL138034 | Hs.102447 | 3.5 |
| | 441834 | AL135740 | Hs.203013 | 3.5 |
| 65 | 421183 | AW135982 | Hs.56782 | 3.5 |
| | 452108 | R13406 | Hs.123956 | 3.5 |
| | 425870 | R44664 | Hs.11217 | 3.5 |
| | 425115 | AB020684 | Hs.93810 | 3.5 |
| | 444471 | U90268 | Hs.39384 | 3.5 |
| 70 | 419929 | AI077715 | Hs.222120 | 3.5 |
| | 407792 | AI148006 | Hs.159142 | 3.5 |
| | 422564 | AA805132 | Hs.12962 | 3.5 |
| | 433323 | T66861 | Hs.38592 | 3.5 |
| | 435743 | AW901347 | Target Exon | 3.5 |
| 75 | 450297 | AI525743 | Hs.345187 | 3.5 |
| | 403341 | R53169 | Hs.80712 | 3.5 |
| | 443761 | AW292271 | Hs.250718 | 3.5 |
| | 458743 | AB028945 | Hs.12696 | 3.5 |
| | 447925 | H98752 | Hs.42568 | 3.5 |
| 80 | 445424 | AA314998 | Hs.241503 | 3.5 |
| | 416874 | AA348947 | Hs.91816 | 3.5 |
| | 430456 | AW205373 | Hs.16443 | 3.5 |
| | 419647 | | | |
| | 412707 | | | |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 444458 | BE041526 | Hs.31746 | hypothetical protein DKFZp547F072 | 3.5 |
| | 451066 | AI758660 | Hs.206132 | ESTs | 3.5 |
| | 425234 | AW152225 | Hs.165909 | ESTs, Weakly similar to I38022 hypothei | 3.5 |
| 5 | 420071 | AB028985 | Hs.94806 | ATP-binding cassette, sub-family A (ABC1 | 3.5 |
| | 432625 | AI243596 | Hs.94830 | ESTs, Moderately similar to T03094 A-kin | 3.5 |
| | 442118 | AA976718 | Hs.202242 | ESTs | 3.5 |
| | 421686 | AB011156 | Hs.106794 | KIAA0584 protein | 3.5 |
| | 428966 | AF059214 | Hs.194687 | cholesterol 25-hydroxylase | 3.5 |
| 10 | 444326 | AI839357 | Hs.270710 | ESTs | 3.5 |
| | 443361 | AI792628 | Hs.133273 | ESTs | 3.5 |
| | 427627 | R87582 | Hs.179915 | guanine nucleotide binding protein (G pr | 3.4 |
| | 434542 | AA769310 | Hs.61260 | hypothetical protein FLJ13164 | 3.4 |
| | 419235 | AW470411 | Hs.288433 | neurotrophin | 3.4 |
| 15 | 440700 | AW952281 | Hs.296184 | guanine nucleotide binding protein (G pr | 3.4 |
| | 417084 | H08370 | Hs.33067 | ESTs | 3.4 |
| | 432925 | AA878324 | | ESTs | 3.4 |
| | 439920 | H05430 | Hs.288433 | neurotrophin | 3.4 |
| | 453710 | AL119136 | Hs.236131 | homeodomain-interacting protein kinase 2 | 3.4 |
| 20 | 412783 | BE276738 | Hs.74578 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypep | 3.4 |
| | 435977 | AL138079 | Hs.5012 | brain-specific membrane-anchored protein | 3.4 |
| | 431725 | X65724 | Hs.2839 | Norrie disease (pseudoglioma) | 3.4 |
| | 449611 | AI970394 | Hs.197075 | ESTs | 3.4 |
| | 448543 | AW897741 | Hs.21380 | Homo sapiens mRNA; cDNA DKFZp586P1124 (f | 3.4 |
| 25 | 430968 | AW972830 | | gb:EST384925 MAGE resequences, MAGL Homo | 3.4 |
| | 413530 | AA130158 | Hs.19977 | ESTs, Moderately similar to ALU8_HUMAN A | 3.4 |
| | 412043 | BE156622 | Hs.333371 | Homo sapiens clone TA40 untranslated mRN | 3.4 |
| | 445666 | R59960 | Hs.282386 | ESTs | 3.4 |
| | 412820 | BE001236 | | gb:CM3-BN0075-240200-101-d11 BN0075 Homo | 3.4 |
| 30 | 458912 | AI911066 | | ESTs | 3.4 |
| | 452449 | AW068658 | Hs.20943 | ESTs | 3.4 |
| | 437085 | AA743935 | Hs.202329 | ESTs | 3.4 |
| | 419852 | AW503756 | Hs.286184 | hypothetical protein dJ551D2.5 | 3.4 |
| | 448750 | U95020 | Hs.21903 | calcium channel, voltage-dependent, beta | 3.4 |
| 35 | 435741 | AI240668 | Hs.113099 | ESTs | 3.4 |
| | 445828 | F05802 | Hs.81907 | ESTs | 3.4 |
| | 419347 | C15944 | Hs.90005 | superiorcervical ganglia, neural specifi | 3.4 |
| | 431733 | AW298410 | Hs.21475 | ESTs | 3.4 |
| | 415949 | H10562 | Hs.21691 | ESTs | 3.4 |
| 40 | 400205 | | | NM_006265*:Homo sapiens RAD21 (S. pombe) | 3.4 |
| | 437528 | N59646 | Hs.169745 | crumbs (Drosophila) homolog 1 | 3.4 |
| | 442593 | R39804 | Hs.31961 | ESTs | 3.4 |
| | 442927 | AI024347 | Hs.131519 | ESTs | 3.4 |
| | 429528 | AI985303 | Hs.99361 | ESTs | 3.4 |
| 45 | 450756 | AI733488 | Hs.144062 | ESTs | 3.4 |
| | 437387 | AI198874 | Hs.28847 | AD026 protein | 3.4 |
| | 430347 | NM_002039 | Hs.239706 | GRB2-associated binding protein 1 | 3.4 |
| | 404283 | | | ENSP00000244751*:Copine-like protein KIA | 3.4 |
| 50 | 433229 | AB040925 | Hs.91625 | KIAA1492 protein | 3.4 |
| | 440274 | R24595 | Hs.7122 | scrapie responsive protein 1 | 3.4 |
| | 436114 | AA778232 | Hs.19515 | ESTs, Highly similar to NRG3_HUMAN PRO-N | 3.4 |
| | 439690 | AA843868 | Hs.190567 | ESTs | 3.4 |
| | 450784 | AW246803 | Hs.47289 | ESTs | 3.4 |
| | 417868 | AI078534 | Hs.122592 | ESTs | 3.3 |
| 55 | 439793 | AA018825 | Hs.7934 | Kruppel-like factor 4 (gut) | 3.3 |
| | 456209 | W60633 | Hs.297792 | ESTs | 3.3 |
| | 421458 | NM_003654 | Hs.104576 | carbohydrate (keratan sulfate Gal-6) sul | 3.3 |
| | 438201 | AA780243 | Hs.54647 | ESTs | 3.3 |
| | 400302 | N48056 | Hs.1915 | folate hydrolase (prostate-specific memb | 3.3 |
| 60 | 425897 | AA935315 | Hs.48965 | Homo sapiens cDNA: FLJ21693 fts, clone C | 3.3 |
| | 423169 | BE047009 | Hs.21837 | ESTs, Weakly similar to KIAA0927 protein | 3.3 |
| | 415539 | AI733881 | Hs.72472 | BMP-R1B | 3.3 |
| | 450337 | AI693256 | Hs.202427 | ESTs | 3.3 |
| | 408447 | AK002089 | Hs.45080 | Homo sapiens cDNA FLJ11227 fts, clone PL | 3.3 |
| 65 | 423420 | AI571364 | Hs.128382 | Homo sapiens mRNA; cDNA DKFZp7611224 (f | 3.3 |
| | 429084 | AJ001443 | Hs.195614 | splicing factor 3b, subunit 3, 130kD | 3.3 |
| | 440435 | AL042201 | Hs.21273 | transcription factor NYD-sp10 | 3.3 |
| | 453785 | AI368236 | Hs.283732 | ESTs, Moderately similar to ALU1_HUMAN A | 3.3 |
| | 448048 | BE281291 | Hs.170408 | ESTs, Moderately similar to A47582 B-cel | 3.3 |
| 70 | 436207 | AA334774 | Hs.12845 | hypothetical protein MGC13159 | 3.3 |
| | 404632 | | | NM_022490:Homo sapiens hypothetical prot | 3.3 |
| | 411565 | AW851728 | | gb:MR2-CT0222-011199-007-d06 CT0222 Homo | 3.3 |
| | 416845 | H95279 | Hs.293788 | gb:yu20h02.s1 Soares fetal liver spleen | 3.3 |
| | 436267 | AW450938 | Hs.180115 | ESTs | 3.3 |
| 75 | 426625 | T78300 | Hs.300642 | serologically defined colon cancer antig | 3.3 |
| | 401272 | | | C9000559*:gq12314195[emb]CAB99338.1 (A | 3.3 |
| | 435071 | D60683 | Hs.35495 | ESTs | 3.3 |
| | 433128 | AB021923 | Hs.23367 | EST-YD1 protein | 3.3 |
| | 426920 | AA393351 | Hs.132121 | ESTs | 3.3 |
| 80 | 423668 | Y10148 | Hs.131138 | neurotensin receptor 2 | 3.3 |
| | 435056 | AW023337 | Hs.5422 | glycoprotein M6B | 3.3 |
| | 445534 | AL038823 | Hs.12840 | Homo sapiens germline mRNA sequence | 3.3 |
| | 425010 | T16837 | Hs.4241 | ESTs | 3.3 |
| | 445260 | AI218133 | Hs.147617 | ESTs | 3.3 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 421094 | AW978202 | Hs.289064 | hypothetical protein FLJ22251 | 3.3 |
| | 450358 | AB010098 | Hs.24907 | coronin, actin-binding protein, 2B | 3.3 |
| | 411048 | AK001742 | Hs.67991 | hypothetical protein DKFZp434G0522 | 3.3 |
| 5 | 432488 | AA551010 | Hs.216640 | ESTs | 3.3 |
| | 443672 | AA323362 | Hs.9667 | butyrobetaine (gamma), 2-oxoglutarate di | 3.3 |
| | 412719 | AW016610 | Hs.816 | ESTs | 3.3 |
| | 420050 | AL118615 | Hs.94653 | neurochondrin | 3.3 |
| | 410082 | AA081594 | Hs.158311 | Musashi (Drosophila) homolog 1 | 3.3 |
| 10 | 408554 | AA836381 | Hs.315111 | nuclear receptor co-repressor/HDAC3 comp | 3.3 |
| | 431462 | AW583672 | Hs.256311 | granin-like neuroendocrine peptide precu | 3.2 |
| | 434574 | AI424458 | Hs.33470 | ESTs | 3.2 |
| | 432715 | AA247152 | Hs.200483 | ESTs, Weakly similar to KIAA1074 protein | 3.2 |
| | 426757 | AW205640 | Hs.158206 | ESTs | 3.2 |
| 15 | 428167 | AA770021 | Hs.16332 | ESTs | 3.2 |
| | 451597 | AW295250 | Hs.207536 | ESTs | 3.2 |
| | 400362 | AF068294 | Hs.272414 | Homo sapiens HDCMB45P mRNA, partial cds | 3.2 |
| | 417675 | AI808607 | Hs.3781 | similar to murine leucine-rich repeat pr | 3.2 |
| | 429550 | AW293055 | Hs.119357 | ESTs | 3.2 |
| 20 | 404120 | | | CS000537*:gii3298595 gb AAC41376.1 (AF0 | 3.2 |
| | 417123 | BE326521 | Hs.159450 | ESTs | 3.2 |
| | 450313 | AI038989 | Hs.332633 | Bardet-Biedl syndrome 2 | 3.2 |
| | 425999 | AW513051 | Hs.332981 | ESTs, Weakly similar to I38022 hypotheti | 3.2 |
| | 430526 | AF181862 | Hs.242407 | G protein-coupled receptor, family C, gr | 3.2 |
| 25 | 452619 | AW298597 | Hs.61884 | Homo sapiens, clone IMAGE:4298026, mRNA, | 3.2 |
| | 415558 | AA885143 | Hs.125719 | ESTs | 3.2 |
| | 451996 | AW514021 | Hs.245510 | ESTs | 3.2 |
| | 420560 | AW207748 | Hs.59115 | ESTs | 3.2 |
| | 432328 | AI572739 | Hs.195471 | 6-phosphofructo-2-kinase/fructose-2,6-bi | 3.2 |
| 30 | 417404 | NM_007350 | Hs.82101 | pleckstrin homology-like domain, family | 3.2 |
| | 414300 | AI304870 | Hs.188680 | ESTs | 3.2 |
| | 437834 | AA769294 | Hs.283854 | gb:nz36g03.s1 NCL CGAP_GCB1 Homo sapiens | 3.2 |
| | 430694 | AA810624 | Hs.30936 | ESTs, Weakly similar to H2BH_HUMAN HISTO | 3.2 |
| | 447714 | AW296313 | Hs.255537 | ESTs | 3.2 |
| 35 | 412021 | AW885592 | | gb:RC4-OT0071-090300-011-g11 OT0071 Homo | 3.2 |
| | 443431 | AI056847 | Hs.20654 | ESTs | 3.2 |
| | 445774 | AI254165 | Hs.339968 | ESTs | 3.2 |
| | 431327 | AW972220 | Hs.105426 | ESTs | 3.2 |
| | 413335 | AI613318 | Hs.48442 | ESTs | 3.2 |
| 40 | 430809 | AI791150 | Hs.262009 | ESTs, Moderately similar to I38022 hypot | 3.2 |
| | 445858 | AL133811 | | solute carrier family 1 (glial high affi | 3.2 |
| | 450692 | H50603 | Hs.94037 | hypothetical protein FLJ23053 | 3.2 |
| | 439039 | AI656707 | Hs.48713 | ESTs | 3.2 |
| | 401720 | | | NM_014587*:Homo sapiens SRY (sex determi | 3.2 |
| 45 | 453740 | AL120295 | Hs.311809 | ESTs, Moderately similar to PC4259 femi | 3.2 |
| | 451032 | W03692 | Hs.323079 | Homo sapiens mRNA; cDNA DKFZp564P116 (fr | 3.2 |
| | 413834 | BE296896 | Hs.224179 | ESTs, Weakly similar to I38022 hypotheti | 3.2 |
| | 438138 | R98299 | Hs.177502 | ESTs | 3.2 |
| | 436338 | W92147 | Hs.118394 | ESTs | 3.2 |
| | 417169 | R13550 | Hs.246773 | ESTs | 3.2 |
| 50 | 424066 | Z99348 | Hs.112461 | ESTs, Weakly similar to I38022 hypotheti | 3.2 |
| | 435767 | H73505 | Hs.117874 | ESTs | 3.2 |
| | 415314 | N88802 | Hs.5422 | glycoprotein M6B | 3.2 |
| | 448475 | BE613134 | Hs.247474 | hypothetical protein FLJ21032 | 3.2 |
| 55 | 414699 | AI815523 | Hs.76930 | synuclein, alpha (non A4 component of am | 3.2 |
| | 438549 | BE386801 | Hs.21858 | trinucleotide repeat containing 3 | 3.2 |
| | 453896 | AW293483 | Hs.255205 | KIAA1853 protein | 3.1 |
| | 419539 | AF070590 | Hs.90869 | Homo sapiens clones 24622 and 24623 mRNA | 3.1 |
| | 428832 | AA578229 | Hs.324239 | ESTs, Moderately similar to ZN91_HUMAN Z | 3.1 |
| 60 | 446636 | AC002563 | Hs.15767 | citron (rho-interacting, serine/threonin | 3.1 |
| | 429046 | X57436 | Hs.194772 | oligodendrocyte myelin glycoprotein | 3.1 |
| | 421896 | N52293 | Hs.45107 | ESTs | 3.1 |
| | 413995 | BE048146 | Hs.75671 | syntaxin 1A (brain) | 3.1 |
| | 414734 | AA151712 | Hs.82572 | ESTs | 3.1 |
| 65 | 446147 | AL133064 | Hs.14051 | Homo sapiens mRNA; cDNA DKFZp434A2417 (f | 3.1 |
| | 427712 | AI368024 | Hs.283696 | ESTs | 3.1 |
| | 406481 | | | Target Exon | 3.1 |
| | 453204 | R10799 | Hs.191990 | ESTs | 3.1 |
| | 422890 | Z43784 | | ankyrin 3, node of Ranvier (ankyrin G) | 3.1 |
| 70 | 422991 | H10940 | Hs.48965 | Homo sapiens cDNA: FLJ21693 fis, clone C | 3.1 |
| | 421030 | AW161357 | | microtubule-associated protein tau | 3.1 |
| | 423603 | AB007880 | Hs.129883 | Homo sapiens KIAA0420 mRNA, complete cds | 3.1 |
| | 413985 | AI018666 | Hs.75667 | synaptophysin | 3.1 |
| | 431721 | AB032996 | Hs.268044 | KIAA1170 protein | 3.1 |
| 75 | 434164 | AW207019 | Hs.148135 | serine/threonine kinase 33 | 3.1 |
| | 429876 | AB028977 | Hs.225974 | KIAA1054 protein | 3.1 |
| | 423175 | W27595 | Hs.347310 | hypothetical protein FLJ14627 | 3.1 |
| | 412799 | AI267606 | | gb:aq91h03.x1 Stanley Frontal SB pool 1 | 3.1 |
| | 459318 | NM_000038 | | gb:Homo sapiens adenomatosis polyposis c | 3.1 |
| 80 | 453324 | W26592 | Hs.232089 | ESTs | 3.1 |
| | 424009 | F11690 | | gb:HSC300041 normalized infant brain cDN | 3.1 |
| | 436222 | AI208737 | Hs.122810 | Homo sapiens cDNA FLJ11489 fis, clone HE | 3.1 |
| | 414884 | R54418 | Hs.183745 | hypothetical protein FLJ13456 | 3.1 |
| | 446862 | AV660697 | Hs.282700 | ESTs | 3.1 |

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|----|--------|-----------|-----------|---|-----|
| 5 | 427241 | AA399988 | Hs.112087 | Human DNA sequence from clone RP11-530N1 | 3.1 |
| | 455388 | AW936234 | | gb:QV0-DT0020-090200-106-g05 DT0020 Homo | 3.1 |
| | 415838 | R44336 | Hs.7093 | ESTs | 3.1 |
| | 451692 | AL137422 | Hs.26849 | Homo sapiens mRNA: cDNA DKFZp761A1623 (f | 3.1 |
| | 445294 | Z45978 | | Human clone Z3826 mRNA sequence | 3.1 |
| 10 | 434460 | AA478486 | Hs.3852 | KIAA0368 protein | 3.1 |
| | 449919 | AI674685 | Hs.200141 | ESTs | 3.1 |
| | 440688 | AW404591 | Hs.147440 | ESTs, Weakly similar to Z192_HUMAN ZINC | 3.1 |
| | 416801 | X98834 | Hs.79971 | sal (Drosophila)-like 2 | 3.1 |
| | 428060 | AA420616 | Hs.249483 | ESTs | 3.1 |
| 15 | 423597 | AL043117 | Hs.129872 | sperm associated antigen 9 | 3.1 |
| | 452454 | AW820480 | | gb:QV2-ST0298-140200-042410 ST0298 Homo | 3.1 |
| | 445337 | NM_013280 | Hs.12523 | fibronectin leucine rich transmembrane p | 3.1 |
| | 413974 | BE208636 | Hs.27788 | ESTs | 3.1 |
| | 422772 | AL119585 | Hs.120228 | KIAA0749 protein | 3.1 |
| 20 | 423872 | AB020316 | Hs.134015 | uronyl 2-sulfotransferase | 3.1 |
| | 435375 | AI733610 | Hs.187832 | ESTs | 3.1 |
| | 450661 | AW952160 | Hs.83849 | ESTs | 3.1 |
| | 428647 | AA830050 | Hs.124344 | ESTs | 3.1 |
| | 400658 | | | ENSP00000237081*:KIAA1217 PROTEIN (FRAGM | 3.0 |
| 25 | 443845 | AI590084 | Hs.148485 | ESTs, Weakly similar to A47161 Mac-2-bin | 3.0 |
| | 446619 | AU076643 | Hs.313 | secreted phosphoprotein 1 (osteopontin, | 3.0 |
| | 433980 | AA137152 | Hs.286049 | phosphoserine aminotransferase | 3.0 |
| | 437738 | AA766914 | Hs.203475 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.0 |
| | 444772 | AW450800 | Hs.178859 | ESTs | 3.0 |
| 30 | 453825 | AL157475 | Hs.35453 | Homo sapiens mRNA: cDNA DKFZp761G151 (fr | 3.0 |
| | 439971 | W32474 | Hs.301746 | RAP2A, member of RAS oncogene family | 3.0 |
| | 408449 | NM_004408 | Hs.166161 | dynamitin 1 | 3.0 |
| | 432821 | BE170702 | Hs.279005 | solute carrier family 21 (organic anion | 3.0 |
| | 453657 | WZ3237 | Hs.296162 | AD037 protein | 3.0 |
| 35 | 407235 | D20569 | Hs.169407 | SAC2 (suppressor of actin mutations 2, y | 3.0 |
| | 428862 | NM_000346 | Hs.2316 | SRY (sex determining region Y)-box 9 (ca | 3.0 |
| | 424726 | AK001007 | Hs.138760 | Homo sapiens cDNA FLJ10145 fis, clone HE | 3.0 |
| | 454253 | AV660717 | Hs.47144 | DKFZP586N0819 protein | 3.0 |
| | 450650 | T65617 | Hs.101257 | hypothetical protein MGC3295 | 3.0 |
| 40 | 418211 | BE244746 | Hs.247474 | hypothetical protein FLJ21032 | 3.0 |
| | 440461 | R52728 | Hs.7193 | KIAA1183 protein | 3.0 |
| | 452850 | H23230 | Hs.22481 | ESTs, Moderately similar to A46010 X-link | 3.0 |
| | 431431 | AL096711 | Hs.252953 | Human DNA sequence from clone RP3-403A15 | 3.0 |
| | 447881 | BE620886 | Hs.75354 | GCN1 (general control of amino-acid synt | 3.0 |
| 45 | 454042 | H22570 | | hypothetical protein FLJ20093 | 3.0 |
| | 429168 | AA984682 | Hs.146589 | ESTs, Weakly similar to JC5238 galactosy | 3.0 |
| | 451391 | AA017410 | Hs.40568 | ESTs | 3.0 |
| | 446377 | AW014022 | Hs.170953 | ESTs | 3.0 |
| | 430251 | AA609246 | Hs.181451 | ESTs | 3.0 |
| 50 | 420658 | AW965215 | Hs.130707 | ESTs | 3.0 |
| | 454119 | BE549773 | Hs.40510 | uncoupling protein 4 | 3.0 |
| | 451018 | AW965599 | Hs.247324 | mitochondrial ribosomal protein S14 | 3.0 |
| | 435321 | R16814 | Hs.112062 | ESTs | 3.0 |
| | 412494 | AL133900 | Hs.792 | ADP-ribosylation factor domain protein 1 | 3.0 |
| 55 | 423858 | AL137326 | Hs.133483 | Homo sapiens mRNA: cDNA DKFZp434B0650 (f | 3.0 |
| | 431242 | AA987742 | Hs.347534 | KIAA1201 protein | 3.0 |
| | 403022 | | | C21000178*:gii7341207[gb]AAF61215.1[AF22 | 3.0 |
| | 445899 | AI263736 | Hs.145626 | ESTs | 3.0 |
| | 440261 | M81886 | Hs.71117 | glutamate receptor, ionotropic, AMPA 1 | 3.0 |
| 60 | 446809 | AW590171 | Hs.101413 | ESTs | 3.0 |
| | 434269 | AK001991 | Hs.3781 | similar to murine leucine-rich repeat pr | 3.0 |
| | 418951 | F07809 | Hs.89506 | paired box gene 6 (aniridia, keratitis) | 3.0 |
| | 448499 | BE613280 | Hs.77550 | hypothetical protein MGC1780 | 3.0 |
| | 432229 | AW290976 | Hs.143587 | ESTs | 3.0 |
| | 443726 | AI083825 | Hs.148382 | ESTs | 3.0 |

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|-------------|---------------------------------------|--|--|--|
| TABLE 13B: | | | | |
| Pkey: | Unique Eos probeset identifier number | | | |
| CAT number: | Gene cluster number | | | |
| Accession: | Genbank accession numbers | | | |

| | | |
|--------|------------|--|
| Pkey | CAT Number | Accession |
| 408065 | 103646_1 | AW954272 AI003154 AA059300 AA046911 |
| 410099 | 117647_1 | AA081630 T08671 AI174254 D83874 AW959843 AA364503 AA693467 AW993370 BE327037 AA167714 N79906 AW901977 AW901980 W52882 |
| | | T07735 AA484549 W60090 D52685 T23811 BE327043 AW901768 BE551237 AA917004 AA716027 AI439658 AA283724 AI805992 AI457096 |
| | | AA084618 BE467736 AI092635 AI887863 AI697593 AA436618 AI167419 AI418634 T31586 AA436630 AA706191 AI041169 AI422304 T03534 |
| | | AA211402 AI204899 AI366472 AW827081 AA788593 T32736 AI767935 AA167791 AA747914 AA663870 AI855504 |
| | | BE169274 AW893230 AA210998 H24222 AA081774 BE000935 BE000834 AA334880 |
| | | AW851728 AW851607 AW851621 AW851702 AW851647 AW851727 AW851658 AW851617 AW851628 |
| | | H08342 R52430 Z42067 AA095285 |
| | | AW885592 AW885594 AW885579 AW885651 |
| | | AJ267606 AA121045 AA126521 |
| | | H06382 AW957730 AA352014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 AI424991 AI693507 AI853108 AA599060 AI091148 AA598689 |
| | | R39887 AA813482 AW016452 H06383 R41807 AI364268 AA620528 AI241940 AW089149 AW090733 AW088875 Z38240 AA121202 R17734 |
| | | BE001236 BE001177 BE001180 BE001234 |
| | | D61119 D81508 D81734 |

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| 418512 | 176394_1 | AW498974 T09332 R58460 AA350990 T33786 T30936 AA350905 T08592 T09274 AA224297 D54678 T08951 R15346 AW953188 AA350074 AW890649 |
| 420111 | 190755_1 | AA255652 AA280911 AW967920 AA262684 |
| 420352 | 192979_1 | BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280 |
| 421030 | 19864_1 | AW161357 AI879062 AI928938 AW161097 AW161167 BE314465 AA351715 F07096 AA179034 F08510 F00653 AI936671 AA476718 AW772454 AI807703 R44253 AA976667 AI585185 AI550254 H38942 R84829 AA018724 AA01000 H85934 AA019126 H85609 AA017000 AA339355 AW950556 D51397 AA213981 BE548002 AI056359 AA001560 AW952113 AA317769 AI857477 AI857475 AW249771 AW162661 H38943 AA018628 R85885 AI984613 AI934765 AI796172 AW157488 AI929191 R85523 D51221 D53851 H85610 AI749674 F21582 AA323145 AA019127 AA687444 T06745 AI699293 H29532 AA214029 AA223656 NM_016834 X14474 R19697 H09695 R17455 R13812 R19056 AI681231 AI590200 R37671 AA861828 AI990023 AI935669 AW005821 AA324581 H17335 R37659 R42802 R46242 R60936 R59731 H28993 AA479907 R44570 AI890696 AA308884 AA507078 R41274 AI365507 T16348 AI560453 F03259 F04722 T16312 AA016081 AW073061 BE314824 W28930 R44098 R51045 Z43784 R13382 AW572911 AA449369 H17037 R19603 AI632565 AW004030 BE502530 Z25032 AA805324 AA449241 AI651825 AI264863 AW196918 AA948267 AI953735 AI263703 AA319159 AW964436 AI903440 AW594171 AI867447 AW204071 AW956110 C15616 D81142 H17038 AW162343 T87230 AI366013 H10064 AI190479 AI093318 AI867923 BE219303 BE048820 AI198397 AA654667 Z39851 F02655 Z28734 F04161 T16575 F10145 AA318815 R40898 |
| 423476 | 22861_1 | AL035633 F11794 F11783 H18042 T66089 H29379 R19493 AW134660 AI299437 AL133995 AA057405 N78357 AA917450 AI002692 T09262 T65008 H29290 AI200874 AA894415 AI732887 AI791768 AI733447 AA988785 N62128 T09261 AW956936 |
| 424009 | 234177_1 | F11690 AW965370 AA333586 D30830 |
| 424572 | 24097_1 | M19650 R18810 R18721 AW896146 AW889520 AA192362 AA176814 F12085 BE255264 BE251393 T65248 AA380585 AA380465 BE408684 AA459037 AW498869 AA776107 BE274289 D45269 M61958 AA378818 AW663180 AW672958 H08611 M78164 BE393721 AA348660 R36303 AW498662 AA019090 AA001087 AA054302 AA019775 AA018808 AA019132 AI858240 R73218 H30477 H17776 AA659570 BE276750 AI118657 AA375861 AA352427 AW581695 AI141188 N63474 AA654162 H17659 AL120696 T28867 AW498868 AI355918 AA902349 AA569098 AI088231 AI042604 AA555133 AI183611 AI608822 AI275941 AW316805 AA349486 AI355233 R85117 AW613626 R49234 AA458846 N20669 H18693 AA977567 T15423 AW002084 AI824721 N36242 AA17281 AI018212 AA912337 F09722 AA749449 AW879172 AA885427 AA916836 AA872560 F00482 H45184 AI217251 AA775807 BE390071 AA303517 AA001050 BE515169 N44066 AL133684 AI807085 AA808009 AA915914 F00007 AA019749 AL121560 AW675544 AW090233 AW072071 AI810932 AI089733 AW026222 AA770155 AI089647 AI085733 AW516061 AI037635 AL037635 AI863947 H50420 R11203 AA019133 N94772 N71842 N29047 AA778138 AA554336 AA179865 N59453 T65212 AA054270 AW806630 AA533375 D13146 AA349487 AU077160 BE255671 BE276795 BE250823 AL120301 BE311390 BE252483 |
| 424945 | 245223_1 | AI221919 Z19967 AA348780 AW964077 AW166028 BE540193 N94800 AA452368 N99604 AI341345 AW298800 AA724961 AA931158 AI741227 AI806660 AI982626 D81263 D53937 D52496 AA974487 AW043854 N50483 Z39997 AI492961 AI361526 F04002 AA452141 T23551 AI472655 AI193667 AI341984 N29658 T32870 R52664 N50428 AW089291 AI934175 AI423737 D60665 |
| 425331 | 250199_1 | AW962128 AA355353 AA427363 |
| 426413 | 266650_1 | AA377823 AW954494 AI022688 |
| 426503 | 268283_1 | AA380153 AA380233 AW953529 |
| 426919 | 273507_1 | AL041228 D82004 D61361 AI203314 AI990307 AW900295 AI018308 AW087473 AW183530 AA393346 H50055 AA935601 |
| 428342 | 290035_2 | AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438 AI092404 AI085630 AA731340 D80642 AA443145 AL119015 AW904500 AL031658 AI693758 AL040619 AW977914 AA811957 AI352198 AW104364 AA648367 AA897604 AW341668 AI201382 AL040620 BE010038 AA676833 AI311783 T86895 W68032 BE064393 BE064394 BE157228 BE183282 AI936370 AA552514 T67280 AA039909 AF084866 AF084870 AF084864 AF084867 AF084869 AF084865 AF084868 AW818206 AW812038 BE144813 BE144812 AW812041 AW812040 AW812067 BE061583 BE061604 T05808 AI352469 AA580921 BE141783 BE141782 BE061601 AW814393 AW885029 AW972830 AA527647 AA489820 AA570362 AW753310 AW974000 AA557840 AA558570 AW751539 AA878324 AI863159 AI619686 AA570406 AI014377 AA761668 AA573621 R92814 R09670 H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320 AA742643 AA808575 AW976668 AI147061 AA743380 AA765223 AW976398 AI083927 AW975186 AA807807 D29548 AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 AI346341 AI867454 N54784 AI655270 AI421279 AW014882 AA775552 N62351 N59253 AA626243 AI341407 BE175639 AA456968 AI358918 AA457077 AA973905 AI299888 AA917019 H63235 T90771 Z45978 U79248 T77277 R24952 AA361008 AW953678 T10376 AW860579 AW860657 AW364889 AW860635 AW860658 AW905164 W21226 AA448954 W69484 AA993098 AA287413 AA449682 AI961815 W57612 AW271363 R45215 AW136256 AI865103 W69577 AI961826 AA747542 AA173746 AI961816 F07706 R39461 F04829 F05938 AA172385 AI133811 M78538 T07792 AW895859 AW895589 AL119422 T79876 R19494 AF131756 H18570 T08285 F11532 Z42038 AW961964 AA683391 M62092 AL119616 Z21141 AA663820 Z19748 H18462 AL120152 R43841 R37594 AA775980 F09194 AI207884 Z38142 F01555 AA020737 AL120362 AW952737 T04912 Z44514 AI352097 AI803984 AW235923 AI965558 AI954637 AI336983 R36075 AI366546 R36167 AI458682 H24420 R14537 R18426 AW867082 AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878 AW118072 AI631982 T15734 AA224195 AI701458 W20198 F26326 AA890570 N90552 AW071907 AI671352 AI375892 T03517 R88265 AI124088 AA224388 AI084316 AI354686 T33652 AI140719 AI720211 T03490 AI372637 T15415 AW205836 AA630384 T03515 T33230 AA017131 AA443303 T33623 AI222556 T33511 T33785 AI419606 D55612 AW820480 AW820288 AI902522 AL120266 AW269469 AW890114 H22570 AW292267 AW137298 AW874199 AI206120 H45263 AA788851 R49056 AW241428 AI921013 AW129293 AI684910 BE466753 AA340613 AW025969 AI202561 AI243913 AW771106 F04969 AI654847 AI944436 AW771447 AW103715 N64350 AA347011 AI431587 AA779107 AA041195 AI358894 AI421678 AI018523 AA707199 AA410309 AI366468 AW020049 AI880103 AL119553 R42410 R55722 T66767 R43035 H17396 H45331 F01659 Z38381 AA708686 AI081305 R53955 AA041432 W27787 AW854832 AW854798 AW854857 AW854816 AW854834 AW854817 AW936234 AW936074 AW936181 AW936179 AW936217 AW936077 AW936227 AW936191 BE064420 BE064435 BE064429 BE064414 BE064400 BE064517 AI911066 AI933734 AI680888 AJ003599 AI821122 AI821866 |

TABLE 13C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
 sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.

Nt_position: Indicates nucleotide positions of predicted exons.

| Pkey | Ref | Strand | Nt_position |
|------|--------|--------|--|
| 5 | 400533 | Minus | 277132-277595 |
| | 400658 | Minus | 73525-73644 |
| | 400777 | Plus | 70745-71121 |
| | 401272 | Minus | 98374-98509 |
| | 401720 | Plus | 7783-8468 |
| 10 | 402145 | Plus | 113086-114800 |
| | 402604 | Plus | 20393-20767 |
| | 402605 | Minus | 47680-47973 |
| | 402855 | Minus | 59763-59909 |
| | 403022 | Plus | 92097-92864 |
| 15 | 403142 | Plus | 89286-90131 |
| | 403341 | Plus | 30699-30910 |
| | 403696 | Minus | 143467-143634 |
| | 404120 | Plus | 135775-136000 |
| | 404185 | Minus | 129171-129327 |
| 20 | 404283 | Minus | 99460-99564 |
| | 404541 | Plus | 103456-103664 |
| | 404584 | Plus | 138651-139153 |
| | 404632 | Plus | 45096-45229 |
| | 404819 | Plus | 16223-16319, 16427-16513, 16736-16859, 16941-17075, 17170-17287, 17389-17529, 18261-18357, 18443-18578 |
| 25 | 405238 | Minus | 51728-51836 |
| | 405239 | Plus | 144345-144464, 144690-144836, 151750-151883, 152407-152484 |
| | 405348 | Minus | 43310-43462 |
| | 405819 | Plus | 2830-2967 |
| 30 | 405481 | Minus | 91439-91579 |

TABLE 14A: ABOUT 1111 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL CENTRAL NERVOUS SYSTEM

Table 14A lists about 1111 genes up-regulated in glioblastoma compared to normal central nervous system (CNS). These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" glioblastoma to "average" CNS tissues was greater than or equal to 2.5. The "average" glioblastoma level was set to the 85th percentile amongst various brain tumors. The "average" normal CNS tissue level was set to the 85th percentile amongst various CNS tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

| | | | |
|----|----------------|---|--|
| | Pkey: | Unique Eos probeset identifier number | |
| | ExAccn: | Exemplar Accession number, Genbank accession number | |
| | UnigeneID: | Unigene number | |
| | Unigene Title: | Unigene gene title | |
| | R1: | Ratio of GLIOBLASTOMA to CNS | |
| 40 | | | |
| | Pkey | ExAccn | UnigeneID |
| | 422737 | M26939 | Hs.119571 |
| | 423961 | D13666 | Hs.136348 |
| | 433001 | AF217513 | Hs.279905 |
| | 414555 | N98569 | Hs.76422 |
| | 424800 | AL035588 | Hs.153203 |
| | 417308 | H60720 | Hs.81892 |
| 50 | 449539 | W80363 | Hs.58446 |
| | 453392 | U23752 | Hs.32964 |
| | 414825 | X06370 | Hs.77432 |
| | 444190 | A1878918 | Hs.10526 |
| | 412420 | AL035668 | Hs.73853 |
| 55 | 417130 | AW276858 | Hs.81256 |
| | 414217 | A1309298 | Hs.279898 |
| | 431941 | AK000106 | Hs.272227 |
| | 425397 | J04088 | Hs.156346 |
| | 446584 | U53445 | Hs.15432 |
| 60 | 422672 | X12784 | Hs.119129 |
| | 402604 | | |
| | 424635 | AA420687 | Hs.115455 |
| | 428330 | L22524 | Hs.2256 |
| | 434078 | AW880709 | Hs.283683 |
| 65 | 414761 | AU077228 | Hs.77256 |
| | 442432 | BE093589 | Hs.38178 |
| | 456759 | BE259150 | Hs.127792 |
| | 409638 | AW450420 | Hs.21335 |
| | 441269 | AW015206 | Hs.178784 |
| 70 | 435020 | AW505076 | Hs.301855 |
| | 422163 | AF027208 | Hs.112360 |
| | 444969 | AI203334 | Hs.160628 |
| | 430132 | AA204586 | Hs.234149 |
| | 433437 | U20536 | Hs.3280 |
| 75 | 445101 | T75202 | Hs.12314 |
| | 413929 | BE501689 | Hs.75617 |
| | 425187 | AW014486 | Hs.22509 |
| | 449722 | BE280074 | Hs.23960 |
| | 449611 | AI970394 | Hs.197075 |
| 80 | 428242 | H55709 | Hs.2250 |
| | 419239 | AA468183 | Hs.184598 |
| | 443731 | AI083928 | Hs.145418 |
| | 402855 | | |
| | | | Unigene Title |
| | | | collagen, type III, alpha 1 (Ehlers-Danl |
| | | | periostin (OSF-2os) |
| | | | clone HQ0310 PRO0310p1 |
| | | | phospholipase A2, group IIA (platelets, |
| | | | MyoD family inhibitor |
| | | | KIAA0101 gene product |
| | | | ESTs |
| | | | SRY (sex determining region Y)-box 11 |
| | | | epidermal growth factor receptor (avian |
| | | | cysteine and glycine-rich protein 2 |
| | | | bone morphogenetic protein 2 |
| | | | S100 calcium-binding protein A4 (calcium |
| | | | Homo sapiens cDNA: FLJ23165 fis, clone L |
| | | | Homo sapiens cDNA FLJ20099 fis, clone CO |
| | | | topoisomerase (DNA) II alpha (170kD) |
| | | | downregulated in ovarian cancer 1 |
| | | | collagen, type IV, alpha 1 |
| | | | Target Exon |
| | | | Homo sapiens cDNA FLJ14259 fis, clone PL |
| | | | matrix metalloproteinase 7 (matrilysin, |
| | | | chromosome 8 open reading frame 4 |
| | | | enhancer of zeste (Drosophila) homolog 2 |
| | | | hypothetical protein FLJ23468 |
| | | | delta (Drosophila)-like 3 |
| | | | ESTs |
| | | | DiGeorge syndrome critical region gene 8 |
| | | | prominin (mouse)-like 1 |
| | | | ESTs |
| | | | hypothetical protein FLJ20647 |
| | | | caspase 6, apoptosis-related cysteine pr |
| | | | Homo sapiens mRNA; cDNA DKFZp586C1019 (f |
| | | | collagen, type IV, alpha 2 |
| | | | ESTs |
| | | | cyclin B1 |
| | | | ESTs |
| | | | leukemia inhibitory factor (cholinergic |
| | | | Homo sapiens cDNA: FLJ23241 fis, clone C |
| | | | ESTs |
| | | | NM_001839*:Homo sapiens catponin 3, acid |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 447342 | AI199268 | Hs.19322 | Homo sapiens, Similar to RIKEN cDNA 2010 | 8.6 |
| | 410102 | AW248508 | Hs.279727 | ESTs, homologue of PEM-3 [Ciona savignyi | 8.5 |
| | 420602 | AF060877 | Hs.99236 | regulator of G-protein signalling 20 | 8.4 |
| | 417426 | NM_002291 | Hs.82124 | laminin, beta 1 | 8.4 |
| 5 | 433800 | AI034361 | Hs.135150 | lung type-I cell membrane-associated gly | 8.3 |
| | 417061 | AI675944 | Hs.188691 | Homo sapiens cDNA FLJ12033 fis, clone HE | 8.1 |
| | 409461 | AA382169 | Hs.54483 | N-myc (and STAT) interactor | 8.1 |
| | 414622 | AI752666 | Hs.76669 | nicotinamide N-methyltransferase | 8.1 |
| | 430691 | C14187 | Hs.103538 | ESTs | 8.0 |
| 10 | 447726 | AL137638 | Hs.19368 | matrilin 2 | 8.0 |
| | 417043 | NM_004369 | Hs.80988 | collagen, type VI, alpha 3 | 7.9 |
| | 447004 | AW296968 | Hs.157539 | ESTs | 7.9 |
| | 409799 | D11928 | Hs.76845 | phosphoserine phosphatase-like | 7.8 |
| | 426075 | AW513691 | Hs.270149 | ESTs, Weakly similar to 2109260A B cell | 7.8 |
| 15 | 419938 | AU076772 | Hs.1279 | complement component 1, r subcomponent | 7.7 |
| | 419508 | AW997938 | Hs.90786 | ATP-binding cassette, sub-family C (CFTR | 7.7 |
| | 411411 | AA345241 | Hs.55950 | ESTs, Weakly similar to KIAA1330 protein | 7.5 |
| | 436291 | BE568452 | Hs.344037 | protein regulator of cytokinesis 1 | 7.5 |
| 20 | 422048 | NM_012445 | Hs.288126 | spondin 2, extracellular matrix protein | 7.5 |
| | 406972 | M32053 | | gb:Human H19 RNA gene, complete cds. | 7.4 |
| | 442802 | AL133035 | Hs.8728 | hypothetical protein DKFZp434G171 | 7.4 |
| | 427581 | NM_014788 | Hs.179703 | KIAA0129 gene product | 7.3 |
| | 409142 | AL136877 | Hs.50758 | SMC4 (structural maintenance of chromoso | 7.3 |
| | 409902 | AI337658 | Hs.156351 | ESTs | 7.3 |
| 25 | 418113 | AI272141 | Hs.83484 | SRY (sex determining region Y)-box 4 | 7.2 |
| | 449961 | AW265634 | Hs.133100 | ESTs | 7.2 |
| | 418203 | X54942 | Hs.83758 | CDC28 protein kinase 2 | 7.2 |
| | 424840 | D79987 | Hs.153479 | extra spindle poles, S. cerevisiae, homo | 7.2 |
| 30 | 428728 | NM_016625 | Hs.191381 | hypothetical protein | 7.1 |
| | 429183 | AB014604 | Hs.197955 | KIAA0704 protein | 7.1 |
| | 439451 | AF086270 | Hs.278554 | heterochromatin-like protein 1 | 7.1 |
| | 422106 | D84239 | Hs.111732 | Fc fragment of IgG binding protein | 7.0 |
| | 406850 | AI624300 | Hs.172928 | collagen, type I, alpha 1 | 7.0 |
| 35 | 453941 | U39817 | Hs.36820 | Bloom syndrome | 6.9 |
| | 425234 | AW152225 | Hs.165909 | ESTs, Weakly similar to I38022 hypotheri | 6.9 |
| | 421977 | W94197 | Hs.110165 | ribosomal protein L26 homolog | 6.8 |
| | 411078 | AI222020 | Hs.182364 | CocoaCrisp | 6.7 |
| | 427019 | AA001732 | Hs.173233 | hypothetical protein FLJ10970 | 6.7 |
| | 448769 | N56037 | Hs.38173 | ESTs | 6.7 |
| 40 | 418400 | BE243026 | Hs.301989 | KIAA0246 protein | 6.6 |
| | 408161 | AW952912 | Hs.300383 | hypothetical protein MGC3032 | 6.6 |
| | 440210 | AW674562 | Hs.125296 | ESTs | 6.6 |
| | 437036 | AI571514 | Hs.133022 | ESTs | 6.6 |
| 45 | 411968 | AI207410 | Hs.69280 | Homo sapiens, clone IMAGE:3636299, mRNA, | 6.6 |
| | 416658 | U03272 | Hs.79432 | fibrillin 2 (congenital contractural ara | 6.6 |
| | 449300 | AI656959 | Hs.346514 | ESTs | 6.5 |
| | 440052 | AI633744 | Hs.195648 | ESTs, Weakly similar to I38022 hypotheri | 6.5 |
| | 412326 | R07566 | Hs.73817 | small inducible cytokine A3 (homologous | 6.5 |
| 50 | 434808 | AF155108 | Hs.256150 | Homo sapiens, Similar to RIKEN cDNA 2810 | 6.5 |
| | 452461 | N78223 | Hs.108106 | transcription factor | 6.5 |
| | 408243 | Y00787 | Hs.624 | interleukin 8 | 6.5 |
| | 424954 | NM_000546 | Hs.1846 | tumor protein p53 (Li-Fraumeni syndrome) | 6.4 |
| | 450375 | AA009647 | | a disintegrin and metalloproteinase doma | 6.4 |
| | 406478 | | | Target Exon | 6.4 |
| 55 | 427528 | AU077143 | Hs.179565 | minichromosome maintenance deficient (S. | 6.4 |
| | 439710 | AF066543 | | gb:Homo sapiens full length insert cDNA | 6.4 |
| | 458814 | AI498957 | Hs.170861 | ESTs, Weakly similar to Z195_HUMAN ZINC | 6.4 |
| | 410276 | AI554545 | Hs.68301 | angiotensin-2 | 6.4 |
| 60 | 425289 | AW139342 | Hs.155530 | interferon, gamma-inducible protein 16 | 6.3 |
| | 427871 | AW992405 | Hs.59622 | Homo sapiens, clone IMAGE:3507281, mRNA, | 6.3 |
| | 436895 | AF037335 | Hs.5338 | carbonic anhydrase XII | 6.3 |
| | 447458 | AI741082 | Hs.158961 | ESTs | 6.3 |
| | 447439 | AA313565 | Hs.145020 | ESTs, Weakly similar to KIAA1205 protein | 6.3 |
| 65 | 413719 | BE439580 | Hs.75498 | small inducible cytokine subfamily A (Cy | 6.3 |
| | 449969 | AW295142 | Hs.180187 | Homo sapiens cDNA FLJ14337 fis, clone PL | 6.2 |
| | 440704 | M69241 | Hs.162 | insulin-like growth factor binding prote | 6.2 |
| | 400419 | AF084545 | | Target | 6.2 |
| | 412140 | AA219691 | Hs.73625 | RAB6 interacting, kinesin-like (rabkines | 6.2 |
| 70 | 409731 | AA125985 | Hs.56145 | thymosin, beta, identified in neuroblast | 6.2 |
| | 424085 | NM_002914 | Hs.139226 | replication factor C (activator 1) 2 (40 | 6.2 |
| | 429469 | M64590 | Hs.27 | glycine dehydrogenase (decarboxylating; | 6.1 |
| | 430630 | AW269920 | Hs.2621 | cystatin A (steffin A) | 6.0 |
| | 410064 | X53416 | Hs.195464 | filamin A, alpha (actin-binding protein- | 6.0 |
| | 432281 | AK001239 | Hs.274263 | hypothetical protein FLJ10377 | 6.0 |
| 75 | 413627 | BE182082 | Hs.246973 | ESTs | 6.0 |
| | 413063 | AL035737 | Hs.75184 | chitinase 3-like 1 (cartilage glycoprote | 5.9 |
| | 421899 | AJ011895 | Hs.109281 | Nef-associated factor 1 | 5.9 |
| | 407182 | AA312551 | Hs.230157 | ESTs | 5.9 |
| 80 | 410286 | AI739159 | Hs.61898 | DKFZP586N2124 protein | 5.9 |
| | 409829 | M33552 | Hs.56729 | lymphocyte-specific protein 1 | 5.9 |
| | 446657 | AI335191 | Hs.260702 | ESTs, Weakly similar to 2109260A B cell | 5.8 |
| | 418097 | R45137 | Hs.21868 | ESTs | 5.8 |
| | 428450 | NM_014791 | Hs.184339 | KIAA0175 gene product | 5.8 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 419741 | NM_007019 | Hs.93002 | ubiquitin carrier protein E2-C | 5.7 |
| | 421988 | AW450481 | Hs.161333 | ESTs | 5.7 |
| | 422283 | AW411307 | Hs.114311 | CDC45 (cell division cycle 45, S.cerevis | 5.7 |
| 5 | 416111 | AA033813 | Hs.79018 | chromatin assembly factor 1, subunit A (| 5.7 |
| | 434846 | AW295389 | Hs.119768 | ESTs | 5.7 |
| | 412567 | AI750979 | Hs.74034 | Homo sapiens clone 24651 mRNA sequence | 5.7 |
| | 452372 | AI885742 | Hs.228474 | ESTs | 5.6 |
| | 443247 | BE614387 | Hs.333893 | c-Myc target JPO1 | 5.6 |
| 10 | 423198 | M81933 | Hs.1634 | cell division cycle 25A | 5.6 |
| | 445873 | AA250970 | Hs.251946 | poly(A)-binding protein, cytoplasmic 1-I | 5.6 |
| | 437034 | AA742643 | | gb:ny91c01.s1 NCI_CGAP_GCB1 Homo sapiens | 5.6 |
| | 429447 | AW812452 | Hs.83286 | ESTs, Weakly similar to S14747 sphingomy | 5.6 |
| | 424687 | J05070 | Hs.151738 | matrix metalloproteinase 9 (gelatinase B | 5.6 |
| 15 | 437695 | AA769202 | Hs.192142 | ESTs | 5.6 |
| | 426935 | NM_000088 | Hs.172928 | collagen, type I, alpha 1 | 5.6 |
| | 453361 | AA035197 | Hs.107375 | ESTs | 5.5 |
| | 418293 | AI224483 | Hs.16063 | hypothetical protein FLJ21877 | 5.5 |
| | 405348 | | | C7001664:gi12698061 dbj BAB21849.1 (AB | 5.5 |
| 20 | 458079 | AI796870 | Hs.54277 | DNA segment on chromosome X (unique) 992 | 5.4 |
| | 452799 | AI948829 | Hs.213786 | ESTs | 5.4 |
| | 448935 | AL078596 | Hs.22591 | nuclear receptor subfamily 2, group E, m | 5.4 |
| | 422809 | AK001379 | Hs.121028 | hypothetical protein FLJ10549 | 5.4 |
| | 442547 | AA306997 | Hs.217484 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 5.4 |
| 25 | 442009 | F11690 | | gb:HSC300041 normalized infant brain cDN | 5.4 |
| | 440332 | AI218517 | Hs.188051 | ESTs | 5.4 |
| | 422094 | AF129535 | Hs.272027 | F-box only protein 5 | 5.4 |
| | 443884 | N20617 | Hs.194397 | leptin receptor | 5.4 |
| | 422493 | AW474183 | Hs.250173 | hypothetical protein FLJ13158 | 5.4 |
| 30 | 432731 | R31178 | Hs.287820 | fibronectin 1 | 5.4 |
| | 426108 | AA622037 | Hs.166468 | programmed cell death 5 | 5.3 |
| | 407624 | AW157431 | Hs.248941 | ESTs | 5.3 |
| | 411048 | AK001742 | Hs.67991 | hypothetical protein DKFZp434G0522 | 5.3 |
| | 412471 | M63193 | Hs.73946 | endothelial cell growth factor 1 (platelet | 5.3 |
| 35 | 414020 | NM_002984 | Hs.75703 | small inducible cytokine A4 (homologous | 5.2 |
| | 414774 | X02419 | Hs.77274 | plasminogen activator, urokinase | 5.2 |
| | 413786 | AW613780 | Hs.13500 | ESTs | 5.2 |
| | 454860 | AW835767 | | gb:QV4-LT0016-240200-110-b08 LT0016 Homo | 5.2 |
| | 428037 | N47474 | Hs.89230 | potassium intermediate/small conductance | 5.2 |
| 40 | 420311 | AW445044 | Hs.38207 | Human DNA sequence from clone RP4-53015 | 5.1 |
| | 416737 | AF154335 | Hs.79691 | LIM domain protein | 5.1 |
| | 445837 | AI261700 | Hs.145544 | ESTs | 5.1 |
| | 425882 | U83115 | Hs.161002 | absent in melanoma 1 | 5.1 |
| | 415682 | AI347128 | Hs.191870 | ESTs | 5.1 |
| 45 | 414053 | BE391635 | Hs.75725 | transgelin 2 | 5.1 |
| | 453884 | AA355925 | Hs.36232 | KIAA0186 gene product | 5.1 |
| | 431512 | BE270734 | Hs.2795 | lactate dehydrogenase A | 5.1 |
| | 432593 | AW301003 | Hs.51483 | ESTs, Weakly similar to hypothetical pro | 5.0 |
| | 433323 | AA805132 | Hs.159142 | ESTs | 5.0 |
| 50 | 443744 | AI084326 | Hs.271548 | ESTs, Weakly similar to I78885 serine/th | 5.0 |
| | 410434 | AF051152 | Hs.63668 | toll-like receptor 2 | 5.0 |
| | 420018 | U56387 | Hs.94376 | proprotein convertase subtilisin/kexin 1 | 5.0 |
| | 419485 | AA489023 | Hs.99807 | ESTs, Weakly similar to unnamed protein | 4.9 |
| | 446131 | NM_000929 | Hs.290 | phospholipase A2, group V | 4.9 |
| 55 | 412777 | AI335773 | Hs.270123 | ESTs | 4.9 |
| | 449246 | AW411209 | Hs.23363 | hypothetical protein FLJ10983 | 4.9 |
| | 433244 | AB040943 | Hs.271285 | KIAA1510 protein | 4.9 |
| | 407235 | D20569 | Hs.169407 | SAC2 (suppressor of actin mutations 2, y | 4.9 |
| | 445118 | AI208762 | Hs.345572 | ESTs | 4.9 |
| 60 | 417404 | NM_007350 | Hs.82101 | pleckstrin homology-like domain, family | 4.9 |
| | 420092 | AA814043 | Hs.88045 | ESTs | 4.9 |
| | 412811 | H06382 | | ESTs | 4.9 |
| | 436607 | AW661783 | Hs.211061 | ESTs | 4.9 |
| | 438456 | AA913381 | Hs.20594 | ESTs | 4.9 |
| 65 | 443883 | AA114212 | Hs.9930 | serine (or cysteine) proteinase inhibito | 4.9 |
| | 431553 | X78075 | Hs.2799 | cartilage linking protein 1 | 4.9 |
| | 439999 | AA115811 | Hs.6838 | ras homolog gene family, member E | 4.9 |
| | 411252 | AB018549 | Hs.69328 | MD-2 protein | 4.9 |
| | 444381 | BE387335 | Hs.283713 | ESTs, Weakly similar to S64054 hypotheti | 4.8 |
| 70 | 429433 | AA452899 | Hs.213586 | ESTs, Weakly similar to KIAA1353 protein | 4.8 |
| | 403349 | NM_001406 | | ephrin-B3 | 4.8 |
| | 402274 | | | C19000498:gi4567179 gb AA23607.1 AC00 | 4.8 |
| | 426044 | AA502490 | Hs.170290 | ESTs | 4.8 |
| | 423600 | AI633559 | Hs.310359 | ESTs | 4.8 |
| 75 | 425905 | AB032959 | Hs.318584 | novel C3HC4 type Zinc finger (ring finger | 4.8 |
| | 431117 | AF003522 | Hs.250500 | delta (Drosophila)-like 1 | 4.8 |
| | 418054 | NM_002318 | Hs.83354 | lysyl oxidase-like 2 | 4.7 |
| | 441703 | AW390054 | Hs.192843 | leucine zipper protein FKSG14 | 4.7 |
| | 439627 | BE621702 | Hs.29076 | hypothetical protein FLJ21841 | 4.7 |
| 80 | 445900 | AF070526 | Hs.125036 | Homo sapiens clone 24787 mRNA sequence | 4.7 |
| | 435937 | AA830893 | Hs.119769 | ESTs | 4.7 |
| | 403961 | | | Target Exon | 4.7 |
| | 407862 | BE548267 | Hs.337986 | Homo sapiens cDNA FLJ10934 fis, clone OV | 4.6 |
| | 408523 | AW833259 | Hs.314287 | ESTs | 4.6 |

| | | | | |
|----|--------|-----------|--|-----|
| | 403481 | | Target Exon | 4.6 |
| | 423529 | T87318 | ESTs | 4.6 |
| | 416847 | L43821 | enhancer of filamentation 1 (cas-like do | 4.6 |
| 5 | 453362 | H14988 | ESTs | 4.6 |
| | 407013 | U35637 | gb:Human nebulin mRNA, partial cds | 4.6 |
| | 423757 | AL049337 | Hs.132571 Homo sapiens mRNA; cDNA DKFZp564P016 (lr | 4.6 |
| | 432363 | AA534489 | gb:n776g11.s1 NCI_CGAP_Co3 Homo sapiens | 4.6 |
| | 408380 | AF123050 | diubiquitin | 4.6 |
| 10 | 429149 | AW193360 | Hs.44532 ESTs, Weakly similar to I38022 hypotheti | 4.6 |
| | 422170 | AI791949 | Hs.197962 anti-Mullerian hormone | 4.6 |
| | 405558 | | Hs.112432 Target Exon | 4.6 |
| | 410295 | AA741357 | Hs.5174 nidogen (enactin) | 4.6 |
| | 450166 | AA429504 | ESTs | 4.6 |
| 15 | 451418 | BE387790 | Hs.26369 hypothetical protein FLJ20287 | 4.5 |
| | 420075 | AF142482 | Hs.203846 TEA domain family member 3 | 4.5 |
| | 422158 | L10343 | Hs.112341 protease inhibitor 3, skin-derived (SKAL | 4.5 |
| | 457465 | AW301344 | Hs.122908 DNA replication factor | 4.5 |
| | 436827 | H72187 | Hs.5322 guanine nucleotide binding protein (G pr | 4.5 |
| 20 | 452620 | AA436504 | Hs.119286 ESTs | 4.5 |
| | 424381 | AA285249 | Hs.146329 protein kinase Chk2 | 4.5 |
| | 444656 | AI277924 | Hs.145199 ESTs | 4.5 |
| | 450639 | AI703186 | Hs.277174 ESTs | 4.5 |
| | 424247 | X14008 | Hs.234734 lysozyme (renal amyloidosis) | 4.5 |
| 25 | 423178 | AJ033140 | Hs.124983 Homo sapiens mRNA; cDNA DKFZp564C142 (lr | 4.5 |
| | 447072 | D61594 | Hs.17279 tyrosylprotein sulfotransferase 1 | 4.5 |
| | 447444 | AK000318 | Hs.18616 hypothetical protein FLJ20311 | 4.4 |
| | 401454 | | NM_014226*:Homo sapiens renal tumor anti | 4.4 |
| | 420560 | AW207748 | Hs.59115 ESTs | 4.4 |
| 30 | 409205 | AJ952884 | Hs.14832 ESTs, Moderately similar to unnamed prot | 4.4 |
| | 451129 | BE072881 | gb:RC2-BT0548-200300-012-e09 BT0548 Homo | 4.4 |
| | 412530 | AA766268 | Hs.266273 hypothetical protein FLJ13346 | 4.4 |
| | 447752 | M73700 | Hs.105938 lactotransferrin | 4.4 |
| | 429083 | Y09397 | Hs.227817 BCL2-related protein A1 | 4.4 |
| 35 | 418283 | S79895 | Hs.83942 cathepsin K (pseudosclerosis) | 4.3 |
| | 424736 | AF230877 | Hs.152701 microtubule-interacting protein that ass | 4.3 |
| | 416379 | N38857 | Hs.203933 ESTs | 4.3 |
| | 452994 | AW962597 | Hs.31305 KIAA1547 protein | 4.3 |
| 40 | 437834 | AA769294 | Hs.283854 gb:nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens | 4.3 |
| | 441035 | AI694309 | Hs.126458 ESTs | 4.3 |
| | 425292 | NM_005824 | Hs.155545 37 kDa leucine-rich repeat (LRR) protein | 4.3 |
| | 418030 | BE207573 | Hs.83321 neuromedin B | 4.3 |
| | 450811 | AI739486 | Hs.245497 ESTs | 4.3 |
| | 438458 | AW975186 | gb:EST387294 MAGE resequences, MAGN Homo | 4.3 |
| 45 | 442201 | AW516704 | Hs.208726 ESTs | 4.3 |
| | 429732 | U20158 | Hs.2488 lymphocyte cytosolic protein 2 (SH2 doma | 4.3 |
| | 435677 | AA694142 | Hs.293726 ESTs, Weakly similar to TSGA RAT TESTIS | 4.3 |
| | 442832 | AW206560 | Hs.253569 ESTs | 4.3 |
| | 449318 | AW236021 | Hs.78531 Homo sapiens, Similar to RIKEN cDNA 5730 | 4.2 |
| 50 | 421027 | AA761198 | Hs.55254 ESTs | 4.2 |
| | 414300 | AI304870 | Hs.188680 ESTs | 4.2 |
| | 452874 | AK001061 | Hs.30925 hypothetical protein FLJ10199 | 4.2 |
| | 444161 | N52543 | Hs.142940 ESTs | 4.2 |
| | 416908 | AA333990 | Hs.80424 coagulation factor XIII, A1 polypeptide | 4.2 |
| 55 | 418483 | W26076 | Hs.221847 ESTs | 4.2 |
| | 443318 | AI051603 | Hs.133141 ESTs | 4.2 |
| | 415079 | R43179 | Hs.22895 hypothetical protein FLJ23548 | 4.2 |
| | 416871 | H98716 | gb:yx13d08.s1 Soares melanocyte 2NbHM Ho | 4.2 |
| | 423678 | AW963357 | Hs.7847 ESTs | 4.2 |
| 60 | 429643 | AA455889 | Hs.167279 FYVE-finger-containing Rab5 effector pro | 4.2 |
| | 438875 | AA827640 | Hs.189059 ESTs | 4.2 |
| | 428600 | AW863261 | Hs.242413 hypothetical protein DKFZp434K1421 | 4.2 |
| | 430968 | AW972830 | gb:EST384925 MAGE resequences, MAGL Homo | 4.2 |
| | 406872 | AI760903 | gb:wi09h08.x1 NCI_CGAP_CLL1 Homo sapiens | 4.2 |
| 65 | 403790 | | NM_001334*:Homo sapiens cathepsin O (CTS | 4.1 |
| | 409112 | BE243971 | Hs.50649 quinone oxidoreductase homolog | 4.1 |
| | 435703 | AW630133 | Hs.83313 GK003 protein | 4.1 |
| | 432625 | AI243596 | Hs.94830 ESTs, Moderately similar to T03094 A-kin | 4.1 |
| | 404407 | | Target Exon | 4.1 |
| 70 | 412568 | AI878826 | Hs.74034 caveolin 1, caveolae protein, 22kD | 4.1 |
| | 422087 | X58968 | Hs.111301 matrix metalloproteinase 2 (gelatinase A | 4.1 |
| | 435143 | R12375 | Hs.194600 ESTs | 4.1 |
| | 447497 | AW167254 | Hs.205722 ESTs | 4.1 |
| | 456304 | AI820973 | gb:nc21c02.y5 NCI_CGAP_Pr1 Homo sapiens | 4.1 |
| 75 | 427676 | AA394062 | Hs.300772 tropomyosin 2 (beta) | 4.1 |
| | 436608 | AA628980 | down syndrome critical region protein DS | 4.1 |
| | 453331 | AI240665 | ESTs | 4.0 |
| | 420004 | AW975532 | Hs.164039 ESTs, Moderately similar to I38022 hypot | 4.0 |
| | 412125 | Y17114 | Hs.73393 eyes absent (Drosophila) homolog 4 | 4.0 |
| 80 | 426215 | AW963419 | Hs.155223 stanniocalcin 2 | 4.0 |
| | 407603 | AW955705 | Hs.62604 Homo sapiens, clone IMAGE:4299322, mRNA, | 4.0 |
| | 450581 | AF081513 | Hs.25195 TGF-beta 4 | 4.0 |
| | 415323 | BE269352 | Hs.949 neutrophil cytosolic factor 2 (65kD, chr | 4.0 |
| | 409893 | AW247090 | Hs.57101 minichromosome maintenance deficient (S. | 4.0 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 432058 | AW665996 | Hs.130729 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 4.0 |
| | 444609 | AW571659 | Hs.278081 | ESTs | 4.0 |
| | 445666 | RS9960 | Hs.282386 | ESTs | 4.0 |
| 5 | 437814 | AI088192 | Hs.135474 | ESTs, Weakly similar to DDX9_HUMAN ATP-D | 4.0 |
| | 414948 | C15240 | Hs.182155 | ESTs | 4.0 |
| | 435542 | AA687376 | | ESTs | 4.0 |
| | 422564 | AI148006 | Hs.222120 | ESTs | 4.0 |
| | 449571 | AW016812 | Hs.200266 | ESTs | 4.0 |
| 10 | 433556 | W56321 | Hs.111460 | calcium/calmodulin-dependent protein kin | 4.0 |
| | 458946 | AA009716 | Hs.42311 | ESTs | 4.0 |
| | 449655 | AI021987 | Hs.59970 | ESTs | 4.0 |
| | 426649 | AI914936 | Hs.97152 | ESTs | 4.0 |
| | 457292 | AI921270 | Hs.281462 | hypothetical protein FLJ14251 | 4.0 |
| 15 | 440435 | AL042201 | Hs.21273 | transcription factor NYD-sp10 | 4.0 |
| | 456977 | AK000252 | Hs.169758 | hypothetical protein FLJ20245 | 4.0 |
| | 420649 | AI866964 | Hs.124704 | ESTs, Moderately similar to S55657 alpha | 4.0 |
| | 416406 | D86961 | Hs.79299 | ipoma HMGC fusion partner-like 2 | 4.0 |
| | 446291 | BE397753 | Hs.14623 | interferon, gamma-inducible protein 30 | 3.9 |
| 20 | 449256 | AA059050 | Hs.59847 | ESTs | 3.9 |
| | 421637 | AF035290 | Hs.106300 | Homo sapiens clone 23556 mRNA sequence | 3.9 |
| | 456306 | AA225313 | Hs.222886 | ESTs, Weakly similar to TRHY_HUMAN TRICH | 3.9 |
| | 438372 | AI140189 | Hs.123191 | ESTs | 3.9 |
| | 427375 | AL035460 | Hs.177536 | metallocarboxypeptidase CPX-1 | 3.9 |
| 25 | 415131 | D61119 | | gb:HUM158C118 Clontech human fetal brain | 3.9 |
| | 439231 | AW581935 | Hs.141480 | Homo sapiens mRNA: cDNA DKFZp434N079 (fr | 3.9 |
| | 424998 | U58515 | Hs.154138 | chitinase 3-like 2 | 3.9 |
| | 433376 | AI249361 | Hs.74122 | caspase 4, apoptosis-related cysteine pr | 3.9 |
| | 455104 | BE064863 | | gb:RC1-BT0313-110300-015-f06 BT0313 Homo | 3.9 |
| 30 | 443426 | AF098158 | Hs.9329 | chromosome 20 open reading frame 1 | 3.9 |
| | 419594 | AA013051 | Hs.91417 | topoisomerase (DNA) II binding protein | 3.9 |
| | 417576 | AA339449 | Hs.82785 | phosphoribosylglycinamide formyltransfer | 3.9 |
| | 416857 | AA188775 | Hs.292453 | ESTs | 3.9 |
| | 434784 | AA649051 | Hs.164007 | ESTs | 3.8 |
| 35 | 438898 | AI819863 | Hs.106243 | ESTs | 3.8 |
| | 408102 | U46351 | Hs.621 | lectin, galactoside-binding, soluble, 3 | 3.8 |
| | 422081 | AW136820 | Hs.196011 | ESTs | 3.8 |
| | 411688 | AW953440 | | gb:EST365510 MAGE resequences, MAGB Homo | 3.8 |
| | 447343 | AA256641 | Hs.236894 | ESTs, Highly similar to S02392 alpha-2-m | 3.8 |
| 40 | 406395 | | | Target Exon | 3.8 |
| | 433675 | AW977653 | Hs.75319 | ribonucleotide reductase M2 polypeptide | 3.8 |
| | 403696 | | | C4001100*:gil5852342[gb]AAD54015.1] (AF0 | 3.8 |
| | 443740 | R56434 | Hs.21062 | ESTs | 3.8 |
| | 413076 | U10564 | Hs.75188 | wee1 (S. pombe) homolog | 3.8 |
| 45 | 409189 | AA125984 | | gb:zn27h06.r1 Stratagene neuroepithelium | 3.8 |
| | 444326 | AI939357 | Hs.270710 | ESTs | 3.8 |
| | 436899 | AA764852 | Hs.291567 | ESTs | 3.8 |
| | 445075 | AI651827 | Hs.344767 | ESTs | 3.8 |
| | 416892 | L24498 | Hs.80409 | growth arrest and DNA-damage-inducible, | 3.8 |
| 50 | 429163 | AA884766 | | gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s | 3.8 |
| | 416114 | AI695549 | Hs.183868 | glucuronidase, beta | 3.8 |
| | 417018 | M16038 | Hs.80887 | v-yes-1 Yamaguchi sarcoma viral related | 3.8 |
| | 446839 | BE091926 | Hs.16244 | mitotic spindle coiled-coil related prot | 3.8 |
| | 454117 | BE410100 | Hs.40368 | adaptor-related protein complex 1, sigma | 3.8 |
| 55 | 416664 | H72780 | Hs.20289 | ESTs | 3.8 |
| | 449444 | AW818436 | Hs.23590 | solute carrier family 16 (monocarboxylic | 3.8 |
| | 419735 | AW750056 | Hs.169577 | Homo sapiens cDNA FLJ14743 fis, clone NT | 3.8 |
| | 448275 | BE514434 | Hs.20830 | kinesin-like 2 | 3.7 |
| | 405141 | Y14443 | | zinc finger protein 200 | 3.7 |
| 60 | 411537 | BE073250 | | gb:MR0-BT0551-060300-102-e05 BT0551 Homo | 3.7 |
| | 422648 | D86983 | Hs.118893 | Melanoma associated gene | 3.7 |
| | 449145 | AI632122 | Hs.198408 | ESTs | 3.7 |
| | 428060 | AA420616 | Hs.249483 | ESTs | 3.7 |
| | 404584 | | | Target Exon | 3.7 |
| 65 | 418596 | AW976721 | Hs.293327 | ESTs | 3.7 |
| | 458072 | AI890347 | Hs.271923 | Homo sapiens cDNA: FLJ22785 fis, clone K | 3.7 |
| | 445908 | R13580 | Hs.13436 | Homo sapiens clone 24425 mRNA sequence | 3.7 |
| | 439979 | AW600291 | Hs.6823 | hypothetical protein FLJ10430 | 3.7 |
| | 431770 | BE221880 | Hs.268555 | 5'-3' exonuclease 2 | 3.7 |
| 70 | 427809 | M26380 | Hs.180878 | lipoprotein lipase | 3.7 |
| | 436674 | AA725002 | Hs.272018 | low molecular mass ubiquinone-binding pr | 3.7 |
| | 413450 | Z99716 | Hs.75372 | N-acetylgalactosaminidase, alpha- | 3.7 |
| | 434467 | BE552368 | Hs.231853 | Homo sapiens cDNA FLJ13445 fis, clone PL | 3.7 |
| | 448048 | BE281291 | Hs.170408 | ESTs, Moderately similar to A47582 B-cel | 3.7 |
| 75 | 422798 | R92347 | Hs.34574 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.7 |
| | 402082 | | | C18000743*:gil6678363[ref]NP_033416.1] t | 3.7 |
| | 448019 | AW947164 | Hs.195641 | ESTs, Moderately similar to I38022 hypot | 3.7 |
| | 428873 | AI701609 | Hs.98908 | ESTs | 3.7 |
| | 437323 | AA371145 | Hs.194397 | leptin receptor | 3.7 |
| 80 | 413095 | AA494359 | Hs.30715 | potassium voltage-gated channel, Isk-rel | 3.7 |
| | 425139 | AW630488 | Hs.25338 | protease, serine, 23 | 3.7 |
| | 452279 | AA286844 | Hs.61260 | hypothetical protein FLJ13164 | 3.7 |
| | 439574 | AI469788 | Hs.165190 | ESTs | 3.7 |
| | 408829 | NM_006042 | Hs.48384 | heparan sulfate (glucosamine) 3-O-sulfot | 3.7 |

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|----|--------|-----------|-----------|--|-----|
| | 407838 | BE146411 | Hs.40342 | putative nuclear protein | 3.7 |
| | 437748 | AF234882 | Hs.5814 | suppression of tumorigenicity 7 | 3.6 |
| | 437470 | AL390147 | Hs.134742 | hypothetical protein DKFZp547D065 | 3.6 |
| | 400288 | X06256 | Hs.149609 | integrin, alpha 5 (fibronectin receptor, | 3.6 |
| 5 | 453438 | AI689935 | Hs.22792 | ESTs | 3.6 |
| | 415024 | AI983981 | Hs.189114 | ESTs | 3.6 |
| | 419713 | AW968058 | Hs.92381 | nudix (nucleoside diphosphate linked moi | 3.6 |
| | 441523 | AW514263 | Hs.301771 | ESTs, Weakly similar to ALUF_HUMAN !!!! | 3.6 |
| | 416427 | BE244050 | Hs.79307 | Rac/Cdc42 guanine exchange factor (GEF) | 3.6 |
| 10 | 448002 | Y15227 | Hs.20149 | deleted in lymphocytic leukemia, 1 | 3.6 |
| | 441362 | BE614410 | Hs.23044 | RAD51 (S. cerevisiae) homolog (E coli Re | 3.6 |
| | 456534 | X91195 | Hs.100623 | phospholipase C, beta 3, neighbor pseudo | 3.6 |
| | 402239 | | | Target Exon | 3.6 |
| | 450297 | AW901347 | Hs.38592 | hypothetical protein FLJ23342 | 3.6 |
| 15 | 443715 | AI583187 | Hs.9700 | cyclin E1 | 3.6 |
| | 403011 | | | ENSP00000215330: Probable serine/threoni | 3.6 |
| | 428403 | AI393048 | Hs.326159 | leucine rich repeat (in FLJ) interactin | 3.6 |
| | 425202 | AW962282 | Hs.152049 | ESTs, Weakly similar to I38022 hypotheti | 3.6 |
| | 409557 | BE182896 | Hs.211193 | ESTs | 3.6 |
| 20 | 453948 | AI970797 | Hs.64859 | ESTs | 3.6 |
| | 440225 | BE295782 | Hs.159 | tumor necrosis factor receptor superfam | 3.6 |
| | 425331 | AW962128 | | gb:EST374201 MAGE resequences, MAGG Homo | 3.6 |
| | 442326 | H92962 | Hs.124813 | hypothetical protein MGC14817 | 3.6 |
| | 437640 | AA764893 | Hs.272155 | ESTs, Weakly similar to I38022 hypotheti | 3.6 |
| 25 | 424051 | AL110203 | Hs.138411 | Homo sapiens mRNA; cDNA DKFZp586J1922 (f | 3.6 |
| | 406481 | | | Target Exon | 3.6 |
| | 433835 | AI806185 | | gb:w26a10.x1 Soares_NFL_T_GBC_S1 Homo s | 3.6 |
| | 456052 | BE311901 | Hs.28935 | gb:601142614F1 NIH_MGC_14 Homo sapiens c | 3.6 |
| 30 | 453857 | AL080235 | Hs.35861 | DKFZP586E1621 protein | 3.5 |
| | 439726 | AW449893 | Hs.293707 | ESTs, Weakly similar to I38598 zinc fing | 3.5 |
| | 416913 | AW934714 | | gb:RC1-DT0001-031299-011-a11 DT0001 Homo | 3.5 |
| | 419402 | Z68155 | Hs.90291 | laminin, beta 2 (laminin S) | 3.5 |
| | 403108 | | | ENSP00000241415: Hypothetical 67.7 kDa p | 3.5 |
| 35 | 426509 | M31166 | Hs.2050 | pentaxin-related gene, rapidly induced b | 3.5 |
| | 418883 | BE387036 | Hs.1211 | acid phosphatase 5, tartrate resistant | 3.5 |
| | 432188 | AI362952 | Hs.2928 | solute carrier family 7 (cationic amino | 3.5 |
| | 448789 | BE539108 | Hs.22051 | hypothetical protein MGC15548 | 3.5 |
| | 427299 | AA830210 | Hs.214263 | ESTs, Moderately similar to ALU1_HUMAN A | 3.5 |
| | 425212 | AW962253 | Hs.171618 | ESTs | 3.5 |
| 40 | 422938 | NM_001809 | Hs.1594 | centromere protein A (17kD) | 3.5 |
| | 442264 | AI278777 | Hs.263455 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.5 |
| | 407253 | AA411175 | Hs.141939 | ESTs, Moderately similar to S65657 alpha | 3.5 |
| | 457211 | AW972565 | Hs.32399 | ESTs, Weakly similar to S51797 vasodilat | 3.5 |
| | 452582 | AA456193 | Hs.9071 | progesterone membrane binding protein | 3.5 |
| 45 | 421247 | BE391727 | Hs.102910 | general transcription factor I1H, polype | 3.5 |
| | 418049 | AA211467 | Hs.190488 | Homo sapiens, Similar to nuclear localiz | 3.5 |
| | 453792 | AL134539 | Hs.254129 | KIAA1678 | 3.5 |
| | 416426 | AA180256 | Hs.210473 | Homo sapiens cDNA FLJ14872 fis, clone PL | 3.5 |
| 50 | 412014 | AI620650 | Hs.43761 | ESTs, Weakly similar to A46010 X-linked | 3.5 |
| | 440370 | AA884000 | Hs.8173 | hypothetical protein FLJ10803 | 3.5 |
| | 407729 | T40707 | Hs.270862 | ESTs | 3.5 |
| | 438527 | AI969251 | Hs.115325 | RAB7, member RAS oncogene family-like 1 | 3.5 |
| | 455646 | BE064420 | | gb:RC4-BT0311-241199-012-c08 BT0311 Homo | 3.5 |
| 55 | 418630 | AI351311 | Hs.251946 | poly(A)-binding protein, cytoplasmic 14 | 3.5 |
| | 432242 | AW022715 | Hs.162160 | ESTs, Weakly similar to ALU4_HUMAN ALU S | 3.5 |
| | 424503 | NM_002205 | Hs.149609 | integrin, alpha 5 (fibronectin receptor, | 3.4 |
| | 449932 | AI675444 | Hs.263024 | ESTs | 3.4 |
| | 427700 | AA262294 | Hs.180383 | dual specificity phosphatase 6 | 3.4 |
| | 403849 | | | Target Exon | 3.4 |
| 60 | 429747 | M87507 | Hs.2490 | caspase 1, apoptosis-related cysteine pr | 3.4 |
| | 451446 | AI826288 | Hs.171637 | hypothetical protein MGC2628 | 3.4 |
| | 434589 | AF147363 | | gb:Homo sapiens full length insert cDNA | 3.4 |
| | 403361 | | | NM_002210: Homo sapiens integrin, alpha | 3.4 |
| | 420841 | AI625251 | Hs.94037 | hypothetical protein FLJ23053 | 3.4 |
| 65 | 438206 | AA780385 | Hs.187885 | ESTs | 3.4 |
| | 425295 | AA431366 | Hs.37251 | ESTs | 3.4 |
| | 411789 | AF245505 | Hs.72157 | Adicican | 3.4 |
| | 440948 | AW188311 | Hs.128619 | ESTs | 3.4 |
| 70 | 439518 | W76326 | | gb:zd60d04.r1 Soares_fetal_heart_NbHH19W | 3.4 |
| | 418821 | AA436002 | Hs.183161 | ESTs | 3.4 |
| | 459650 | M79082 | | ESTs | 3.4 |
| | 404209 | | | Target Exon | 3.4 |
| | 443950 | NM_001425 | Hs.9999 | epithelial membrane protein 3 | 3.4 |
| 75 | 430694 | AA810624 | Hs.30936 | ESTs, Weakly similar to H2BH_HUMAN HISTO | 3.4 |
| | 425300 | AW601773 | Hs.270259 | ESTs | 3.4 |
| | 420300 | AA258245 | Hs.127573 | Homo sapiens FKSG41 (FKSG41) mRNA, compl | 3.4 |
| | 458438 | AI141520 | Hs.151464 | ESTs, Weakly similar to ALUC_HUMAN !!!! | 3.4 |
| | 444911 | U08117 | Hs.250 | xanthine dehydrogenase | 3.4 |
| 80 | 421064 | AI245432 | Hs.101382 | tumor necrosis factor, alpha-induced pro | 3.4 |
| | 441287 | AW293132 | Hs.131373 | ESTs | 3.4 |
| | 446960 | AW294936 | Hs.156762 | ESTs | 3.4 |
| | 405605 | | | C2001342:gi127814[sp]P26434[NAH4_RAT SO | 3.4 |
| | 433791 | AA719352 | Hs.112718 | ESTs | 3.4 |

| | | | | | |
|----|--------|-----------|-------------|--|-----|
| | 405238 | | Target Exon | 3.4 | |
| | 412986 | X81120 | Hs.75110 | cannabinoid receptor 1 (brain) | 3.4 |
| | 414372 | AA143654 | | gb:zo65a02.r1 Stratagene pancreas (93720 | 3.4 |
| 5 | 435523 | T62849 | Hs.11090 | membrane-spanning 4-domains, subfamily A | 3.4 |
| | 406739 | AI566709 | Hs.182426 | ribosomal protein S2 | 3.4 |
| | 442710 | AI015631 | Hs.23210 | ESTs | 3.4 |
| | 452526 | W38537 | Hs.280740 | hypothetical protein MGC3040 | 3.4 |
| | 456060 | C14904 | Hs.45184 | Homo sapiens cDNA FLJ12284 fis, clone MA | 3.4 |
| 10 | 435005 | U80743 | Hs.306094 | trinucleotide repeat containing 12 | 3.4 |
| | 421674 | T10707 | Hs.296355 | hypothetical protein FLJ23138 | 3.4 |
| | 425242 | D13635 | Hs.155287 | KIAA0010 gene product | 3.4 |
| | 436805 | AA731533 | Hs.270751 | ESTs | 3.4 |
| | 418641 | BE243136 | Hs.86947 | a disintegrin and metalloproteinase doma | 3.4 |
| 15 | 430809 | AI791150 | Hs.262009 | ESTs, Moderately similar to I38022 hypot | 3.4 |
| | 428878 | AA436884 | Hs.48926 | ESTs | 3.3 |
| | 413774 | AA131782 | Hs.182314 | ESTs | 3.3 |
| | 400533 | | | ENSP00000209376*:PRED65 protein (Fragmen | 3.3 |
| | 422448 | AW372922 | Hs.116774 | integrin, alpha 1 | 3.3 |
| 20 | 423905 | AW579960 | Hs.135150 | lung type-I cell membrane-associated gly | 3.3 |
| | 430637 | BE160081 | Hs.256290 | S100 calcium-binding protein A11 (calgiz | 3.3 |
| | 427899 | AA829286 | Hs.332053 | serum amyloid A1 | 3.3 |
| | 434206 | AW136973 | Hs.180479 | ESTs, Weakly similar to S69890 mitogen i | 3.3 |
| | 453387 | AI990741 | Hs.252809 | ESTs | 3.3 |
| 25 | 436265 | AA731331 | Hs.190668 | ESTs | 3.3 |
| | 412971 | AA889628 | Hs.35125 | ESTs | 3.3 |
| | 441701 | AW339828 | Hs.127497 | ESTs | 3.3 |
| | 418967 | NM_001725 | Hs.89535 | bactericidal/permeability-increasing pro | 3.3 |
| | 434577 | R37316 | Hs.179769 | Homo sapiens cDNA: FLJ22487 fis, clone H | 3.3 |
| 30 | 418216 | AA662240 | Hs.283099 | AF15q14 protein | 3.3 |
| | 436137 | AI056769 | Hs.133512 | ESTs | 3.3 |
| | 428715 | AW293716 | Hs.53126 | ESTs | 3.3 |
| | 449249 | T52285 | Hs.193115 | Homo sapiens mRNA for KIAA1764 protein, | 3.3 |
| | 440074 | AA863045 | Hs.10669 | ESTs, Weakly similar to T00050 hypotheti | 3.3 |
| 35 | 405046 | | | C3000978:gi9280045 dbj BAB01579.1 (AB0 | 3.3 |
| | 437816 | AI823445 | Hs.280699 | ESTs | 3.3 |
| | 401272 | | | C9000559*:gi12314195 emb CAB99338.1 (A | 3.3 |
| | 408896 | AI610447 | Hs.48778 | riban protein | 3.3 |
| | 432343 | NM_002960 | Hs.2961 | S100 calcium-binding protein A3 | 3.3 |
| 40 | 407881 | AW072003 | Hs.40968 | heparan sulfate (glucosamine) 3-O-sulfot | 3.3 |
| | 439978 | BE139460 | Hs.124673 | Homo sapiens cDNA FLJ11477 fis, clone HE | 3.3 |
| | 421094 | AW978202 | Hs.289064 | hypothetical protein FLJ22251 | 3.3 |
| | 428722 | U76456 | Hs.190787 | tissue inhibitor of metalloproteinase 4 | 3.3 |
| | 446134 | AW161234 | Hs.13993 | TBP-like 1 | 3.3 |
| 45 | 412281 | AI810054 | Hs.14119 | ESTs | 3.3 |
| | 436282 | R91913 | Hs.272104 | ESTs, Moderately similar to ALU1_HUMAN A | 3.3 |
| | 452203 | X57522 | | transporter 1, ATP-binding cassette, sub | 3.3 |
| | 421307 | BE539976 | Hs.103305 | Homo sapiens mRNA; cDNA DKFZp434B0425 (f | 3.3 |
| | 409463 | AI458165 | Hs.17296 | hypothetical protein MGC2376 | 3.3 |
| 50 | 411565 | AW851728 | | gb:MR2-CT0222-011199-007-d06 CT0222 Homo | 3.3 |
| | 410422 | AL042014 | Hs.63348 | Homo sapiens, clone MGC:15203, mRNA, com | 3.3 |
| | 450506 | NM_004460 | | fibroblast activation protein, alpha | 3.3 |
| | 451254 | AI571016 | Hs.172967 | ESTs | 3.3 |
| | 423784 | AK000039 | Hs.132826 | Homo sapiens cDNA FLJ14913 fis, clone PL | 3.3 |
| 55 | 433325 | AW206986 | Hs.143905 | ESTs | 3.3 |
| | 419896 | Z99362 | | gb:HSZ99362 DKFZphamy1 Homo sapiens cDNA | 3.3 |
| | 420552 | AK000492 | Hs.98806 | hypothetical protein | 3.3 |
| | 451778 | AI826131 | Hs.62954 | ESTs, Weakly similar to zinc finger prot | 3.3 |
| | 427584 | BE410293 | Hs.179718 | v-myb avian myeloblastosis viral oncogen | 3.2 |
| 60 | 433507 | AI817336 | Hs.191791 | ESTs | 3.2 |
| | 418661 | NM_001949 | Hs.1189 | E2F transcription factor 3 | 3.2 |
| | 440933 | AI208217 | Hs.142879 | ESTs | 3.2 |
| | 426746 | J03626 | Hs.2057 | uridine monophosphate synthetase (orotat | 3.2 |
| | 404120 | | | C5000537*:gi3298595 gb AAC41376.1 (AF0 | 3.2 |
| 65 | 453920 | AI133148 | Hs.36602 | I factor (complement) | 3.2 |
| | 437014 | AA808757 | Hs.222531 | ESTs, Weakly similar to S59501 interfero | 3.2 |
| | 424479 | AF064238 | Hs.149098 | smoothenin | 3.2 |
| | 413278 | BE563085 | Hs.833 | interferon-stimulated protein, 15 kDa | 3.2 |
| | 425922 | AL157466 | Hs.162751 | Homo sapiens mRNA; cDNA DKFZp761E2423 (f | 3.2 |
| 70 | 407304 | AA565832 | Hs.271649 | gb:nj32b03.s1 NCI_CGAP_AA1 Homo sapiens | 3.2 |
| | 411671 | BE049094 | | ESTs | 3.2 |
| | 420352 | BE258835 | | gb:501117374F1 NIH_MGC_16 Homo sapiens c | 3.2 |
| | 454765 | AW819629 | | gb:RCS-ST0293-140200-014-H05 ST0293 Homo | 3.2 |
| | 410407 | X66839 | Hs.63287 | carbonic anhydrase IX | 3.2 |
| 75 | 412490 | AW803564 | Hs.288850 | Homo sapiens cDNA: FLJ22528 fis, clone H | 3.2 |
| | 434563 | AW083994 | Hs.9469 | pleckstrin homology domain-containing, f | 3.2 |
| | 417124 | BE122762 | Hs.25338 | ESTs | 3.2 |
| | 407378 | AA299264 | Hs.57776 | ESTs, Moderately similar to I38022 hypot | 3.2 |
| | 439764 | T26535 | Hs.22744 | hypothetical protein MGC13105 | 3.2 |
| 80 | 445936 | BE543594 | Hs.61478 | hypothetical protein FLJ22329 | 3.2 |
| | 446523 | NM_003063 | Hs.334629 | sarcophilin | 3.2 |
| | 406060 | | | Target Exon | 3.2 |
| | 432250 | AA452088 | Hs.274170 | Opa-interacting protein 2 | 3.2 |
| | 437269 | AA334384 | Hs.149420 | ESTs | 3.2 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 449115 | AW959952 | Hs.37528 | ESTs, Weakly similar to AF090944.1 PRO06 | 3.2 |
| | 425146 | AW954627 | | gb:EST366697 MAGE resequences, MAGC Homo | 3.2 |
| | 436210 | A1825420 | Hs.197824 | ESTs | 3.2 |
| | 437698 | R61837 | Hs.7990 | ESTs, Moderately similar to I64505 catci | 3.2 |
| 5 | 444371 | BE540274 | Hs.239 | forkhead box M1 | 3.2 |
| | 410006 | AW732308 | Hs.57783 | eukaryotic translation initiation factor | 3.2 |
| | 445828 | F05802 | Hs.81907 | ESTs | 3.2 |
| | 450810 | BE207588 | Hs.334360 | transforming growth factor beta 1 induce | 3.2 |
| 10 | 439533 | W76021 | | gb:zd54c04.r1 Soares_fetal_heart_NbHH19W | 3.2 |
| | 418079 | R40058 | Hs.6911 | ESTs | 3.2 |
| | 418781 | T41160 | Hs.8404 | ESTs | 3.2 |
| | 422765 | AW409701 | Hs.1578 | baculoviral IAP repeat-containing 5 (sur | 3.2 |
| | 431319 | AA873350 | Hs.302232 | ESTs | 3.2 |
| | 445413 | AA151342 | Hs.12677 | CGI-147 protein | 3.2 |
| 15 | 424947 | R77952 | | ESTs, Weakly similar to alternatively sp | 3.2 |
| | 429490 | A1971131 | Hs.23889 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 3.2 |
| | 426765 | AA743603 | Hs.172108 | nucleoporin 88kD | 3.2 |
| | 419726 | U50330 | Hs.1274 | bone morphogenetic protein 1 | 3.2 |
| 20 | 425849 | AJ000512 | Hs.296323 | serum/glucocorticoid regulated kinase | 3.1 |
| | 439566 | AF086387 | | gb:Homo sapiens full length insert cDNA | 3.1 |
| | 452574 | AF127481 | Hs.301946 | lymphoid blast crisis oncogene | 3.1 |
| | 439753 | BE262233 | Hs.7423 | hypothetical protein from EUROIMAGE 2168 | 3.1 |
| | 435256 | AF193766 | Hs.13872 | cytokine-like protein C17 | 3.1 |
| 25 | 439570 | T79925 | Hs.269165 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.1 |
| | 443431 | A1056847 | Hs.20654 | ESTs | 3.1 |
| | 428289 | M26301 | Hs.2253 | complement component 2 | 3.1 |
| | 415849 | R20529 | Hs.6806 | ESTs | 3.1 |
| | 419652 | AL157485 | Hs.91973 | hypothetical protein | 3.1 |
| 30 | 429500 | X78565 | Hs.289114 | hexabrachion (tenascin C, cytactin) | 3.1 |
| | 457579 | AB030816 | Hs.36761 | HRAS-like suppressor | 3.1 |
| | 420579 | AA278449 | Hs.137429 | ESTs | 3.1 |
| | 408116 | AA251393 | Hs.289052 | Homo sapiens, Similar to RIKEN cDNA 5430 | 3.1 |
| | 408247 | AA053451 | Hs.225632 | leucine zipper protein 3 | 3.1 |
| 35 | 405183 | | | NM_016358:Homo sapiens iroquois homeobo | 3.1 |
| | 420676 | AA434780 | Hs.4248 | vav 2 oncogene | 3.1 |
| | 440286 | U29589 | Hs.7138 | cholinergic receptor, muscarinic 3 | 3.1 |
| | 431176 | A1026984 | Hs.293662 | ESTs | 3.1 |
| | 417918 | AA209205 | Hs.163754 | hypothetical protein FLJ12606 | 3.1 |
| 40 | 437945 | T78519 | | gb:yd68c08.r1 Soares fetal liver spleen | 3.1 |
| | 404632 | | | NM_022490:Homo sapiens hypothetical prot | 3.1 |
| | 428917 | AA437337 | Hs.16689 | ESTs | 3.1 |
| | 429940 | W25215 | | gb:zb87a09.r1 Soares_senescent_fibroblas | 3.1 |
| | 444016 | AA448154 | | gb:zw82h09.r1 Soares_testis_NHT Homo sap | 3.1 |
| 45 | 430701 | A1760833 | Hs.293971 | ESTs | 3.1 |
| | 402229 | BE262804 | | mitochondrial ribosomal protein S2 | 3.1 |
| | 454177 | AW807321 | | gb:MR4-ST0062-240300-003-g05 ST0062 Homo | 3.1 |
| | 400090 | | | Eos Control | 3.1 |
| | 419326 | W94915 | Hs.42419 | ESTs | 3.1 |
| 50 | 435644 | AA700867 | Hs.269659 | ESTs | 3.1 |
| | 433042 | AW193534 | Hs.281895 | Homo sapiens cDNA FLJ11660 fis, clone HE | 3.1 |
| | 458810 | BE407125 | Hs.231510 | ESTs | 3.1 |
| | 414403 | AW969551 | Hs.76064 | ribosomal protein L27a | 3.1 |
| | 449670 | F07693 | Hs.85603 | Homo sapiens mRNA; cDNA DKFZp434K2172 (I | 3.1 |
| 55 | 403288 | | | C1001737:gi7511201 pir T27904 hypothe | 3.1 |
| | 430535 | AW968485 | | gb:EST380561 MAGE resequences, MAGJ Homo | 3.1 |
| | 455899 | BE155112 | | gb:PM1-HT0350-151299-003-a03 HT0350 Homo | 3.1 |
| | 432044 | AW972727 | | gb:EST384819 MAGE resequences, MAGL Homo | 3.1 |
| | 443105 | X96753 | Hs.9004 | chondroitin sulfate proteoglycan 4 (mela | 3.1 |
| 60 | 423789 | AK002084 | Hs.132851 | hypothetical protein FLJ11222 | 3.1 |
| | 439538 | AA837323 | Hs.56407 | ESTs | 3.1 |
| | 437681 | A1207958 | Hs.166556 | Homo sapiens, Similar to TEA domain fami | 3.1 |
| | 433577 | AW007080 | Hs.284192 | ESTs | 3.1 |
| | 443021 | AA368546 | Hs.8904 | Ig superfamily protein | 3.1 |
| 65 | 433894 | A1907682 | Hs.243293 | ESTs | 3.1 |
| | 414884 | R54418 | Hs.183745 | hypothetical protein FLJ13456 | 3.1 |
| | 408996 | A1979168 | Hs.344096 | glycoprotein (transmembrane) nmb | 3.1 |
| | 449162 | A1632740 | Hs.10476 | ESTs | 3.1 |
| | 417893 | AA290605 | Hs.190002 | ESTs | 3.1 |
| 70 | 433578 | BE336886 | Hs.3416 | adipose differentiation-related protein | 3.0 |
| | 438380 | T06430 | Hs.6194 | chondroitin sulfate proteoglycan BEHAB/b | 3.0 |
| | 450756 | A1733488 | Hs.144062 | ESTs | 3.0 |
| | 422631 | BE218919 | Hs.118793 | hypothetical protein FLJ10688 | 3.0 |
| | 414733 | BE514535 | Hs.77171 | minichromosome maintenance deficient (S. | 3.0 |
| 75 | 431019 | NM_005249 | Hs.2714 | forkhead box G1B | 3.0 |
| | 434503 | T96231 | Hs.17762 | ESTs | 3.0 |
| | 455481 | AW948317 | | gb:RCO-MT0015-280300-021-a09 MT0015 Homo | 3.0 |
| | 427413 | BE547647 | Hs.177781 | hypothetical protein MGC5618 | 3.0 |
| | 414396 | BE548266 | Hs.76057 | galactose-4-epimerase, UDP- | 3.0 |
| 80 | 458760 | A1498631 | Hs.111334 | feritin, light polypeptide | 3.0 |
| | 410555 | U92649 | Hs.64311 | a disintegrin and metalloproteinase doma | 3.0 |
| | 411543 | AW851248 | | gb:IL3-CT0220-160200-066-F01 CT0220 Homo | 3.0 |
| | 435375 | A1733610 | Hs.187832 | ESTs | 3.0 |
| | 407047 | X65965 | | gb:H.sapiens SOD-2 gene for manganese su | 3.0 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| 5 | 432065 | AA401039 | Hs.2903 | protein phosphatase 4 (formerly X), cata | 3.0 |
| | 443338 | R99575 | Hs.302908 | ESTs | 3.0 |
| | 433062 | AK001757 | Hs.281348 | hypothetical protein FLJ10895 | 3.0 |
| | 412135 | AW895309 | | gb:QV4-NN0038-300300-155-e07 NN0038 Homo | 3.0 |
| | 418669 | U85992 | Hs.87197 | Human clone IMAGE:35527 unknown protein | 3.0 |
| 10 | 449385 | AJ650471 | Hs.347290 | ESTs | 3.0 |
| | 426384 | AJ472078 | Hs.303662 | hypothetical protein FLJ13189 (FLJ13189) | 3.0 |
| | 436267 | AW450938 | Hs.180115 | ESTs | 3.0 |
| | 440388 | AJ693520 | Hs.223000 | ESTs | 3.0 |
| | 427235 | AJ126288 | Hs.192232 | ESTs | 3.0 |
| 15 | 420116 | NM_013241 | Hs.95231 | FH1/FH2 domain-containing protein | 3.0 |
| | 419764 | BE262524 | Hs.93183 | vasodilator-stimulated phosphoprotein | 3.0 |
| | 406673 | M34996 | Hs.198253 | major histocompatibility complex, class | 3.0 |
| | 445921 | AW015211 | Hs.146181 | ESTs | 3.0 |
| | 427695 | R88483 | Hs.172862 | ESTs | 3.0 |
| 20 | 453324 | W26592 | Hs.232089 | ESTs | 3.0 |
| | 404272 | | | Target Exon | 3.0 |
| | 428538 | AA446440 | Hs.98643 | ESTs | 3.0 |
| | 442786 | H50733 | Hs.256261 | ESTs, Moderately similar to ALU8_HUMAN A | 3.0 |
| | 444396 | T65213 | Hs.4257 | ESTs | 3.0 |
| 25 | 440483 | AJ200836 | Hs.150386 | ESTs | 3.0 |
| | 429973 | AJ423317 | Hs.164680 | ESTs | 3.0 |
| | 450125 | AA005418 | Hs.158186 | ESTs | 3.0 |
| | 417409 | BE272506 | Hs.82109 | syndecan 1 | 3.0 |
| | 429569 | AA54993 | Hs.138343 | ESTs, Weakly similar to I78885 serine th | 3.0 |
| 30 | 455778 | BE088746 | | gb:CM2-BT0693-210300-123-d09 BT0693 Homo | 3.0 |
| | 427954 | J03060 | Hs.247551 | metaxin 1 | 3.0 |
| | 422418 | AK001383 | Hs.116385 | hypothetical protein FLJ10521 | 3.0 |
| | 427527 | AJ809057 | Hs.293441 | immunoglobulin heavy constant mu | 3.0 |
| | 416677 | T83470 | Hs.334840 | ESTs, Moderately similar to I78885 serin | 3.0 |
| 35 | 451130 | AJ762250 | Hs.345554 | ESTs | 3.0 |
| | 431431 | AL096711 | Hs.252953 | Human DNA sequence from clone RP3-403A15 | 3.0 |
| | 425248 | AW957442 | Hs.252766 | ESTs | 3.0 |
| | 422757 | AJ909935 | Hs.65551 | Homo sapiens, Similar to DNA segment, Ch | 3.0 |
| | 431836 | AF178532 | Hs.271411 | beta-site APP-cleaving enzyme 2 | 3.0 |
| 40 | 416355 | H49875 | Hs.268906 | ESTs | 3.0 |
| | 426406 | AJ742501 | Hs.169756 | complement component 1, s subcomponent | 3.0 |
| | 419829 | AJ924228 | Hs.115185 | ESTs, Moderately similar to PC4259 femi | 3.0 |
| | 412646 | NM_006825 | Hs.74368 | transmembrane protein (63kD), endoplasmic | 3.0 |
| | 423869 | BE409301 | Hs.134012 | C1q-related factor | 2.9 |
| 45 | 422710 | AW936566 | Hs.201876 | ESTs | 2.9 |
| | 445906 | N28939 | Hs.13434 | Homo sapiens clone 24418 mRNA sequence | 2.9 |
| | 429751 | M55210 | Hs.214982 | laminin, gamma 1 (formerly LAMB2) | 2.9 |
| | 430413 | AW842182 | Hs.241392 | small inducible cytokine A5 (RANTES) | 2.9 |
| | 443433 | R44743 | Hs.301667 | ESTs | 2.9 |
| 50 | 444145 | BE153823 | Hs.282385 | ESTs, Weakly similar to 2004399A chromos | 2.9 |
| | 425262 | D87119 | Hs.155418 | GS3955 protein | 2.9 |
| | 442476 | AF069475 | | gb:AF069475 Homo sapiens astrocytoma lib | 2.9 |
| | 443361 | AJ792628 | Hs.133273 | ESTs | 2.9 |
| | 427144 | X95097 | Hs.2126 | vasoactive intestinal peptide receptor 2 | 2.9 |
| 55 | 415709 | AA649850 | Hs.278558 | ESTs | 2.9 |
| | 453385 | AW296101 | Hs.252806 | ESTs | 2.9 |
| | 442609 | AL020996 | Hs.8518 | setonoprotein N | 2.9 |
| | 443378 | AW392550 | Hs.9280 | proteasome (prosome, macropain) subunit, | 2.9 |
| | 414416 | AW409985 | Hs.76084 | hypothetical protein MGC2721 | 2.9 |
| 60 | 443502 | AJ074528 | Hs.133949 | ESTs | 2.9 |
| | 444143 | AW747996 | Hs.160999 | ESTs, Moderately similar to A56194 throm | 2.9 |
| | 416308 | AW291942 | Hs.23628 | 3 beta-hydroxy-delta 5-C27-steroid oxido | 2.9 |
| | 447674 | BE270640 | Hs.19192 | cyclin-dependent kinase 2 | 2.9 |
| | 408989 | AW361666 | Hs.49500 | KIAA0746 protein | 2.9 |
| 65 | 427418 | AA402587 | Hs.325520 | LAT1-3TM protein | 2.9 |
| | 408788 | AL134947 | Hs.213956 | Homo sapiens BAC clone RP11-10205 from Y | 2.9 |
| | 426827 | AW067805 | Hs.172665 | methyltetrahydrofolate dehydrogenase | 2.9 |
| | 403290 | | | C10001011::gij4758212[pre][NP_004411.1] d | 2.9 |
| | 430890 | X54232 | Hs.2699 | glypican 1 | 2.9 |
| 70 | 441217 | AJ922183 | Hs.213246 | ESTs | 2.9 |
| | 418287 | AJ872319 | Hs.78935 | methionine aminopeptidase; eIF-2-associa | 2.9 |
| | 443836 | BE221613 | Hs.140553 | ESTs | 2.9 |
| | 451527 | AF022813 | Hs.26518 | transmembrane 4 superfamily member 7 | 2.9 |
| | 418110 | R43523 | Hs.217754 | hypothetical protein FLJ22202 | 2.9 |
| 75 | 420886 | AA805453 | | ESTs, Weakly similar to T29012 hypotheti | 2.9 |
| | 439379 | AA835002 | Hs.125611 | ESTs | 2.9 |
| | 426197 | AA004410 | Hs.100009 | acyl-Coenzyme A oxidase 1, palmitoyl | 2.9 |
| | 406679 | AA070786 | | gb:zm66b07.r1 Stratagene neuroepithelium | 2.9 |
| | 454120 | AB032990 | Hs.40719 | hypothetical protein KIAA1164 | 2.9 |
| 80 | 457244 | AA581385 | Hs.162473 | ESTs, Weakly similar to I38022 hypotheti | 2.9 |
| | 432036 | AF224266 | Hs.272373 | interleukin 20 | 2.9 |
| | 457364 | AW971037 | | gb:EST383123 MAGE resequences, MAGK Homo | 2.9 |
| | 437860 | AA333063 | Hs.279898 | Homo sapiens cDNA: FLJ23165 fis, clone L | 2.9 |
| | 453544 | AA831785 | Hs.171914 | Homo sapiens cDNA FLJ14209 fis, clone NT | 2.9 |
| | 454968 | AW849046 | | gb:IL3-CT0214-150300-085-H06 CT0214 Homo | 2.9 |
| | 437528 | N59646 | Hs.169745 | crumbs (Drosophila) homolog 1 | 2.9 |
| | 400850 | | | Target Exon | 2.9 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| 5 | 428896 | AW291932 | Hs.98936 | ESTs | 2.9 |
| | 426140 | AF131798 | Hs.343768 | Homo sapiens clone 25119 mRNA sequence | 2.9 |
| | 408872 | AJ476139 | Hs.13291 | ESTs | 2.9 |
| | 414799 | AI752416 | Hs.77326 | insulin-like growth factor binding prote | 2.9 |
| | 406646 | M33600 | Hs.308026 | major histocompatibility complex, class | 2.9 |
| | 416569 | H64891 | | gb:yr68n03.r1 Soares fetal liver spleen | 2.9 |
| | 439130 | AA306090 | Hs.124707 | ESTs | 2.9 |
| | 451433 | AA021140 | Hs.269265 | ESTs, Weakly similar to A46010 X-linked | 2.9 |
| 10 | 430314 | AA369601 | Hs.239138 | pre-B-cell colony-enhancing factor | 2.9 |
| | 424308 | AW975531 | Hs.154443 | minichromosome maintenance deficient (S. | 2.9 |
| | 420172 | AA601122 | Hs.95655 | secreted and transmembrane 1 | 2.9 |
| | 442485 | BE092285 | Hs.29724 | hypothetical protein FLJ13187 | 2.9 |
| | 416505 | H66470 | Hs.16004 | ESTs | 2.9 |
| 15 | 415198 | AW009480 | Hs.943 | natural killer cell transcript 4 | 2.9 |
| | 420674 | NM_000055 | Hs.1327 | butyrylcholinesterase | 2.9 |
| | 452139 | AA099969 | Hs.16331 | Homo sapiens cDNA: FLJ21482 fis, clone C | 2.8 |
| | 447499 | AW262580 | Hs.147674 | protocadherin beta 16 | 2.8 |
| | 411373 | BE326276 | Hs.8861 | ESTs | 2.8 |
| 20 | 456816 | AK001509 | Hs.144391 | hypothetical protein FLJ10647 | 2.8 |
| | 414232 | W86946 | Hs.238246 | hypothetical protein FLJ22479 | 2.8 |
| | 416188 | BE157260 | Hs.79070 | v-myc avian myelocytomatosis viral oncog | 2.8 |
| | 447733 | AF157482 | Hs.19400 | MAD2 (mitotic arrest deficient, yeast, h | 2.8 |
| | 438624 | AA889055 | Hs.123468 | ESTs | 2.8 |
| 25 | 452102 | U04343 | Hs.27954 | CD86 antigen (CD28 antigen ligand 2, B7- | 2.8 |
| | 408716 | AI587839 | Hs.151714 | Homo sapiens mRNA for KIAA1769 protein, | 2.8 |
| | 424028 | AF055084 | Hs.153692 | Homo sapiens cDNA FLJ14354 fis, clone Y7 | 2.8 |
| | 421679 | AI475110 | Hs.203933 | ESTs | 2.8 |
| | 450651 | W79000 | Hs.44545 | ESTs, Weakly similar to B34087 hypotheti | 2.8 |
| 30 | 452785 | AL359942 | Hs.296434 | erythroid differentiation and denudeati | 2.8 |
| | 432842 | AW674093 | Hs.334822 | hypothetical protein MGC4485 | 2.8 |
| | 403291 | | | Target Exon | 2.8 |
| | 453096 | AW294631 | Hs.11325 | ESTs | 2.8 |
| | 422545 | X02761 | Hs.287820 | fibronectin 1 | 2.8 |
| 35 | 440296 | D30829 | Hs.180610 | splicing factor proline/glutamine rich (| 2.8 |
| | 427154 | AL137262 | Hs.325630 | hypothetical protein MGC4289 | 2.8 |
| | 422282 | AF019225 | Hs.114309 | apolipoprotein L | 2.8 |
| | 434868 | R50032 | Hs.159263 | collagen, type VI, alpha 2 | 2.8 |
| | 414727 | BE466904 | Hs.190162 | gb:h28i03.x1 NCI_CGAP_G06 Homo sapiens | 2.8 |
| 40 | 437437 | AA226869 | | hypothetical protein DKFzP762L0311 | 2.8 |
| | 427722 | AK000123 | Hs.180479 | hypothetical protein FLJ20116 | 2.8 |
| | 443623 | AA345519 | Hs.9641 | complement component 1, q subcomponent, | 2.8 |
| | 444006 | BE395085 | Hs.10086 | type I transmembrane protein Fn14 | 2.8 |
| | 448432 | AI783586 | Hs.208575 | ESTs | 2.8 |
| 45 | 453682 | T79703 | | gb:yd71e08.r1 Soares fetal liver spleen | 2.8 |
| | 447527 | AI702896 | Hs.42091 | ESTs | 2.8 |
| | 418557 | BE140602 | Hs.246645 | ESTs | 2.8 |
| | 409157 | AA064631 | | gb:zf72c03.s1 Soares_pineal_gland_N3HPG | 2.8 |
| | 457653 | AI820719 | Hs.154662 | DnaJ (Hsp40) homolog, subfamily A, membe | 2.8 |
| 50 | 456908 | AI953671 | Hs.220994 | hypothetical protein FLJ14129 | 2.8 |
| | 439220 | AW295340 | Hs.130417 | ESTs, Weakly similar to Z195_HUMAN ZINC | 2.8 |
| | 418312 | AW972468 | Hs.170307 | Ral guanine nucleotide exchange factor R | 2.8 |
| | 454581 | AW809189 | | gb:MR4-ST0118-261099-012-e10 ST0118 Homo | 2.8 |
| | 419169 | AW851980 | Hs.262346 | ESTs, Weakly similar to S72482 hypotheti | 2.8 |
| | 400645 | | | Target Exon | 2.8 |
| 55 | 413951 | AW051200 | Hs.75640 | natriuretic peptide precursor A | 2.8 |
| | 441360 | AI091713 | Hs.106597 | Homo sapiens, Similar to RIKEN cDNA 1110 | 2.8 |
| | 404150 | | | Target Exon | 2.8 |
| | 402936 | | | ENSP00000217246*:DJ803K15.1 (novel prote | 2.8 |
| 60 | 454457 | AW753456 | | gb:QV2-CT0261-261099-011-d11 CT0261 Homo | 2.8 |
| | 439544 | W26354 | Hs.28891 | hypothetical protein FLJ11360; artemis p | 2.8 |
| | 403969 | | | ENSP0000034663:Zinc finger protein 131 | 2.8 |
| | 447183 | AI554733 | Hs.173182 | ESTs | 2.8 |
| | 446566 | H95741 | Hs.17914 | membrane-spanning 4-domains, subfamily A | 2.8 |
| 65 | 426141 | C05886 | Hs.293972 | ESTs | 2.8 |
| | 440146 | AW014231 | Hs.90790 | Homo sapiens cDNA: FLJ22930 fis, clone K | 2.8 |
| | 430335 | D80007 | Hs.239499 | KIAA0185 protein | 2.8 |
| | 447071 | AW236867 | Hs.244376 | ESTs | 2.8 |
| | 428899 | AA744610 | Hs.194431 | palladin | 2.8 |
| 70 | 400658 | | | ENSP00000237081*:KIAA1217 PROTEIN (FRAGM | 2.8 |
| | 403942 | | | Target Exon | 2.8 |
| | 420565 | AI806770 | Hs.30258 | ESTs | 2.8 |
| | 409734 | BE161664 | Hs.56155 | hypothetical protein | 2.8 |
| | 456645 | AF227156 | Hs.110103 | RNA polymerase I transcription factor RR | 2.8 |
| 75 | 401841 | | | NM_015113:Homo sapiens KIAA0399 protein | 2.8 |
| | 447247 | AW369351 | Hs.287955 | Homo sapiens cDNA FLJ13090 fis, clone NT | 2.8 |
| | 450150 | AI754391 | Hs.23510 | Kruppel-like factor 12 | 2.8 |
| | 409154 | U72882 | Hs.50842 | interferon-induced protein 35 | 2.8 |
| | 410267 | AW978005 | Hs.12600 | N-ethylmaleimide-sensitive factor attach | 2.8 |
| 80 | 448224 | R48700 | Hs.20733 | Homo sapiens cDNA: FLJ2356 fis, clone H | 2.8 |
| | 410268 | AA316181 | Hs.61635 | six transmembrane epithelial antigen of | 2.8 |
| | 447512 | AW958148 | Hs.129454 | ESTs | 2.8 |
| | 417749 | U09196 | Hs.82520 | polymerase (DNA-directed), delta 4 | 2.8 |
| | 415293 | R49462 | Hs.106541 | ESTs | 2.8 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 416207 | NM_014745 | Hs.79077 | Homo sapiens, clone MGC.2908, mRNA, comp | 2.8 |
| | 423337 | NM_004655 | Hs.127337 | axin 2 (conductin, axil) | 2.8 |
| | 425128 | BE561929 | Hs.154718 | tumor protein D52-like 2 | 2.7 |
| 5 | 444491 | AI151091 | Hs.270714 | ESTs | 2.7 |
| | 428311 | NM_005651 | Hs.183671 | tryptophan 2,3-dioxygenase | 2.7 |
| | 430377 | NM_001922 | Hs.301865 | dopachrome tautomerase (dopachrome delta | 2.7 |
| | 417944 | AU077195 | Hs.82985 | collagen, type V, alpha 2 | 2.7 |
| | 444153 | AK001610 | Hs.10414 | hypothetical protein FLJ10748 | 2.7 |
| 10 | 438138 | R98299 | Hs.177502 | ESTs | 2.7 |
| | 425421 | L11669 | Hs.157145 | tetracycline transporter-like protein | 2.7 |
| | 431070 | AW408164 | Hs.249184 | transcription factor 19 (SC1) | 2.7 |
| | 451748 | AK001612 | Hs.26962 | Homo sapiens cDNA FLJ10750 fs, clone NT | 2.7 |
| | 452085 | AW239140 | Hs.25614 | ESTs, Weakly similar to PC4396 mucin 3 T | 2.7 |
| 15 | 405941 | | | Target Exon | 2.7 |
| | 417395 | BE564245 | Hs.82084 | integrin beta 3 binding protein (beta3-e | 2.7 |
| | 449667 | AB023227 | Hs.23860 | KIAA1010 protein | 2.7 |
| | 428808 | AA436007 | Hs.188780 | ESTs | 2.7 |
| | 425843 | BE313280 | Hs.159627 | death associated protein 3 | 2.7 |
| 20 | 438025 | AW501360 | Hs.258910 | ESTs | 2.7 |
| | 400924 | | | Target Exon | 2.7 |
| | 412898 | AI129903 | Hs.74669 | vesicle-associated membrane protein 5 (m | 2.7 |
| | 413834 | BE296896 | Hs.224179 | ESTs, Weakly similar to I38022 hypothe | 2.7 |
| | 453785 | AI368236 | Hs.283732 | ESTs, Moderately similar to ALU1_HUMAN A | 2.7 |
| 25 | 406736 | AI254733 | Hs.182426 | ribosomal protein S2 | 2.7 |
| | 414280 | BE410769 | Hs.75873 | zyrin | 2.7 |
| | 434203 | BE262677 | Hs.283558 | hypothetical protein PRO1855 | 2.7 |
| | 442621 | AI004333 | Hs.130553 | ESTs, Weakly similar to ALUA_HUMAN !!! | 2.7 |
| | 414591 | AI888490 | Hs.55902 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 2.7 |
| 30 | 416547 | H62914 | Hs.268946 | ESTs, Weakly similar to PC4259 ferritin | 2.7 |
| | 416784 | AA334592 | Hs.79914 | lumican | 2.7 |
| | 413851 | AW897510 | Hs.137387 | ESTs | 2.7 |
| | 451767 | AI625014 | Hs.187328 | ESTs | 2.7 |
| | 441668 | AI611973 | Hs.136313 | ESTs | 2.7 |
| 35 | 435664 | AI032087 | Hs.269819 | ESTs | 2.7 |
| | 435046 | AA662772 | Hs.174330 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.7 |
| | 439467 | AW292275 | Hs.158365 | ESTs | 2.7 |
| | 441329 | AI203575 | Hs.46821 | hypothetical protein FLJ20086 | 2.7 |
| | 426925 | NM_001196 | Hs.315689 | Homo sapiens cDNA: FLJ22373 fs, clone H | 2.7 |
| 40 | 427241 | AA399988 | Hs.112087 | Human DNA sequence from clone RP11-530N1 | 2.7 |
| | 449919 | AI674685 | Hs.200141 | ESTs | 2.7 |
| | 458070 | AW503578 | Hs.209406 | ESTs, Weakly similar to I38600 zinc fing | 2.7 |
| | 444794 | AI419991 | Hs.145225 | ESTs | 2.7 |
| | 410781 | AI375672 | Hs.165028 | ESTs | 2.7 |
| 45 | 449520 | R34993 | Hs.226666 | ESTs, Moderately similar to I54374 gene | 2.7 |
| | 439481 | AF086294 | Hs.125844 | ESTs | 2.7 |
| | 401702 | | | NM_001171*:Homo sapiens ATP-binding cass | 2.7 |
| | 432890 | NM_014442 | Hs.279751 | sialic acid binding Ig-like lectin 8 | 2.7 |
| 50 | 435545 | AA687415 | Hs.28107 | ESTs | 2.7 |
| | 416422 | H60457 | | ESTs, Moderately similar to ZN91_HUMAN Z | 2.7 |
| | 429415 | NM_002593 | Hs.202097 | procollagen C-endopeptidase enhancer | 2.7 |
| | 420982 | AW576160 | Hs.100729 | KIAA0692 protein | 2.7 |
| | 431421 | AW969118 | Hs.108144 | ESTs, Weakly similar to unnamed protein | 2.7 |
| | 444168 | AW379879 | | gb:RC1-HT0256-081199-011-01 HT0256 Homo | 2.7 |
| 55 | 419964 | AA811657 | Hs.220913 | ESTs | 2.7 |
| | 424480 | AA341442 | Hs.205299 | ESTs | 2.7 |
| | 436314 | AI983409 | Hs.189226 | ESTs | 2.7 |
| | 405516 | | | ENSP00000200457*:Thyroid receptor intera | 2.7 |
| | 449340 | AW235786 | Hs.195359 | hypothetical protein MGC10954 | 2.7 |
| 60 | 457876 | AI821940 | | ESTs, Moderately similar to ALU8_HUMAN A | 2.7 |
| | 423799 | AW026300 | Hs.132906 | 19A24 protein | 2.7 |
| | 422551 | AW967284 | | gb:EST379359 MAGE resequences, MAGJ Homo | 2.7 |
| | 404592 | | | NM_022739*:Homo sapiens E3 ubiquitin lig | 2.7 |
| | 424200 | AA337221 | | gb:EST41944 Endometrial tumor Homo sapie | 2.7 |
| 65 | 428612 | AA770001 | Hs.188778 | ESTs | 2.7 |
| | 446139 | H77395 | Hs.39749 | ESTs | 2.7 |
| | 440478 | AI733047 | Hs.130005 | ESTs | 2.7 |
| | 429612 | AF062649 | Hs.252587 | pituitary tumor-transforming 1 | 2.7 |
| | 422530 | AW972300 | Hs.118110 | bone marrow stromal cell antigen 2 | 2.7 |
| 70 | 423713 | AW754182 | | gb:RC2-CT0321-131199-011-c01 CT0321 Homo | 2.7 |
| | 402032 | | | ENSP00000251056*:Plasma membrane calcium | 2.7 |
| | 424186 | AI536021 | Hs.288706 | Homo sapiens cDNA FLJ10281 fs, clone HE | 2.7 |
| | 402799 | | | Target Exon | 2.7 |
| | 423352 | AA324808 | Hs.193576 | ESTs | 2.7 |
| 75 | 412021 | AW885592 | | gb:RC4-OT0071-090300-011-g11 OT0071 Homo | 2.7 |
| | 458617 | Z25900 | Hs.18724 | Homo sapiens mRNA: cDNA DKFZp564F093 (fr | 2.7 |
| | 404170 | | | NM_000636*:Homo sapiens superoxide dismu | 2.7 |
| | 410886 | AW809324 | | gb:MR4-ST0121-141099-010-G06_1 ST0121 Ho | 2.7 |
| | 414988 | C17535 | | gb:C17535 Human placenta cDNA (TFujiwara | 2.7 |
| 80 | 450325 | AI935962 | Hs.26289 | ESTs | 2.7 |
| | 458918 | H56499 | Hs.252692 | ESTs, Weakly similar to I38022 hypothesi | 2.7 |
| | 405760 | | | Target Exon | 2.7 |
| | 406789 | AI041403 | | ribosomal protein L29 | 2.7 |
| | 424686 | AA345504 | | gb:EST51529 Gall bladder II Homo sapiens | 2.7 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 400335 | Y13187 | Hs.248068 | Homo sapiens dmd gene, intron 11 | 2.7 |
| | 435065 | BE064391 | | gb:RC4-BT0310-110300-015-b08 BT0310 Homo | 2.7 |
| | 419373 | NM_003244 | Hs.90077 | TG-interacting factor (TALE family homeo | 2.7 |
| | 406785 | AA588061 | | gb:nk10d03.s1 NCL_CGAP_Co2 Homo sapiens | 2.7 |
| 5 | 433006 | BE242758 | Hs.190223 | ESTs, Moderately similar to T29285 hypot | 2.7 |
| | 428690 | AI948490 | Hs.98765 | ESTs | 2.7 |
| | 432692 | AW974944 | Hs.200577 | ESTs | 2.7 |
| | 439699 | AF086534 | Hs.187561 | ESTs, Moderately similar to ALU1_HUMAN A | 2.7 |
| | 452811 | AA937079 | Hs.118983 | hypothetical protein FLJ12150 | 2.6 |
| 10 | 457035 | AA398074 | Hs.119143 | ESTs, Moderately similar to KIAA1513 pro | 2.6 |
| | 427725 | U66839 | Hs.180533 | mitogen-activated protein kinase kinase | 2.6 |
| | 433681 | AI004377 | Hs.200360 | Homo sapiens cDNA FLJ13027 fs, clone NT | 2.6 |
| | 423748 | AI149048 | Hs.30211 | hypothetical protein FLJ22313 | 2.6 |
| | 422764 | AI767727 | Hs.47522 | ESTs | 2.6 |
| 15 | 403431 | | | Target Exon | 2.6 |
| | 439332 | AW842747 | Hs.300870 | Homo sapiens mRNA; cDNA DKFZp547M072 (fr | 2.6 |
| | 412749 | AA378417 | Hs.74564 | signal sequence receptor, beta (transloc | 2.6 |
| | 409703 | NM_006187 | Hs.56009 | 2'-5'-oligoadenylate synthetase 3 (100 k | 2.6 |
| | 405717 | | | CX000838.gij10092633[ref]NP_055314.1 pu | 2.6 |
| 20 | 426503 | AA380153 | | gb:EST93093 Skin tumor 1 Homo sapiens cD | 2.6 |
| | 414039 | M83221 | Hs.858 | v-rel avian reticuloendotheliosis viral | 2.6 |
| | 452683 | AI089575 | Hs.9071 | progesterone membrane binding protein | 2.6 |
| | 447587 | AW292139 | Hs.115789 | ESTs | 2.6 |
| | 408605 | AF025374 | Hs.46465 | T-cell, immune regulator 1 | 2.6 |
| 25 | 407103 | AA424881 | Hs.256301 | hypothetical protein MGC13170 | 2.6 |
| | 427395 | AW298741 | Hs.97861 | ESTs, Moderately similar to I38022 hypot | 2.6 |
| | 435113 | AA665469 | Hs.117136 | ESTs | 2.6 |
| | 419015 | T79262 | Hs.14463 | ESTs | 2.6 |
| | 427648 | AI376722 | Hs.180062 | proteasome (prosome, macropain) subunit, | 2.6 |
| 30 | 453707 | AW003879 | Hs.126522 | Homo sapiens, clone MGC:16722, mRNA, com | 2.6 |
| | 411927 | BE274009 | Hs.772 | glycogen synthase 1 (muscle) | 2.6 |
| | 404053 | | | Target Exon | 2.6 |
| | 415069 | AA159831 | Hs.29286 | ESTs, Weakly similar to I49636 DNA-bindi | 2.6 |
| 35 | 449625 | NM_014253 | | odx (odd Oz/ten-m, Drosophila) homolog 1 | 2.6 |
| | 438033 | T26483 | Hs.6059 | EGF-containing fibulin-like extracellular | 2.6 |
| | 451593 | AF151879 | Hs.26706 | CGI-121 protein | 2.6 |
| | 435828 | AA700705 | Hs.13852 | ESTs | 2.6 |
| | 443753 | AW367578 | Hs.134749 | ESTs | 2.6 |
| | 416097 | BE387371 | Hs.118964 | hypothetical protein FLJ20085 | 2.6 |
| 40 | 413986 | Z43567 | | gb:HSC1FC021 normalized infant brain cDN | 2.6 |
| | 439755 | AW748482 | Hs.77873 | B7 homolog 3 | 2.6 |
| | 408371 | AF161545 | Hs.44439 | hypothetical protein | 2.6 |
| | 445658 | AI469062 | Hs.172660 | ESTs | 2.6 |
| | 438166 | N30158 | Hs.122645 | ESTs | 2.6 |
| 45 | 449426 | T92251 | Hs.198882 | ESTs | 2.6 |
| | 422605 | H16646 | Hs.118666 | hypothetical protein PP591 | 2.6 |
| | 415788 | AW628686 | Hs.78851 | KIAA0217 protein | 2.6 |
| | 448966 | AW372914 | Hs.86149 | phosphoinositol 3-phosphate-binding prot | 2.6 |
| 50 | 400295 | W72838 | | AI905687:IL-BT095-190199-019 BT095 Homo | 2.6 |
| | 441128 | AA570256 | | ESTs, Weakly similar to T23273 hypothi | 2.6 |
| | 420372 | AW960049 | Hs.293660 | Homo sapiens, clone IMAGE:3535476, mRNA, | 2.6 |
| | 428977 | AK001404 | Hs.194698 | cyclin B2 | 2.6 |
| | 424278 | AK000723 | Hs.144517 | hypothetical protein FLJ20716 | 2.6 |
| | 445211 | BE045601 | Hs.118248 | ESTs, Weakly similar to YC18_HUMAN HYPOT | 2.6 |
| 55 | 412715 | NM_000947 | Hs.74519 | primase, polypeptide 2A (58kD) | 2.6 |
| | 417838 | R24713 | Hs.22514 | ESTs | 2.6 |
| | 420670 | AW973577 | | ESTs | 2.6 |
| | 403267 | | | Target Exon | 2.6 |
| 60 | 454354 | AW389896 | | gb:RC4-ST0173-191099-032-e12 ST0173 Homo | 2.6 |
| | 452903 | AI953425 | Hs.345291 | ESTs, Weakly similar to I38022 hypothi | 2.6 |
| | 427830 | AA416598 | Hs.98233 | ESTs | 2.6 |
| | 435953 | AI767087 | Hs.114142 | ESTs | 2.6 |
| | 430744 | AA485229 | Hs.105649 | ESTs | 2.6 |
| 65 | 413335 | AI613318 | Hs.48442 | ESTs | 2.6 |
| | 416370 | N90470 | Hs.203697 | ESTs, Weakly similar to I38022 hypothi | 2.6 |
| | 431865 | AA521106 | Hs.136375 | ESTs, Weakly similar to S65824 reverse t | 2.6 |
| | 434274 | AA628539 | Hs.116252 | ESTs, Moderately similar to ALU1_HUMAN A | 2.6 |
| | 447854 | AW138454 | Hs.11594 | ESTs | 2.6 |
| 70 | 412799 | AI267606 | | gb:aq91h03.x1 Stanley Frontal S8 pool 1 | 2.6 |
| | 455409 | AW936832 | | gb:PM2-DT0023-050400-003-h03 DT0023 Homo | 2.6 |
| | 408212 | AA297567 | Hs.43728 | hypothetical protein | 2.6 |
| | 453055 | AW291436 | Hs.31917 | Homo sapiens, clone MGC:9658, mRNA, comp | 2.6 |
| | 443539 | AI076182 | Hs.134074 | ESTs, Moderately similar to ALU6_HUMAN A | 2.6 |
| | 434898 | AW500458 | Hs.29956 | KIAA0460 protein | 2.6 |
| 75 | 438118 | AW753311 | Hs.346690 | ESTs | 2.6 |
| | 431786 | AW452784 | Hs.220718 | ESTs | 2.6 |
| | 421689 | N87820 | Hs.106826 | KIAA1696 protein | 2.6 |
| | 429597 | NM_003816 | Hs.2442 | a disintegrin and metalloproteinase doma | 2.6 |
| | 424684 | AW752714 | Hs.5174 | ribosomal protein S17 | 2.6 |
| 80 | 439823 | AW665287 | Hs.124514 | ESTs | 2.6 |
| | 411962 | AA099050 | | gb:z85d12.r1 Soares_pregnant_uterus_NbH | 2.6 |
| | 445774 | AI254165 | Hs.339968 | ESTs | 2.6 |
| | 400492 | | | C10001573:gi7302749[gb]AAF57827.1 (AE | 2.6 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 450625 | AW970107 | | gb:EST382188 MAGE resequences, MAGK Homo | 2.6 |
| | 426931 | NM_003416 | Hs.2076 | zinc finger protein 7 (KOX 4, clone HF.1 | 2.6 |
| | 440131 | AI023425 | Hs.222225 | ESTs | 2.6 |
| 5 | 438525 | AW368528 | Hs.100855 | ESTs | 2.6 |
| | 412247 | AF022375 | Hs.73793 | vascular endothelial growth factor | 2.6 |
| | 406662 | X62006 | Hs.172550 | polypyrimidine tract binding protein (he | 2.6 |
| | 443725 | AW245680 | Hs.9701 | growth arrest and DNA-damage-inducible, | 2.6 |
| | 402260 | | | NM_001436*:Homo sapiens fibrillarin (FBL | 2.6 |
| 10 | 429599 | AA806106 | Hs.123664 | ESTs | 2.6 |
| | 429562 | AJ732767 | Hs.158101 | Homo sapiens cDNA FLJ14673 fis, clone NT | 2.6 |
| | 432527 | AW975028 | Hs.102754 | ESTs | 2.6 |
| | 434420 | AA688278 | Hs.194864 | hypothetical protein FLJ22578 | 2.6 |
| | 452732 | BE300078 | Hs.80449 | Homo sapiens, clone IMAGE:3535294, mRNA, | 2.6 |
| 15 | 424408 | AI754813 | Hs.146428 | collagen, type V, alpha 1 | 2.6 |
| | 413151 | H47969 | Hs.141971 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.6 |
| | 416244 | N39535 | Hs.32748 | ESTs | 2.6 |
| | 403104 | | | C8000064*:gii10432393[emb]CAC10283.1[(A | 2.6 |
| | 400780 | | | NM_007325*:Homo sapiens glutamate recept | 2.6 |
| 20 | 433009 | AA761668 | | gb:nz24c08.s1 NCL_CGAP_GCB1 Homo sapiens | 2.6 |
| | 424090 | X99699 | Hs.139262 | XIAP associated factor-1 | 2.6 |
| | 403212 | | | NM_019595:Homo sapiens intersectin 2 (IT | 2.6 |
| | 407855 | R54126 | Hs.40500 | similar to S. cerevisiae RER1 | 2.6 |
| | 406849 | AA454809 | Hs.172928 | collagen, type I, alpha 1 | 2.6 |
| 25 | 443462 | AI064690 | Hs.171176 | ESTs | 2.6 |
| | 439963 | AW247529 | Hs.6793 | platelet-activating factor acetylhydrola | 2.6 |
| | 450089 | AI681883 | Hs.209546 | ESTs, Weakly similar to 2109260A B cell | 2.6 |
| | 419571 | AW674962 | Hs.91146 | protein kinase D2 | 2.6 |
| | 448140 | AF146761 | Hs.20450 | BCM-like membrane protein precursor | 2.6 |
| 30 | 444881 | AI623288 | Hs.192805 | ESTs | 2.6 |
| | 420658 | AW965215 | Hs.130707 | ESTs | 2.6 |
| | 437634 | AW293046 | Hs.255158 | ESTs | 2.6 |
| | 426894 | AI204209 | Hs.143911 | ESTs | 2.6 |
| | 428467 | AK002121 | Hs.184465 | hypothetical protein FLJ11259 | 2.6 |
| 35 | 434171 | BE247688 | Hs.347349 | KIAA0948 protein | 2.6 |
| | 410174 | AA306007 | Hs.59461 | DKFZP434C245 protein | 2.6 |
| | 427245 | AA421022 | Hs.97739 | ESTs | 2.6 |
| | 437085 | AA743935 | Hs.202329 | ESTs | 2.5 |
| | 400362 | AF068294 | Hs.272414 | Homo sapiens HDCMB45P mRNA, partial cds | 2.5 |
| 40 | 452221 | C21322 | Hs.288057 | hypothetical protein FLJ22242 | 2.5 |
| | 439079 | AF085937 | Hs.38348 | ESTs | 2.5 |
| | 437287 | AA748180 | Hs.159346 | hypothetical protein FLJ21369 | 2.5 |
| | 411852 | AA528140 | Hs.107515 | ESTs, Weakly similar to T00329 hypotheti | 2.5 |
| | 427624 | AA406245 | Hs.24895 | ESTs | 2.5 |
| 45 | 435177 | AI018174 | Hs.42936 | ESTs | 2.5 |
| | 449433 | AI672096 | Hs.9012 | ESTs, Weakly similar to S26650 DNA-bindi | 2.5 |
| | 447853 | AI434204 | Hs.164285 | ESTs, Weakly similar to AFG1_YEAST AFG1 | 2.5 |
| | 416704 | H77795 | Hs.39785 | ESTs | 2.5 |
| | 401696 | | | Target Exon | 2.5 |
| 50 | 445677 | H96577 | Hs.6838 | ras homolog gene family, member E | 2.5 |
| | 413840 | AI301558 | Hs.146381 | RNA binding motif protein, X chromosome | 2.5 |
| | 437916 | BE566249 | Hs.20999 | hypothetical protein FLJ23142 | 2.5 |
| | 420289 | N55394 | Hs.96398 | 8-oxoguanine DNA glycosylase | 2.5 |
| | 421848 | X15880 | Hs.108885 | collagen, type VI, alpha 1 | 2.5 |
| 55 | 421234 | AA907153 | Hs.190060 | ESTs | 2.5 |
| | 414598 | AI094221 | Hs.135150 | lung type-I cell membrane-associated gly | 2.5 |
| | 420162 | BE378432 | Hs.95577 | cyclin-dependent kinase 4 | 2.5 |
| | 458199 | AW136417 | | hypothetical protein FLJ14464 | 2.5 |
| | 433523 | H29882 | | ESTs | 2.5 |
| 60 | 429125 | AA446854 | Hs.271004 | ESTs, Weakly similar to I38022 hypotheti | 2.5 |
| | 418399 | AF131781 | Hs.84753 | hypothetical protein FLJ12442 | 2.5 |
| | 404748 | | | ENSP00000238177*:Similar to kynurenine 3 | 2.5 |
| | 413507 | BE145360 | Hs.190064 | ESTs, Weakly similar to I38022 hypotheti | 2.5 |
| | 418886 | AA993982 | Hs.130858 | ESTs | 2.5 |
| 65 | 429359 | W00482 | Hs.2399 | matrix metalloproteinase 14 (membrane-in | 2.5 |
| | 452367 | U71207 | Hs.29279 | eyes absent (Drosophila) homolog 2 | 2.5 |
| | 436258 | AW867491 | Hs.107125 | plasmalemma vesicle associated protein | 2.5 |
| | 459527 | AW977556 | Hs.291735 | ESTs, Weakly similar to I78885 serine/th | 2.5 |
| | 450543 | AI394037 | Hs.170296 | Homo sapiens cDNA: FLJ22090 fis, clone H | 2.5 |
| 70 | 434818 | AA650097 | Hs.5996 | ESTs | 2.5 |
| | 444534 | AW271626 | Hs.42294 | ESTs | 2.5 |
| | 452113 | AI859393 | | gb:wm11a02.x1 NCL_CGAP_Ut4 Homo sapiens | 2.5 |
| | 429115 | AA446728 | Hs.289020 | Homo sapiens cDNA FLJ14098 fis, clone MA | 2.5 |
| | 434012 | AA621425 | Hs.186256 | ESTs | 2.5 |
| 75 | 447143 | AW292408 | Hs.152290 | ESTs, Highly similar to JC2463 vasoactiv | 2.5 |
| | 449505 | AI653006 | Hs.195374 | ESTs | 2.5 |
| | 419817 | AA743434 | Hs.193778 | ESTs | 2.5 |
| | 457986 | AA781745 | Hs.126920 | Homo sapiens, clone IMAGE:4299555, mRNA, | 2.5 |
| | 431454 | AW975980 | Hs.292918 | ESTs | 2.5 |
| 80 | 425018 | BE245277 | Hs.154196 | E4F transcription factor 1 | 2.5 |
| | 427513 | AI476318 | Hs.192480 | ESTs | 2.5 |
| | 441318 | AI078234 | Hs.176130 | ESTs | 2.5 |
| | 424830 | AW270580 | Hs.189311 | ESTs, Weakly similar to putative p150 [H | 2.5 |
| | 414271 | AK000275 | Hs.75871 | protein kinase C binding protein 1 | 2.5 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| 5 | 446089 | AI860021 | Hs.345028 | ESTs, Moderately similar to A47582 B-cel | 2.5 |
| | 415983 | AI436798 | Hs.117078 | Homo sapiens cDNA: FLJ23028 fs, clone L | 2.5 |
| | 408292 | AW178363 | | gb:RC3-HT0105-010999-002-H06 HT0105 Homo | 2.5 |
| | 446862 | AV660697 | Hs.282700 | ESTs | 2.5 |
| | 448970 | AW138582 | | gb:U1-H-B11-acw-a-06-0-U1.s1 NCI_CGAP_Su | 2.5 |
| | 459200 | Y09306 | Hs.30148 | homeodomain-interacting protein kinase 3 | 2.5 |
| | 422627 | BE336857 | Hs.118787 | transforming growth factor, beta-induced | 2.5 |
| | 433388 | AI432672 | Hs.288539 | hypothetical protein FLJ22191 | 2.5 |
| 10 | 436222 | AI208737 | Hs.122810 | Homo sapiens cDNA FLJ11489 fs, clone HE | 2.5 |
| | 441255 | R06350 | Hs.171635 | ESTs | 2.5 |
| | 441627 | AA947552 | Hs.58086 | branched chain aminotransferase 1, cytos | 2.5 |
| | 438714 | AA814859 | Hs.294112 | ESTs | 2.5 |
| | 441020 | W79283 | Hs.35962 | ESTs | 2.5 |
| 15 | 418291 | BE300369 | Hs.289038 | hypothetical protein MGC4126 | 2.5 |
| | 434267 | AI206589 | Hs.116243 | ESTs | 2.5 |
| | 446821 | W03766 | | tropomodulin 3 (ubiquitous) | 2.5 |
| | 402615 | | | C1003844":gij6912550(ref NP_036483.1) ol | 2.5 |
| | 416845 | H95279 | Hs.293788 | gb:yu20h02.s1 Soares fetal liver spleen | 2.5 |
| 20 | 408253 | AW807476 | Hs.21051 | Homo sapiens mRNA for FLJ00012 protein, | 2.5 |
| | 444884 | AI201094 | Hs.148540 | ESTs | 2.5 |
| | 440826 | AW383618 | Hs.346256 | ESTs, Moderately similar to ALU2_HUMAN A | 2.5 |
| | 431374 | BE258532 | Hs.251871 | CTP synthase | 2.5 |
| | 458093 | AI207788 | Hs.343628 | sialyltransferase 4B (beta-galactosidase | 2.5 |
| 25 | 422484 | AA568770 | Hs.123158 | Homo sapiens cDNA FLJ12830 fs, clone NT | 2.5 |
| | 442804 | AW300118 | Hs.131257 | ESTs | 2.5 |
| | 420949 | AA934063 | Hs.13836 | ESTs, Weakly similar to I38022 hypotheti | 2.5 |
| | 451350 | AI791447 | | gb:ni13a05.y5 NCI_CGAP_Co4 Homo sapiens | 2.5 |
| | 410855 | X97795 | Hs.66718 | RAD54 (S.cerevisiae)-like | 2.5 |
| 30 | 430426 | AA478807 | Hs.125173 | ESTs | 2.5 |
| | 418526 | BE019020 | Hs.85838 | solute carrier family 16 (monocarboxylic | 2.5 |
| | 406290 | | | Target Exon | 2.5 |
| | 442085 | AA975688 | Hs.159955 | ESTs | 2.5 |
| | 448148 | NM_016578 | Hs.20509 | HBV pX associated protein-8 | 2.5 |
| 35 | 432888 | T86823 | | gb:yd81a08.s1 Soares fetal liver spleen | 2.5 |
| | 424126 | AA335635 | Hs.96917 | ESTs | 2.5 |
| | 459727 | AI906494 | | gb:RC-BT113-060499-024 BT113 Homo sapien | 2.5 |
| | 407989 | AW135208 | Hs.256092 | ESTs | 2.5 |
| | 404571 | | | NM_015902: Homo sapiens progesteron induce | 2.5 |
| 40 | 429139 | F09092 | Hs.66087 | ESTs | 2.5 |
| | 435232 | NM_001262 | Hs.4854 | cyclin-dependent kinase inhibitor 2C (p1 | 2.5 |
| | 420608 | BE548277 | Hs.103104 | ESTs | 2.5 |
| | 432668 | AA558601 | Hs.43296 | ESTs | 2.5 |
| | 406871 | AA993857 | Hs.180842 | ribosomal protein L13 | 2.5 |
| 45 | 443516 | AA305821 | Hs.9527 | apoptosis related protein APR-3 | 2.5 |
| | 445985 | BE621800 | Hs.29444 | putative small membrane protein NID67 | 2.5 |
| | 424614 | X54486 | Hs.151242 | serine (or cysteine) proteinase inhibitor | 2.5 |
| | 437267 | AW511443 | Hs.258110 | ESTs | 2.5 |
| | 458251 | AL040927 | Hs.210422 | ESTs | 2.5 |
| 50 | 431198 | AL047634 | Hs.231913 | ESTs | 2.5 |
| | 413944 | AW001579 | Hs.9645 | Homo sapiens mRNA for KIAA1741 protein, | 2.5 |
| | 420796 | L34355 | Hs.99931 | sarcoglycan, alpha (50kD dystrophin-asso | 2.5 |
| | 428032 | AW997704 | Hs.11493 | Homo sapiens cDNA FLJ13536 fs, clone PL | 2.5 |
| | 422017 | NM_003877 | Hs.110776 | STAT induced STAT inhibitor-2 | 2.5 |
| 55 | 424662 | NM_002870 | Hs.151536 | RAB13, member RAS oncogene family | 2.5 |
| | 423779 | AW071837 | Hs.57971 | ESTs | 2.5 |
| | 405863 | | | Target Exon | 2.5 |
| | 458421 | AI279978 | Hs.22547 | ESTs | 2.5 |
| | 439019 | AF085902 | Hs.271737 | ESTs | 2.5 |
| 60 | 412577 | Z22968 | Hs.74076 | CD163 antigen | 2.5 |
| | 404891 | | | Target Exon | 2.5 |
| | 419043 | T19167 | Hs.89566 | ets variant gene 1 | 2.5 |
| | 448482 | AW294078 | Hs.171092 | ESTs | 2.5 |
| | 426030 | BE243933 | Hs.108642 | zinc finger protein 22 (KOX 15) | 2.5 |
| 65 | 429109 | AL008637 | Hs.196352 | neutrophil cytosolic factor 4 (40kD) | 2.5 |
| | 450597 | AI701635 | Hs.207077 | ESTs | 2.5 |
| | 414386 | X00442 | Hs.75990 | haptoglobin | 2.5 |
| | 440473 | BE562314 | Hs.98711 | Homo sapiens, clone IMAGE:3677165, mRNA, | 2.5 |
| | 406851 | AA609784 | | major histocompatibility complex, class | 2.5 |
| 70 | 414821 | M63835 | Hs.77424 | Fc fragment of IgG, high affinity Ia, re | 2.5 |
| | 417663 | R07483 | Hs.180461 | ESTs | 2.5 |
| | 429341 | X73874 | Hs.2393 | phosphorylase kinase, alpha 1 (muscle) | 2.5 |
| | 450663 | H43540 | Hs.25292 | ribonuclease H1, large subunit | 2.5 |
| | 407198 | H91679 | | gb:yy04g07.s1 Soares fetal liver spleen | 2.5 |
| 75 | 411742 | AW247593 | Hs.71819 | eukaryotic translation initiation factor | 2.5 |
| | 409449 | H11341 | Hs.13366 | Homo sapiens cDNA: FLJ23567 fs, clone L | 2.5 |

TABLE 14B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey CAT Number Accession
408292 1050507_1 AW178363 AW846011 AW845964 AW845988 AW845977 AW846002

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| | 409157 | 110363_1 | AA064631 AA722000 AA064793 |
| | 409189 | 110687_1 | AA125984 AA127189 AA065075 AA070377 AA100017 AA079891 AA113255 AA075168 AA082764 AA083380 N84829 AA084752 AA076512 AA085119 |
| 5 | 410886 | 1225822_1 | AA085208 AA085045 |
| | 411537 | 1248899_1 | AW809324 BE144977 BE144956 |
| | 411543 | 1249127_1 | BE073250 BE073378 BE073379 AW850533 AW850529 |
| | 411565 | 1249756_1 | AW851248 AW851425 AW850805 AW851021 AW850905 |
| | 411671 | 125369_1 | AW851728 AW851607 AW851621 AW851702 AW851647 AW851727 AW851658 AW851617 AW851628 |
| 10 | 411688 | 1254076_1 | BE049094 AA700765 H86770 AA094646 R02483 C03868 N56170 |
| | 411962 | 126744_1 | AW953440 T08189 AW857085 |
| | 412021 | 1272156_1 | AA099050 AA099526 T47733 |
| | 412135 | 1279148_1 | AW885592 AW885594 AW885579 AW885651 |
| 15 | 412799 | 132817_1 | AW895309 AW895290 AW895307 AW895397 AW895378 AW895402 AW895403 AW895311 AW895298 AW895390 AW895488 AW895468 AW895481 |
| | 412811 | 132943_1 | AW895288 |
| | 413986 | 140720_1 | AI267606 AA121045 AA126521 |
| | 414372 | 143909_1 | H06382 AW957730 AA352014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 AI424991 AI693507 AI863108 AA599060 AI091148 AA598689 |
| 20 | 414988 | 1511316_1 | R39887 AA813482 AW016452 H06383 R41807 AI364268 AA620528 AI241940 AW089149 AW090733 AW088875 Z38240 AA121202 R17734 |
| | 415131 | 1523680_1 | Z43567 H24159 AA134240 |
| | 416422 | 1593811_1 | AA143654 AW753140 AA213770 AW970865 AA569075 AA492132 |
| | 416569 | 1601567_1 | C17535 D59244 D58878 D79090 |
| | 416871 | 1626761_1 | D61119 D81508 D81734 |
| 25 | 416913 | 163001_1 | H60457 H68709 H73528 H54335 R87154 |
| | 419896 | 1888662_1 | H64891 R93444 R93458 R05590 |
| | 420352 | 192979_1 | H98716 N90792 N24283 |
| | 420670 | 195442_1 | AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499 |
| | 420886 | 197344_1 | Z9362 Z9363 |
| 30 | 422551 | 217767_1 | BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280 |
| | 423713 | 231290_1 | AW973577 AA553621 AA279187 |
| | 424009 | 234177_1 | AA805453 AA281379 |
| | 424200 | 236595_1 | AW967284 AA312192 AA312203 |
| 35 | 424686 | 242486_1 | AW754182 AW754198 AA329983 |
| | 424947 | 245247_1 | F11690 AW965370 AA333586 D30830 |
| | 425146 | 247244_1 | AA337221 AA336756 AW966196 |
| | 425331 | 250199_1 | AA345504 AA345251 AW963243 |
| | 426503 | 268283_1 | R77952 AA348809 AW959960 AW959962 AI565552 AW070702 AA973910 R85973 |
| 40 | 429163 | 300543_1 | AW954627 AW954629 AA351258 R25935 |
| | 429940 | 310884_1 | AW962128 AA355353 AA427363 |
| | 430535 | 319643_1 | AA380153 AA380233 AW963529 |
| | 430968 | 326269_1 | AA884766 AW974271 AA592975 AA447312 |
| | 432044 | 340773_1 | W25215 AA461079 AA461391 |
| | 432363 | 345469_1 | AW968485 AW968670 AA480922 BE350425 |
| 45 | 432888 | 355780_1 | AW972830 AA527647 AA489820 AA570362 |
| | 433009 | 357371_1 | AW972727 AA524829 AW972733 |
| | 433523 | 368873_1 | AA534489 AW970240 AW970323 |
| | 433835 | 374758_1 | T86823 AI821425 AI732232 AA569589 AA570737 |
| 50 | 434589 | 38929_1 | AA761668 AA573621 R92814 R09670 |
| | 435065 | 399329_1 | H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320 |
| | 435542 | 407744_1 | AI806185 AA610063 AI693089 AI693075 |
| | 436608 | 42361_3 | AF147363 T47219 T47218 |
| | 437034 | 431713_1 | BE064391 BE064395 AA663613 N99644 |
| 55 | 437437 | 43709_1 | AA687376 H74234 AW975503 |
| | 437945 | 44580_1 | AA628980 AI126603 BE504035 |
| | 438458 | 457837_1 | AA742643 AA808575 AW976668 |
| | 439518 | 47334_1 | AA226869 AA296516 AW959753 AA186390 AL359619 AA356195 AA148427 R22748 AI033624 BE548853 H95327 AW579751 BE561649 AA397533 |
| 60 | 439533 | 47349_1 | BE617136 AA236444 T89946 AA247450 N55777 W38725 AI743846 AI808406 AA922229 AI051464 W04713 R11251 W19656 AI042319 AA489276 |
| | 439566 | 47387_1 | AI224533 H |
| | 439710 | 47550_1 | T78519 H59898 U72516 |
| | 441128 | 51021_2 | AW975186 AA807807 D29548 |
| 65 | 442476 | 543547_1 | W76326 AF086341 W72300 |
| | 444016 | 58899_1 | W76021 AF088052 W72465 |
| | 444168 | 593829_1 | AF086387 W77884 W72711 |
| | 446821 | 69435_1 | AF086543 W96291 W96225 |
| | 448970 | 791254_1 | AA570256 AW014761 AA573721 AI473237 AI022165 AA554071 AA127551 N90525 AW973623 AA447991 AA243852 BE328850 AI148171 AI359627 |
| 70 | 449625 | 8113_1 | AI005068 AI356567 AA232991 AW016855 AA906902 AA233101 AA127550 BE512923 |
| | 450166 | 82677_1 | AF069475 AF069477 AF069476 |
| | 450375 | 83327_1 | AA448154 AV647571 |
| 75 | 450506 | 836_1 | AW379879 AI126285 H12014 |
| | 450625 | 84032_1 | W03766 AI357775 AV660500 AV660731 |
| | 451129 | 859870_1 | AW138582 AI638298 AI631640 AI963868 AI611082 |
| 80 | 451350 | 866945_1 | NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 |
| | 452113 | 899664_1 | AA429504 R41904 AA279467 H09648 AA007236 |
| | 452203 | 903_2 | AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 |
| | | | AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 AI161014 AA099554 R69067 |
| | | | NM_004460 U09278 U76833 AW630055 AW471133 C02434 W45237 AW793518 BE070112 AI587479 AI624429 AW190535 AI446661 AI478772 |
| | | | AW022667 AA528235 AA599775 AW613820 AI435793 AW594230 AI051768 AI200109 AI680296 AA436611 AW609728 W42634 AI682584 AA405569 |
| | | | AI685653 AW0 |
| | | | AW970107 AA513951 AA010406 |
| | | | BE072881 BE072946 AI762181 |
| | | | AI791447 AI791327 AW886809 |
| | | | AI859393 BE177742 |
| | | | X57522 AW295947 AI346197 AI304693 L21205 L21206 L21207 L21208 L21204 NM_000593 F06770 F12630 X57521 R18264 T74452 AA346259 |
| | | | AW602508 AA904076 F08426 H23432 AA313737 AA393782 M78052 AA847441 AA487637 AA135770 AA353161 AI819778 AA054458 AI346733 |
| | | | AW361447 AI4 |

| | | | |
|----|--------|-----------|---|
| 5 | 453331 | 96214_1 | AI240665 T53681 N77468 H51833 AA147247 R75732 C18450 R73999 AI095755 T49904 H03868 AA411580 R33395 AA410586 T48869 D63292 R31981 H12498 H02668 AA035018 R75957 AI803329 R27528 R36203 AI809932 AI808765 R78948 AA411449 AA976929 AI378760 AI378620 T48870 R7390 |
| 10 | 453682 | 977454_1 | T79703 T96307 AL079725 |
| 15 | 454177 | 1049351_1 | AW807321 AW807262 AW177104 AW807319 AW807115 AW807344 AW807324 AW178116 BE141575 AW845849 AW807105 AW845868 BE140942 AW807178 AW807167 AW807398 AW807320 AW807306 AW845866 |
| 20 | 454354 | 1129859_1 | AW389896 AW389898 AW389906 AW609203 AW389873 |
| 25 | 454457 | 1207274_1 | AW753456 AW753036 AW854868 AW854862 |
| 30 | 454581 | 1225710_1 | AW809189 AW809219 AW813574 |
| 35 | 454765 | 1233905_1 | AW819629 AW854320 |
| 40 | 454860 | 1237732_1 | AW835767 AW835537 BE160187 |
| 45 | 454968 | 1247029_1 | AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033 |
| 50 | 455104 | 1253737_1 | BE064863 BE153698 AW856751 BE153820 BE064737 BE153674 BE064730 BE065062 BE153536 AW856622 BE155079 BE064651 BE153665 BE064650 BE064691 |
| 55 | 455409 | 1288355_1 | AW936832 AW936509 AW936657 AW936611 AW936739 AW936734 AW936779 AW936688 AW936659 AW936738 AW936827 AW936737 AW936736 AW936740 AW936833 AW936777 AW936830 AW936834 AW936829 AW936772 AW936638 AW936658 AW936636 AW936774 AW936778 AW936766 AW936776 AW936831 AW9 |
| 60 | 455481 | 1293182_1 | AW948317 AW948322 AW948329 AW948316 AW948298 AW948330 AW948325 AW948324 |
| 65 | 455646 | 1348557_1 | BE064420 BE064435 BE064429 BE064414 BE064400 BE064517 |
| 70 | 455778 | 1364506_1 | BE088746 BE088802 BE088755 BE088876 BE088947 BE088881 BE088952 |
| 75 | 455899 | 1381547_1 | BE155112 BE155154 BE155087 BE155247 BE155499 BE155367 BE155452 |
| 80 | 456304 | 176820_1 | AI820973 AI734077 AI820984 AA225796 AA225060 AA225101 |
| 85 | 457364 | 328154_1 | AW971037 AA508019 AA492345 |
| 90 | 457876 | 42814_2 | AI821940 N67106 AI744264 AA808846 AA643417 AA643416 Z70715 |
| 95 | 458199 | 504866_1 | AW136417 AI141026 AI340960 AI091670 AI523802 AW572908 AI458860 AI924374 AI830572 AI400702 AI337539 AI968111 AI521308 AI492336 AI540779 AI672594 AW665077 AA971810 AA909139 AW082128 AI335251 AI807192 AW511744 AI023232 AI536899 AW207791 AI670910 AI002047 AW4 |

TABLE 14C:

| | | |
|----|--------------|---|
| 30 | Pkey: | Unique number corresponding to an Eos probeset |
| 35 | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. |
| 40 | Strand: | Indicates DNA strand from which exons were predicted. |
| 45 | NI_position: | Indicates nucleotide positions of predicted exons. |

| Pkey | Ref | Strand | NI_position |
|--------|---------|--------|---|
| 400492 | 9213749 | Minus | 123881-124090 |
| 400533 | 6981826 | Minus | 277132-277595 |
| 400645 | 8117693 | Minus | 58471-58716 |
| 400658 | 8118459 | Minus | 73525-73644 |
| 400780 | 8131663 | Minus | 118372-118619 |
| 400850 | 1927150 | Minus | 4506-4691 |
| 400924 | 7107613 | Minus | 30309-30498 |
| 401272 | 9797373 | Minus | 98374-98509 |
| 401454 | 9186923 | Minus | 114659-114832 |
| 401696 | 3417290 | Minus | 46209-46401 |
| 401702 | 1871197 | Minus | 68182-68325 |
| 401841 | 7684597 | Plus | 89868-90006,91920-92085 |
| 402032 | 7656761 | Plus | 62293-62475 |
| 402082 | 8117478 | Minus | 190046-190183 |
| 402229 | 9965022 | Minus | 15739-15951,16166-16779 |
| 402239 | 7690131 | Plus | 38175-38304,42133-42266 |
| 402260 | 3399665 | Minus | 113765-113910,115653-115765,116808-116940 |
| 402274 | 2935596 | Plus | 5604-6527 |
| 402604 | 9909420 | Plus | 20393-20767 |
| 402615 | 9926801 | Plus | 131390-132157 |
| 402799 | 3355547 | Plus | 35718-35899 |
| 402855 | 9662953 | Minus | 59763-59909 |
| 402936 | 8894303 | Plus | 51655-51771 |
| 403011 | 6693597 | Minus | 3468-3623 |
| 403104 | 7331404 | Minus | 41800-41973 |
| 403108 | 8980955 | Plus | 93253-93667 |
| 403212 | 7630897 | Minus | 156037-156210 |
| 403267 | 7887182 | Plus | 116078-121885 |
| 403288 | 8081479 | Plus | 133763-133899,135813-135958 |
| 403290 | 8083176 | Plus | 19288-20076 |
| 403291 | 7230870 | Plus | 95177-95435 |
| 403349 | 8569773 | Minus | 167815-168374 |
| 403361 | 8570313 | Minus | 112496-112687 |
| 403431 | 7139839 | Plus | 56509-56860 |
| 403481 | 9965004 | Plus | 93496-93633 |
| 403696 | 3135242 | Minus | 143467-143634 |
| 403790 | 8084957 | Minus | 87826-87947,89835-90002 |
| 403849 | 7708855 | Plus | 95043-96519 |
| 403942 | 7711825 | Minus | 99606-99757 |
| 403961 | 7596976 | Minus | 110393-110603 |
| 403969 | 8569909 | Plus | 31237-31375,32405-32506 |
| 404053 | 3548785 | Plus | 61797-64205 |
| 404120 | 7342152 | Plus | 135775-136000 |
| 404150 | 7534008 | Plus | 165811-165943 |
| 404170 | 9930793 | Plus | 168836-169248 |
| 404209 | 5006246 | Minus | 11247-11514 |
| 404272 | 9885189 | Plus | 83207-83355,84358-84496,90519-90720,91371-91447 |

| | | | | |
|----|--------|---------|-------|------------------------------|
| 5 | 404407 | 7329316 | Minus | 48154-48499 |
| | 404571 | 7249169 | Minus | 112450-112648 |
| | 404584 | 9857511 | Plus | 138651-139153 |
| | 404592 | 9943965 | Minus | 39067-39225 |
| | 404632 | 9796668 | Plus | 45096-45229 |
| | 404748 | 7263437 | Plus | 11446-11591 |
| | 404891 | 7329392 | Plus | 84974-85125 |
| | 405046 | 7596829 | Minus | 4373-4528 |
| 10 | 405141 | 8980911 | Plus | 99861-100054 |
| | 405183 | 7209940 | Plus | 12335-12653 |
| | 405238 | 7249119 | Minus | 51728-51836 |
| | 405348 | 2914717 | Minus | 43310-43462 |
| | 405516 | 9454624 | Plus | 112707-112876, 113676-113854 |
| | 405558 | 1621110 | Plus | 4502-4644, 5983-6083 |
| 15 | 405605 | 5836195 | Minus | 117070-117270 |
| | 405717 | 9588573 | Plus | 11275-11973 |
| | 405760 | 6066938 | Minus | 37424-38045 |
| | 405863 | 7657810 | Plus | 49410-49620 |
| 20 | 405941 | 6758796 | Plus | 2798-3444 |
| | 406060 | 6899623 | Minus | 20339-20746 |
| | 406290 | 5686274 | Plus | 8711-9358 |
| | 406395 | 9256242 | Minus | 20805-20960 |
| | 406478 | 9857502 | Plus | 68314-68523, 68853-68950 |
| 25 | 406481 | 9864741 | Minus | 91439-91579 |

TABLE 15A: ABOUT 1033 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT TISSUES

Table 15A lists about 1033 genes up-regulated in glioblastoma compared to normal normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" glioblastoma to "average" normal tissues was greater than or equal to 3.0. The "average" glioblastoma level was set to the 85th percentile amongst various brain tumors. The "average" normal tissue level was set to the 85th percentile amongst various non-malignant adult tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of GLIOBLASTOMA to NORMAL ADULT TISSUES

| | | | | | |
|----|--------|-----------|-----------|--|------|
| 40 | Pkey | ExAccn | UnigenelD | Unigene Title | R1 |
| | 427343 | A1880044 | Hs.176977 | protein kinase C binding protein 2 | 60.5 |
| | 431917 | D16181 | Hs.2868 | peripheral myelin protein 2 | 54.9 |
| | 418375 | NM_003081 | Hs.84389 | synaptosomal-associated protein, 25kD | 53.1 |
| | 428321 | A1699994 | Hs.2868 | peripheral myelin protein 2 | 49.6 |
| 45 | 409389 | AB007979 | Hs.301281 | Homo sapiens mRNA, chromosome 1 specific | 45.4 |
| | 435147 | AL133731 | Hs.4774 | Homo sapiens mRNA; cDNA DKFZp761C1712 (f | 43.9 |
| | 413472 | BE242870 | Hs.75379 | solute carrier family 1 (glial high affi | 42.7 |
| | 415817 | U88967 | Hs.78867 | protein tyrosine phosphatase, receptor-t | 42.3 |
| | 456759 | BE259150 | Hs.127792 | della (Drosophila)-like 3 | 39.1 |
| 50 | 430838 | N46664 | Hs.169395 | hypothetical protein FLJ12015 | 37.9 |
| | 417183 | R52089 | Hs.172717 | ESTs | 37.6 |
| | 426325 | D28114 | Hs.169309 | myelin-associated oligodendrocyte basic | 36.5 |
| | 425088 | AA663372 | Hs.169395 | hypothetical protein FLJ12015 | 34.3 |
| | 429007 | D80642 | | gb:HUM092E09B Human fetal brain (TFujw | 33.9 |
| 55 | 449494 | AW237014 | Hs.315369 | Homo sapiens cDNA: FLJ23075 fis, clone L | 33.9 |
| | 423849 | AL157425 | Hs.133315 | Homo sapiens mRNA; cDNA DKFZp761J1324 (f | 32.7 |
| | 429276 | AF056085 | Hs.198612 | G protein-coupled receptor 51 | 32.3 |
| | 413333 | M74028 | Hs.75297 | fibroblast growth factor 1 (acidic) | 29.0 |
| | 450133 | AW969769 | Hs.105201 | ESTs | 27.9 |
| 60 | 412733 | AA984472 | Hs.74554 | KIAA0080 protein | 27.6 |
| | 425842 | AI587490 | Hs.159623 | NK-2 (Drosophila) homolog B | 27.3 |
| | 416829 | AB013805 | Hs.80220 | catenin (cadherin-associated protein), d | 27.1 |
| | 424140 | Z48051 | Hs.141308 | myelin oligodendrocyte glycoprotein | 25.2 |
| | 402604 | | | Target Exon | 24.3 |
| 65 | 437204 | AL110216 | Hs.22826 | ESTs, Weakly similar to I55214 salivary | 24.3 |
| | 422656 | AI870435 | Hs.1569 | LIM homeobox protein 2 | 23.6 |
| | 447359 | NM_012093 | Hs.18268 | adenylate kinase 5 | 23.3 |
| | 436878 | BE465204 | Hs.47448 | ESTs | 22.9 |
| | 435708 | AI362949 | Hs.75169 | ESTs | 22.9 |
| 70 | 429903 | AL134197 | Hs.93597 | cyclin-dependent kinase 5, regulatory su | 22.7 |
| | 439239 | AI031540 | Hs.235331 | ESTs | 22.4 |
| | 409395 | U46745 | Hs.336678 | dystrobrevin, alpha | 22.2 |
| | 425799 | T08133 | Hs.182906 | Homo sapiens mRNA for KIAA1872 protein, | 21.9 |
| | 425057 | AA826434 | Hs.1619 | achaete-scute complex (Drosophila) homol | 21.3 |
| 75 | 444378 | R41339 | Hs.47860 | neurotrophic tyrosine kinase, receptor, | 21.2 |
| | 444513 | AL120214 | Hs.7117 | glutamate receptor, ionotropic, AMPA 1 | 21.0 |
| | 419078 | M93119 | Hs.89584 | insulinoma-associated 1 | 21.0 |
| | 425048 | H05468 | Hs.164502 | ESTs | 20.9 |
| | 453392 | U23752 | Hs.32964 | SRY (sex determining region Y)-box 11 | 19.3 |
| 80 | 423853 | AB011537 | Hs.133466 | slit (Drosophila) homolog 1 | 19.3 |
| | 418110 | R43523 | Hs.217754 | hypothetical protein FLJ22202 | 19.2 |
| | 447004 | AW296968 | Hs.157539 | ESTs | 18.6 |
| | 439415 | F05538 | Hs.4273 | ESTs | 18.6 |
| | 441497 | R51064 | Hs.23172 | ESTs | 18.5 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 425523 | AB007948 | Hs.158244 | KIAA0479 protein | 18.3 |
| | 413597 | AW302885 | Hs.117183 | ESTs | 18.2 |
| | 433551 | AI985544 | Hs.12450 | protocadherin 9 | 17.7 |
| 5 | 428392 | H10233 | Hs.2265 | secretory granule, neuroendocrine protei | 17.3 |
| | 453642 | AI370936 | Hs.34074 | dipeptidylpeptidase VI | 17.3 |
| | 418338 | NM_002522 | Hs.84154 | neuronal pentraxin I | 17.1 |
| | 437268 | AI754847 | Hs.227571 | regulator of G-protein signalling 4 | 16.8 |
| | 408604 | D51408 | Hs.21925 | ESTs | 16.6 |
| 10 | 424581 | M52062 | Hs.150917 | catenin (cadherin-associated protein), a | 16.6 |
| | 422980 | N46569 | Hs.76722 | CCAAT/enhancer binding protein (C/EBP), | 16.5 |
| | 448302 | AI480208 | Hs.182906 | Homo sapiens mRNA for KIAA1872 protein, | 16.4 |
| | 429466 | M85835 | Hs.12827 | ESTs | 16.3 |
| | 441350 | AB020690 | Hs.7782 | paraneoplastic antigen MA2 | 15.9 |
| 15 | 448672 | AI955511 | Hs.225106 | ESTs | 15.8 |
| | 448743 | AB032962 | Hs.21896 | KIAA1136 protein | 15.7 |
| | 415910 | U20350 | Hs.78913 | chemokine (C-X3-C) receptor 1 | 15.3 |
| | 441285 | NM_002374 | Hs.167 | microtubule-associated protein 2 | 15.2 |
| | 431019 | NM_005249 | Hs.2714 | forkhead box G1B | 14.8 |
| 20 | 431941 | AK000106 | Hs.272227 | Homo sapiens cDNA FLJ20099 fis, clone CO | 14.3 |
| | 433800 | AI034361 | Hs.135150 | lung type-I cell membrane-associated gly | 14.3 |
| | 416370 | N90470 | Hs.203697 | ESTs, Weakly similar to I38022 hypotheti | 14.1 |
| | 439979 | AW600291 | Hs.6823 | hypothetical protein FLJ10430 | 14.0 |
| | 444471 | AB020684 | Hs.11217 | KIAA0877 protein | 13.9 |
| 25 | 444783 | AK001468 | Hs.62180 | anillin (Drosophila Scraps homolog), act | 13.8 |
| | 448595 | AB014544 | Hs.21572 | KIAA0644 gene product | 13.6 |
| | 441440 | AI807981 | Hs.30495 | ESTs | 13.6 |
| | 428982 | NM_005097 | Hs.194704 | leucine-rich, glioma inactivated 1 | 13.5 |
| | 424790 | AL119344 | Hs.13326 | ESTs, Weakly similar to 2004399A chromos | 13.3 |
| | 459516 | AI049662 | Hs.246858 | EST | 13.2 |
| 30 | 421264 | AL039123 | Hs.103042 | microtubule-associated protein 1B | 13.2 |
| | 428342 | AI739168 | | Homo sapiens cDNA FLJ13458 fis, clone PL | 13.1 |
| | 408562 | AI436323 | Hs.31141 | Homo sapiens mRNA for KIAA1568 protein, | 12.9 |
| | 412959 | D87458 | Hs.75090 | KIAA0282 protein | 12.9 |
| | 439199 | R40373 | Hs.26299 | ESTs | 12.8 |
| 35 | 423419 | R55336 | Hs.23539 | ESTs | 12.5 |
| | 445495 | BE622641 | Hs.38489 | ESTs, Weakly similar to I38022 hypotheti | 12.4 |
| | 415849 | R20529 | Hs.6806 | ESTs | 12.4 |
| | 452372 | AI885742 | Hs.228474 | ESTs | 12.4 |
| 40 | 452744 | AI267652 | Hs.246107 | Homo sapiens mRNA; cDNA DKFZp434E082 (fr | 12.3 |
| | 426344 | H41821 | Hs.322469 | transcriptional activator of the c-fos p | 12.2 |
| | 415734 | NM_014747 | Hs.78748 | KIAA0237 gene product | 12.1 |
| | 426269 | H15302 | Hs.168950 | Homo sapiens mRNA; cDNA DKFZp566A1046 (f | 12.1 |
| | 444119 | R41231 | Hs.184261 | ESTs, Weakly similar to T26586 hypotheti | 12.0 |
| | 409049 | AI423132 | Hs.146343 | ESTs | 11.9 |
| 45 | 434277 | X77748 | Hs.3786 | glutamate receptor, metabotropic 3 | 11.9 |
| | 427897 | NM_017413 | Hs.303084 | apelin; peptide ligand for APJ receptor | 11.8 |
| | 453941 | U39817 | Hs.36820 | Bloom syndrome | 11.8 |
| | 424120 | T80579 | Hs.290270 | ESTs | 11.7 |
| 50 | 418738 | AW388633 | Hs.6682 | solute carrier family 7, (cationic amino | 11.7 |
| | 411305 | BE241596 | Hs.69547 | myelin basic protein | 11.7 |
| | 424945 | AI221919 | | hypothetical protein FLJ10582 | 11.6 |
| | 449539 | W80363 | Hs.58446 | ESTs | 11.5 |
| | 409638 | AW450420 | Hs.21335 | ESTs | 11.5 |
| | 441016 | AW138653 | Hs.25845 | ESTs | 11.4 |
| 55 | 429037 | X81895 | Hs.194765 | H.sapiens GENX-5624 mRNA, 3' UTR | 11.3 |
| | 407034 | U84540 | | gb:Human dystrobrevin isoform DTN-3 (DTN | 11.2 |
| | 446372 | AB020644 | Hs.14945 | long fatty acyl-CoA synthetase 2 gene | 11.2 |
| | 425984 | AW836277 | Hs.165636 | hypothetical protein DKFZp761C07121 | 11.2 |
| 60 | 424432 | AB037821 | Hs.146858 | protocadherin 10 | 11.1 |
| | 424893 | AW295112 | Hs.153648 | Homo sapiens cDNA FLJ13303 fis, clone OV | 11.1 |
| | 425649 | U30930 | Hs.158540 | UDP glycosyltransferase 8 (UDP-galactose | 11.1 |
| | 438380 | T06430 | Hs.6194 | chondroitin sulfate proteoglycan BEHAB/b | 11.1 |
| | 423678 | AW963357 | Hs.7847 | ESTs | 10.7 |
| 65 | 446692 | Z44514 | | Homo sapiens mRNA for KIAA1763 protein, | 10.7 |
| | 430691 | C14187 | Hs.103538 | ESTs | 10.7 |
| | 428728 | NM_016625 | Hs.191381 | hypothetical protein | 10.6 |
| | 427701 | AA411101 | Hs.243886 | nuclear autoantigenic sperm protein (his | 10.6 |
| | 431988 | AC002302 | Hs.77202 | protein kinase C, beta 1 | 10.5 |
| | 433896 | AW294729 | Hs.274461 | ESTs | 10.5 |
| 70 | 431467 | N71831 | Hs.256398 | Homo sapiens mRNA; cDNA DKFZp434E0528 (f | 10.4 |
| | 419249 | X14767 | Hs.89768 | gamma-aminobutyric acid (GABA) A recepto | 10.3 |
| | 445041 | T64183 | Hs.282982 | solute carrier | 10.3 |
| | 446782 | AI653048 | Hs.144006 | ESTs | 10.2 |
| 75 | 451952 | AL120173 | Hs.301663 | ESTs | 10.2 |
| | 446711 | AF169692 | Hs.12450 | protocadherin 9 | 10.1 |
| | 438054 | AA776626 | Hs.169309 | ESTs | 10.1 |
| | 443785 | AW449952 | Hs.190125 | basic-helix-loop-helix-PAS protein | 10.1 |
| | 451099 | R52795 | Hs.25954 | interleukin 13 receptor, alpha 2 | 10.0 |
| 80 | 419863 | AW952691 | Hs.93485 | Homo sapiens mRNA; cDNA DKFZp761D191 (fr | 10.0 |
| | 416857 | AA188775 | Hs.292453 | ESTs | 10.0 |
| | 435191 | R15912 | Hs.4817 | Homo sapiens clone 24461 mRNA sequence | 10.0 |
| | 419271 | N34901 | Hs.238532 | ESTs | 9.9 |
| | 429927 | NM_001115 | Hs.2522 | adenylate cyclase 8 (brain) | 9.9 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 415293 | R49462 | Hs.106541 | ESTs | |
| | 440184 | AB002297 | Hs.7022 | dedicator of cyto-kinesis 3 | 9.9 |
| | 452526 | W38537 | Hs.280740 | hypothetical protein MGC3040 | 9.8 |
| 5 | 427304 | AA761526 | Hs.163853 | ESTs | 9.8 |
| | 420547 | AF155140 | Hs.98738 | gonadotropin-regulated testicular RNA he | 9.7 |
| | 421659 | NM_014459 | Hs.106511 | protocadherin 17 | 9.6 |
| | 426847 | S78723 | Hs.298623 | 5-hydroxytryptamine (serotonin) receptor | 9.6 |
| | 429656 | X05608 | Hs.211584 | neurofilament, light polypeptide (68kD) | 9.6 |
| 10 | 447101 | N72185 | Hs.44189 | ESTs | 9.5 |
| | 442613 | AI004002 | Hs.130522 | Kv channel-interacting protein 1 | 9.5 |
| | 454027 | R40192 | Hs.21527 | Human DNA sequence from clone GS1-115M3 | 9.5 |
| | 445102 | AW204610 | Hs.22270 | ESTs | 9.5 |
| | 435793 | AB037734 | Hs.4993 | KIAA1313 protein | 9.5 |
| 15 | 437948 | AA772920 | Hs.303527 | ESTs | 9.5 |
| | 438209 | AL120659 | Hs.6111 | aryl-hydrocarbon receptor nuclear transi | 9.5 |
| | 415170 | R44386 | Hs.164578 | ESTs | 9.4 |
| | 415486 | H12214 | Hs.13284 | ESTs, Weakly similar to 2109260A B cell | 9.3 |
| | 435501 | AW051819 | Hs.129908 | KIAA0591 protein | 9.2 |
| 20 | 416072 | AL110370 | Hs.79000 | growth associated protein 43 | 9.2 |
| | 442910 | AI365130 | Hs.11307 | ESTs, Weakly similar to T19326 hypotheti | 9.2 |
| | 438080 | AA777381 | Hs.291530 | ESTs, Weakly similar to ALUC_HUMAN !!! | 9.1 |
| | 425187 | AW014486 | Hs.22509 | ESTs | 9.1 |
| | 424028 | AF055084 | Hs.153692 | Homo sapiens cDNA FLJ14354 fis, clone Y7 | 9.1 |
| 25 | 430091 | AB032958 | Hs.233023 | KIAA1132 protein | 9.0 |
| | 427540 | R12014 | Hs.20976 | ESTs | 9.0 |
| | 447198 | D61523 | Hs.283435 | ESTs | 9.0 |
| | 449611 | AI970394 | Hs.197075 | ESTs | 9.0 |
| | 444124 | R43097 | Hs.6818 | ESTs | 8.9 |
| 30 | 451996 | AW514021 | Hs.245510 | ESTs | 8.9 |
| | 454048 | H05626 | Hs.6921 | ESTs | 8.8 |
| | 412266 | N59006 | Hs.26133 | ESTs | 8.8 |
| | 433597 | AA708205 | Hs.100343 | ESTs | 8.8 |
| | 447342 | AI199268 | Hs.19322 | Homo sapiens, Similar to RIKEN cDNA 2010 | 8.7 |
| 35 | 450154 | R15891 | Hs.281587 | Human (clone CTG-A4) mRNA sequence | 8.6 |
| | 410102 | AW248508 | Hs.279727 | ESTs; homologue of PEM-3 (Ciona savignyi | 8.6 |
| | 423135 | N67655 | Hs.26411 | ESTs | 8.5 |
| | 418097 | R45137 | Hs.21868 | ESTs | 8.5 |
| | 420602 | AF060877 | Hs.99236 | regulator of G-protein signalling 20 | 8.4 |
| 40 | 419721 | NM_001650 | Hs.288650 | aquaporin 4 | 8.4 |
| | 449300 | AI656959 | Hs.346514 | ESTs | 8.4 |
| | 436954 | AA740151 | Hs.130425 | ESTs | 8.4 |
| | 425354 | U62027 | Hs.155935 | complement component 3a receptor 1 | 8.3 |
| | 424997 | AL138167 | Hs.96920 | ESTs | 8.3 |
| 45 | 442710 | AI015631 | Hs.23210 | ESTs | 8.3 |
| | 449625 | NM_014253 | | odt (odd Ozten-m, Drosophila) homolog 1 | 8.2 |
| | 451625 | R56793 | Hs.106576 | alanine-glyoxylate aminotransferase 2-l | 8.2 |
| | 413063 | AL035737 | Hs.75184 | chitinase 3-like 1 (cartilage glycoprote | 8.2 |
| | 449605 | AW138581 | Hs.198416 | ESTs | 8.0 |
| 50 | 407886 | AW969688 | Hs.100826 | ESTs | 8.0 |
| | 414175 | AI308876 | Hs.103849 | hypothetical protein DKFZp761D112 | 8.0 |
| | 429946 | R49390 | Hs.254129 | KIAA1678 | 7.9 |
| | 400293 | N51002 | Hs.306480 | Homo sapiens mRNA; cDNA DKFZp761E2112 (f | 7.9 |
| 55 | 455601 | AI368680 | Hs.816 | SRY (sex determining region Y)-box 2 | 7.9 |
| | 409799 | D11928 | Hs.76845 | phosphoserine phosphatase-like | 7.9 |
| | 415279 | F04237 | Hs.1447 | glial fibrillary acidic protein | 7.8 |
| | 429918 | AW873986 | Hs.119383 | ESTs | 7.8 |
| | 449433 | AI672096 | Hs.9012 | ESTs, Weakly similar to S26650 DNA-bindi | 7.8 |
| | 422411 | AW749443 | Hs.22511 | ESTs | 7.8 |
| 60 | 448902 | Z45998 | Hs.22543 | Homo sapiens mRNA; cDNA DKFZp761I1912 (f | 7.7 |
| | 452355 | N54926 | Hs.29202 | G protein-coupled receptor 34 | 7.7 |
| | 447414 | D82343 | Hs.74376 | neuroblastoma (nerve tissue) protein | 7.7 |
| | 407168 | R45175 | Hs.117183 | ESTs | 7.7 |
| | 448555 | AI536697 | Hs.159863 | ESTs | 7.6 |
| 65 | 428536 | AI143139 | Hs.2288 | visinin-like 1 | 7.6 |
| | 408947 | AL080093 | Hs.49117 | Homo sapiens mRNA; cDNA DKFZp564N1662 (f | 7.6 |
| | 420362 | U79734 | Hs.97206 | huntinglin interacting protein 1 | 7.6 |
| | 435624 | AF218942 | Hs.24889 | formin 2 | 7.6 |
| | 440105 | AA694010 | Hs.6932 | Homo sapiens clone 23809 mRNA sequence | 7.6 |
| 70 | 412058 | S72043 | Hs.73133 | metallothionein 3 (growth inhibitory fac | 7.6 |
| | 445568 | H00918 | Hs.268744 | KIAA1796 protein | 7.6 |
| | 417160 | N76497 | Hs.1787 | proteolipid protein 1 (Pelizaeus-Merzbac | 7.5 |
| | 423361 | AW170055 | Hs.47628 | ESTs | 7.5 |
| | 456965 | AW131888 | Hs.172792 | ESTs, Weakly similar to hypothetical pro | 7.5 |
| 75 | 458332 | AI000341 | Hs.220491 | ESTs | 7.5 |
| | 409902 | AI337658 | Hs.156351 | ESTs | 7.4 |
| | 448321 | NM_005883 | Hs.20912 | adenomatous polyposis coli like | 7.3 |
| | 420345 | AW295230 | Hs.25231 | ESTs | 7.3 |
| | 402855 | | | NM_001839: Homo sapiens calponin 3, acid | 7.3 |
| 80 | 424481 | R19453 | Hs.1787 | proteolipid protein 1 (Pelizaeus-Merzbac | 7.2 |
| | 425741 | AF052152 | Hs.159412 | Homo sapiens clone 24628 mRNA sequence | 7.2 |
| | 448986 | H42169 | Hs.347310 | hypothetical protein FLJ14627 | 7.2 |
| | 415651 | AI207162 | Hs.3815 | stathmin-like-protein RB3 | 7.2 |
| | 412709 | AL022327 | Hs.74518 | KIAA0027 protein | 7.1 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 451621 | AI879148 | Hs.26770 | fatty acid binding protein 7, brain | 7.1 |
| | 445745 | AB007924 | Hs.13245 | KIAA0455 gene product | 7.1 |
| | 439451 | AF086270 | Hs.278554 | heterochromatin-like protein 1 | 7.1 |
| 5 | 418030 | BE207573 | Hs.83321 | neuromedin B | 7.1 |
| | 400292 | AA250737 | Hs.72472 | BMP-R1B | 7.1 |
| | 407748 | AL079409 | Hs.38176 | KIAA0606 protein; SCN Circadian Oscillat | 7.0 |
| | 440435 | AL042201 | Hs.21273 | transcription factor NYD-sp10 | 7.0 |
| | 414696 | AF002020 | Hs.76918 | Niemann-Pick disease, type C1 | 7.0 |
| 10 | 417417 | F05745 | Hs.89512 | ATPase, Ca transporting, plasma membrane | 7.0 |
| | 440152 | AB002376 | Hs.7006 | KIAA0378 protein | 7.0 |
| | 422960 | AW890487 | Hs.63984 | cadherin 13, H-cadherin (heart) | 7.0 |
| | 454293 | H49739 | Hs.134013 | ESTs, Moderately similar to HK61_HUMAN H | 7.0 |
| | 447197 | R36075 | | gb:yh88b01.s1 Soares placenta Nb2HP Homo | 7.0 |
| 15 | 426814 | AF036943 | Hs.172619 | myelin transcription factor 1-like | 6.9 |
| | 416836 | D54745 | Hs.80247 | cholecystokinin | 6.9 |
| | 447350 | AI375572 | Hs.172634 | ESTs | 6.9 |
| | 440074 | AA863045 | Hs.10669 | ESTs, Weakly similar to T00050 hypotheti | 6.9 |
| | 436039 | AW023323 | Hs.121070 | ESTs | 6.9 |
| 20 | 444396 | T65213 | Hs.4257 | ESTs | 6.9 |
| | 425234 | AW152225 | Hs.165909 | ESTs, Weakly similar to I38022 hypotheti | 6.9 |
| | 438330 | AW450572 | Hs.257316 | ESTs | 6.8 |
| | 410305 | AF030409 | Hs.62185 | solute carrier family 9 (sodium/hydrogen | 6.8 |
| | 421141 | AW117261 | Hs.125914 | ESTs | 6.7 |
| 25 | 412788 | AA120960 | Hs.198416 | ESTs | 6.7 |
| | 411078 | AI222020 | Hs.182364 | CocoaCrisp | 6.7 |
| | 443455 | AB001025 | Hs.9349 | ryanodine receptor 3 | 6.7 |
| | 448769 | N66037 | Hs.38173 | ESTs | 6.7 |
| | 441523 | AW514263 | Hs.301771 | ESTs, Weakly similar to ALUF_HUMAN !!!! | 6.7 |
| 30 | 414214 | D49958 | Hs.75819 | glycoprotein M6A | 6.6 |
| | 439845 | AL355743 | Hs.56663 | Homo sapiens EST from clone 41214, full | 6.6 |
| | 437036 | AI571514 | Hs.133022 | ESTs | 6.6 |
| | 429239 | AA448419 | Hs.45209 | ESTs | 6.6 |
| | 434164 | AW207019 | Hs.148135 | serine/threonine kinase 33 | 6.6 |
| 35 | 412155 | R38167 | Hs.12449 | Homo sapiens transmembrane protein HTMP1 | 6.5 |
| | 452834 | AI638627 | Hs.105685 | KIAA1688 protein | 6.5 |
| | 441916 | AA993571 | Hs.129075 | ESTs | 6.5 |
| | 451516 | AI800515 | Hs.12024 | ESTs | 6.5 |
| | 434808 | AF155108 | Hs.256150 | Homo sapiens, Similar to RIKEN cDNA 2810 | 6.5 |
| 40 | 452461 | N78223 | Hs.108106 | transcription factor | 6.5 |
| | 450375 | AA009647 | | a disintegrin and metalloproteinase doma | 6.4 |
| | 434811 | AW971205 | Hs.114280 | ESTs | 6.4 |
| | 424624 | AB032947 | Hs.151301 | Ca2-dependent activator protein for secr | 6.4 |
| | 429250 | H56585 | Hs.198308 | tryptophan rich basic protein | 6.3 |
| 45 | 414245 | BE148072 | Hs.75850 | WAS protein family, member 1 | 6.3 |
| | 433447 | U29195 | Hs.3281 | neuronal pentraxin II | 6.3 |
| | 424922 | BE386547 | Hs.217112 | hypothetical protein MGC10825 | 6.3 |
| | 426919 | AL041228 | | ELAV (embryonic lethal, abnormal vision, | 6.3 |
| | 411411 | AA345241 | Hs.55950 | ESTs, Weakly similar to KIAA1330 protein | 6.3 |
| 50 | 415669 | NM_005025 | Hs.78589 | serine (or cysteine) proteinase inhibito | 6.2 |
| | 449048 | Z45051 | Hs.22920 | similar to S68401 (cattle) glucose induc | 6.2 |
| | 433929 | AI375499 | Hs.27379 | ESTs | 6.2 |
| | 423346 | AI267677 | Hs.127416 | synaptojanin 1 | 6.2 |
| | 448148 | NM_016578 | Hs.20509 | HBV pX associated protein-8 | 6.2 |
| 55 | 412140 | AA219691 | Hs.73625 | RAB6 interacting, kinesin-like (rabkines | 6.2 |
| | 409731 | AA125985 | Hs.56145 | thymosin, beta, identified in neuroblast | 6.2 |
| | 420608 | BE548277 | Hs.103104 | ESTs | 6.2 |
| | 424085 | NM_002914 | Hs.139226 | replication factor C (activator 1) 2 (40 | 6.2 |
| | 422175 | N79885 | Hs.6382 | ESTs, Highly similar to T00391 hypotheti | 6.1 |
| 60 | 428845 | AL157579 | Hs.153610 | KIAA0751 gene product | 6.1 |
| | 439274 | AF086092 | Hs.48372 | ESTs | 6.1 |
| | 447499 | AW262580 | Hs.147674 | protocadherin beta 16 | 6.1 |
| | 425977 | R15138 | Hs.165570 | Homo sapiens clone 25052 mRNA sequence | 6.1 |
| | 453924 | R49295 | Hs.24886 | ESTs | 6.1 |
| 65 | 449340 | AW235786 | Hs.195359 | hypothetical protein MGC10954 | 6.1 |
| | 420077 | AW512260 | Hs.87767 | ESTs | 6.1 |
| | 431721 | AB032996 | Hs.268044 | KIAA1170 protein | 6.1 |
| | 433701 | AW445023 | Hs.15155 | ESTs | 6.1 |
| | 430968 | AW972830 | | gb:EST384925 MAGE resequences, MAGL Homo | 6.1 |
| 70 | 429469 | M64590 | Hs.27 | glycine dehydrogenase (decarboxylating; | 6.1 |
| | 456723 | Z43902 | Hs.4748 | adenylate cyclase activating polypeptide | 6.0 |
| | 448681 | AL109781 | Hs.21754 | Homo sapiens mRNA full length insert cDN | 6.0 |
| | 429900 | AA460421 | Hs.30875 | ESTs | 6.0 |
| | 410909 | AW898161 | Hs.53112 | ESTs, Moderately similar to ALU8_HUMAN A | 6.0 |
| 75 | 432281 | AK001239 | Hs.274263 | hypothetical protein FLJ10377 | 6.0 |
| | 448243 | AW369771 | Hs.52620 | integrin, beta 8 | 6.0 |
| | 416427 | BE244050 | Hs.79307 | Rac/Cdc42 guanine exchange factor (GEF) | 6.0 |
| | 419704 | AA429104 | Hs.45057 | ESTs | 6.0 |
| | 436936 | AL134451 | Hs.197478 | ESTs | 6.0 |
| 80 | 428409 | AW117207 | Hs.98523 | ESTs | 6.0 |
| | 433244 | AB040943 | Hs.271285 | KIAA1510 protein | 6.0 |
| | 439772 | AL365406 | Hs.10268 | Homo sapiens mRNA full length insert cDN | 6.0 |
| | 408096 | BE250162 | Hs.83765 | dihydrofolate reductase | 6.0 |
| | 419929 | U90268 | Hs.93810 | cerebral cavernous malformations 1 | 6.0 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 422544 | AB018259 | Hs.118140 | KIAA0716 gene product | 6.0 |
| | 413627 | BE182082 | Hs.246973 | ESTs | 6.0 |
| | 419985 | H66373 | Hs.5856 | ESTs, Highly similar to bA393J16.3 [H.sa | 6.0 |
| 5 | 410366 | AI267589 | Hs.302689 | hypothetical protein | 6.0 |
| | 429183 | AB014604 | Hs.197955 | KIAA0704 protein | 5.9 |
| | 430188 | AL049242 | Hs.234794 | Homo sapiens mRNA; cDNA DKFZp564B083 (fr | 5.9 |
| | 441102 | AA973905 | | intermediate filament protein syncoilin | 5.9 |
| | 448533 | AL119710 | Hs.21365 | nucleosome assembly protein 1-like 3 | 5.9 |
| 10 | 407182 | AA312551 | Hs.230157 | ESTs | 5.9 |
| | 437372 | AA323968 | Hs.283631 | hypothetical protein DKFZp547G183 | 5.9 |
| | 433523 | H29882 | | ESTs | 5.9 |
| | 444165 | AL137443 | Hs.10441 | hypothetical protein FLJ11236 | 5.9 |
| | 424343 | AW956360 | Hs.4748 | adenylate cyclase activating polypeptide | 5.9 |
| 15 | 420156 | AW449258 | Hs.6187 | ESTs | 5.9 |
| | 422864 | AA318323 | Hs.12827 | gb:EST20390 Retina II Homo sapiens cDNA | 5.8 |
| | 446727 | AB011095 | Hs.16032 | KIAA0523 protein | 5.8 |
| | 448543 | AW897741 | Hs.21380 | Homo sapiens mRNA; cDNA DKFZp586P1124 (f | 5.8 |
| | 430132 | AA204686 | Hs.234149 | hypothetical protein FLJ20647 | 5.8 |
| 20 | 425782 | U66468 | Hs.159525 | cell growth regulatory with EF-hand doma | 5.8 |
| | 419629 | AB020695 | Hs.91662 | KIAA0888 protein | 5.8 |
| | 452279 | AA286844 | Hs.61260 | hypothetical protein FLJ13164 | 5.8 |
| | 407808 | AA663559 | Hs.279789 | histone deacetylase 3 | 5.8 |
| | 414737 | AI160386 | Hs.125087 | ESTs | 5.8 |
| 25 | 432154 | AI701523 | Hs.112577 | ESTs | 5.8 |
| | 410099 | AA081630 | | KIAA0036 gene product | 5.8 |
| | 411379 | AI816344 | Hs.12554 | ESTs, Weakly similar to NPL4_HUMAN NUCLE | 5.8 |
| | 440492 | R39127 | Hs.21433 | hypothetical protein DKFZp547J036 | 5.8 |
| | 424560 | AA158727 | Hs.150555 | protein predicted by clone 23733 | 5.7 |
| 30 | 419498 | AL036591 | Hs.20887 | hypothetical protein FLJ10392 | 5.7 |
| | 436643 | AA757626 | Hs.10941 | ESTs, Weakly similar to IPP1_HUMAN PROTE | 5.7 |
| | 416111 | AA033813 | Hs.79018 | chromatin assembly factor 1, subunit A (| 5.7 |
| | 419088 | AI538323 | Hs.52620 | integrin, beta 8 | 5.7 |
| | 436109 | AA922153 | Hs.132760 | hypothetical protein MGC15729 | 5.7 |
| 35 | 428588 | F12101 | Hs.185701 | Homo sapiens mRNA full length insert cDN | 5.7 |
| | 451752 | AB032997 | Hs.26966 | KIAA1171 protein | 5.7 |
| | 413492 | D87470 | Hs.75400 | KIAA0280 protein | 5.7 |
| | 414683 | S78296 | Hs.76888 | hypothetical protein MGC12702 | 5.7 |
| | 418079 | R40058 | Hs.6911 | ESTs | 5.6 |
| 40 | 445873 | AA250970 | Hs.251946 | poly(A)-binding protein, cytoplasmic 14 | 5.6 |
| | 437034 | AA742643 | | gb:ny91c01.s1 NCL_CGAP_GCB1 Homo sapiens | 5.6 |
| | 419544 | AI909154 | | gb:CV-BT200-010499-007 BT200 Homo sapien | 5.6 |
| | 452785 | AL359942 | Hs.296434 | erythroid differentiation and denucleati | 5.6 |
| | 408081 | AW451597 | Hs.167409 | ESTs | 5.6 |
| 45 | 436887 | AW953157 | Hs.193235 | hypothetical protein DKFZp547D155 | 5.6 |
| | 413589 | AW452631 | Hs.313803 | ESTs, Highly similar to AF157833 1 noncl | 5.6 |
| | 418506 | AA084248 | Hs.85339 | G protein-coupled receptor 39 | 5.6 |
| | 433556 | W56321 | Hs.111460 | calcium/calmodulin-dependent protein kin | 5.6 |
| | 448299 | AA497044 | Hs.20887 | hypothetical protein FLJ10392 | 5.5 |
| 50 | 425154 | NM_001851 | Hs.154850 | collagen, type IX, alpha 1 | 5.5 |
| | 447773 | AI423930 | Hs.36790 | ESTs, Weakly similar to putative p150 [H | 5.5 |
| | 422421 | AA325138 | Hs.235873 | hypothetical protein FLJ22672 | 5.5 |
| | 453128 | AW026516 | Hs.31791 | acylphosphatase 2, muscle type | 5.5 |
| | 453220 | AB033089 | Hs.32452 | Homo sapiens mRNA for KIAA1263 protein, | 5.5 |
| 55 | 440866 | AI703103 | Hs.271360 | hypothetical protein MGC16275 | 5.4 |
| | 428976 | AL037824 | Hs.194695 | ras homolog gene family, member I | 5.4 |
| | 419723 | AL120193 | Hs.339810 | longevity assurance (LAG1, S. cerevisiae | 5.4 |
| | 452799 | AI948829 | Hs.213786 | ESTs | 5.4 |
| | 429038 | AL023513 | Hs.194766 | seizure related gene 6 (mouse)-like | 5.4 |
| 60 | 445255 | NM_014841 | Hs.12477 | synaptosomal-associated protein, 91 kDa | 5.4 |
| | 424332 | AA338919 | Hs.101615 | ESTs | 5.4 |
| | 440210 | AW674562 | Hs.125296 | ESTs | 5.4 |
| | 414825 | X06370 | Hs.77432 | epidermal growth factor receptor (avian | 5.4 |
| | 448935 | AL078596 | Hs.22591 | nuclear receptor subfamily 2, group E, m | 5.4 |
| 65 | 452786 | R61362 | Hs.106642 | ESTs, Weakly similar to T09052 hypotheti | 5.4 |
| | 408790 | AW580227 | Hs.47860 | neurotrophic tyrosine kinase, receptor, | 5.4 |
| | 423476 | AL035633 | | Human DNA sequence from clone RP5-1046G1 | 5.4 |
| | 448507 | AL133109 | Hs.21333 | Homo sapiens mRNA; cDNA DKFZp566N1047 (f | 5.4 |
| | 419683 | AA248897 | Hs.48784 | ESTs | 5.4 |
| 70 | 407728 | AW071502 | Hs.175931 | ESTs | 5.4 |
| | 453313 | BE005771 | Hs.153746 | hypothetical protein FLJ22490 | 5.4 |
| | 422094 | AF129535 | Hs.272027 | F-box only protein 5 | 5.4 |
| | 452856 | AF034799 | Hs.30881 | protein tyrosine phosphatase, receptor t | 5.4 |
| | 434792 | AA649253 | Hs.132458 | ESTs | 5.4 |
| 75 | 412190 | R16180 | Hs.274461 | ESTs | 5.4 |
| | 425588 | F07396 | Hs.46627 | ESTs | 5.3 |
| | 444190 | AI878918 | Hs.10526 | cysteine and glycine-rich protein 2 | 5.3 |
| | 429698 | AI685086 | Hs.26339 | ESTs, Weakly similar to S21348 probable | 5.3 |
| | 424458 | M29273 | Hs.1780 | myelin associated glycoprotein | 5.3 |
| 80 | 446997 | AA383439 | Hs.16758 | Spir-1 protein | 5.3 |
| | 427302 | AA400540 | Hs.135282 | Homo sapiens cDNA FLJ11554 fis, clone HE | 5.3 |
| | 439607 | BE540565 | Hs.159460 | ESTs | 5.3 |
| | 448499 | BE613280 | Hs.77550 | hypothetical protein MGC1780 | 5.3 |
| | 410037 | AB020725 | Hs.58009 | KIAA0918 protein | 5.3 |

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|----|--------|-----------|-----------|---|-----|
| | 451407 | AA131376 | Hs.343809 | fibroblast growth factor 12B | 5.3 |
| | 430287 | AW182459 | Hs.125759 | ESTs, Weakly similar to LEU5_HUMAN LEUKE | 5.3 |
| | 428784 | Y12851 | Hs.193470 | purinergic receptor P2X, ligand-gated to | 5.3 |
| 5 | 418512 | AW498974 | | diacylglycerol kinase, zeta (104kD) | 5.3 |
| | 435538 | AB011540 | Hs.4930 | low density lipoprotein receptor-related | 5.3 |
| | 420285 | AA258124 | Hs.293878 | ESTs, Moderately similar to ZNS1_HUMAN Z | 5.2 |
| | 407896 | D76435 | Hs.41154 | Zic family member 1 (odd-paired Drosophi | 5.2 |
| | 404819 | | | NM_002688*:Homo sapiens peanut (Drosophi | 5.2 |
| 10 | 426503 | AA380153 | | gb:EST93093 Skin tumor 1 Homo sapiens cD | 5.2 |
| | 405348 | | | C7001664.gij12698061 dbj BAB21849.1 (AB | 5.2 |
| | 431552 | A1815863 | Hs.259873 | axonal transport of synaptic vesicles | 5.2 |
| | 418677 | S83308 | Hs.87224 | SRY (sex determining region Y)-box 5 | 5.2 |
| | 427250 | R35941 | Hs.25418 | ESTs | 5.2 |
| 15 | 428037 | N47474 | Hs.89230 | potassium intermediate/small conductance | 5.2 |
| | 445740 | T78281 | Hs.13226 | Homo sapiens clone 25181 mRNA sequence | 5.2 |
| | 430130 | AL137311 | Hs.234074 | Homo sapiens mRNA; cDNA DKFZp761G02121 (| 5.2 |
| | 423869 | BE409301 | Hs.134012 | C1q-related factor | 5.2 |
| | 416220 | N49776 | Hs.170994 | hypothetical protein MGC10946 | 5.2 |
| 20 | 457005 | AJ007421 | Hs.172597 | sal (Drosophila)-like 3 | 5.1 |
| | 447072 | D61594 | Hs.17279 | tyrosylprotein sulfotransferase 1 | 5.1 |
| | 414372 | AA143654 | | gb:z065a02.r1 Stratagene pancreas (93720 | 5.1 |
| | 410631 | AA086469 | Hs.47171 | ESTs | 5.1 |
| | 414821 | M63835 | Hs.77424 | Fc fragment of IgG, high affinity Ia, re | 5.1 |
| 25 | 420133 | AA426117 | Hs.155543 | ESTs | 5.1 |
| | 453884 | AA355925 | Hs.36232 | KIAA0186 gene product | 5.1 |
| | 414922 | D00723 | Hs.77631 | glycine cleavage system protein H (amino | 5.1 |
| | 414727 | BE466904 | Hs.190162 | gb:hz28f03.x1 NCL_CGAP_GC6 Homo sapiens | 5.1 |
| | 441869 | NM_003947 | Hs.8004 | huntingtin-associated protein interactin | 5.1 |
| 30 | 437387 | A198874 | Hs.28847 | AD026 protein | 5.0 |
| | 400533 | | | ENSP00000209376*:PRE065 protein (Fragmen | 5.0 |
| | 430979 | A1479755 | Hs.129010 | ESTs | 5.0 |
| | 448944 | AB014605 | Hs.22599 | atrophin-1 interacting protein 1; activi | 5.0 |
| | 444600 | R41398 | Hs.6996 | ESTs | 5.0 |
| 35 | 453785 | A1368236 | Hs.283732 | ESTs, Moderately similar to ALU1_HUMAN A | 5.0 |
| | 428878 | AA436884 | Hs.48926 | ESTs | 5.0 |
| | 444670 | H58373 | Hs.332938 | hypothetical protein MGC5370 | 5.0 |
| | 440471 | AA886146 | Hs.307944 | ESTs | 5.0 |
| | 410434 | AF051152 | Hs.63668 | tol1-like receptor 2 | 5.0 |
| 40 | 441390 | AU692560 | Hs.131175 | ESTs | 4.9 |
| | 448765 | R15337 | Hs.21958 | Homo sapiens mRNA; cDNA DKFZp547D086 (tr | 4.9 |
| | 422263 | AA307639 | Hs.129908 | KIAA0591 protein | 4.9 |
| | 431117 | AF003522 | Hs.250500 | delta (Drosophila)-like 1 | 4.9 |
| | 407235 | D20569 | Hs.169407 | SAC2 (suppressor of actin mutations 2, y | 4.9 |
| 45 | 417404 | NM_007350 | Hs.82101 | pleckstrin homology-like domain, family | 4.9 |
| | 448548 | R13209 | Hs.21413 | solute carrier family 12, (potassium-chl | 4.9 |
| | 420092 | AA814043 | Hs.88045 | ESTs | 4.9 |
| | 449571 | AW016812 | Hs.200266 | ESTs | 4.9 |
| | 412811 | H06382 | | ESTs | 4.9 |
| 50 | 409100 | H98216 | Hs.42245 | ESTs, Moderately similar to I38022 hypot | 4.9 |
| | 403142 | | | NM_002706*:Homo sapiens protein phosphat | 4.9 |
| | 414300 | A1304870 | Hs.188680 | ESTs | 4.9 |
| | 436607 | AW661783 | Hs.211061 | ESTs | 4.9 |
| | 431553 | X78075 | Hs.2799 | cartilage linking protein 1 | 4.9 |
| 55 | 449328 | A1962493 | Hs.345303 | ESTs | 4.9 |
| | 420805 | L10333 | Hs.99947 | reticulin 1 | 4.9 |
| | 421688 | AK000307 | Hs.106825 | hypothetical protein FLJ20300 | 4.9 |
| | 452898 | AA814497 | Hs.78792 | ESTs | 4.9 |
| | 427958 | AA418000 | Hs.98280 | potassium intermediate/small conductance | 4.9 |
| 60 | 432328 | A1572739 | Hs.195471 | 6-phosphofructo-2-kinase/fructose-2,6-bi | 4.9 |
| | 408453 | A1369838 | Hs.45127 | chondroitin sulfate proteoglycan 5 (neur | 4.8 |
| | 428841 | A418430 | Hs.104935 | ESTs | 4.8 |
| | 416439 | AA180363 | Hs.118769 | ESTs | 4.8 |
| | 447458 | A1741082 | Hs.158961 | ESTs | 4.8 |
| 65 | 429433 | AA452899 | Hs.213586 | ESTs, Weakly similar to KIAA1353 protein | 4.8 |
| | 409746 | NM_004794 | Hs.56294 | RAB33A, member RAS oncogene family | 4.8 |
| | 436511 | AA721252 | Hs.291502 | ESTs | 4.8 |
| | 443392 | A1055821 | Hs.293420 | ESTs | 4.8 |
| | 423600 | A1633559 | Hs.310359 | ESTs | 4.8 |
| 70 | 425905 | AB032959 | Hs.318584 | novel C3HC4 type Zinc finger (ring finger | 4.8 |
| | 414706 | AW340125 | Hs.76589 | KIAA0097 gene product | 4.8 |
| | 407385 | AA610150 | Hs.272072 | ESTs, Weakly similar to I38022 hypothesi | 4.8 |
| | 439340 | AB032436 | Hs.6535 | brain-specific Na-dependent inorganic ph | 4.7 |
| | 427624 | AA406245 | Hs.24895 | ESTs | 4.7 |
| 75 | 413248 | T64858 | Hs.21433 | hypothetical protein DKFZp547J036 | 4.7 |
| | 408670 | AF160967 | Hs.46784 | potassium large conductance calcium-acti | 4.7 |
| | 440491 | R35252 | Hs.130558 | ESTs, Weakly similar to 2109260A B cell | 4.7 |
| | 411555 | AF113537 | Hs.70669 | HMP19 protein | 4.7 |
| | 430471 | AF064845 | Hs.241523 | hypothetical protein FLJ10142 | 4.7 |
| 80 | 413530 | AA130158 | Hs.19977 | ESTs, Moderately similar to ALU8_HUMAN A | 4.7 |
| | 445900 | AF070526 | Hs.125036 | Homo sapiens clone 24787 mRNA sequence | 4.7 |
| | 426457 | AW894667 | Hs.169965 | chimerin (chimaerin) 1 | 4.7 |
| | 459527 | AW977556 | Hs.291735 | ESTs, Weakly similar to I78885 serine/th | 4.7 |
| | 453096 | AW294631 | Hs.11325 | ESTs | 4.7 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 409125 | R17268 | Hs.343567 | axonal transport of synaptic vesicles | 4.7 |
| | 428001 | H97428 | Hs.219907 | ESTs, Moderately similar to Transforming | 4.7 |
| | 410276 | AI554545 | Hs.68301 | angiopoietin-2 | 4.7 |
| 5 | 421637 | AF035290 | Hs.106300 | Homo sapiens clone 23556 mRNA sequence | 4.7 |
| | 421633 | AF121860 | Hs.106260 | sorting nexin 10 | 4.7 |
| | 440052 | AI633744 | Hs.195648 | ESTs, Weakly similar to I38022 hypothe | 4.7 |
| | 439566 | AF086387 | | gb:Homo sapiens full length insert cDNA | 4.7 |
| | 432890 | NM_014442 | Hs.279751 | sialic acid binding Ig-like lectin 8 | 4.6 |
| | 402145 | | | Target Exon | 4.6 |
| 10 | 409892 | AW956113 | Hs.7149 | gb:EST368183 MAGE resequences, MAGD Homo | 4.6 |
| | 458760 | AI498631 | Hs.111334 | ferritin, light polypeptide | 4.6 |
| | 453362 | H14988 | Hs.107375 | ESTs | 4.6 |
| | 436734 | AI937612 | Hs.273758 | hypothetical protein FLJ23112 | 4.6 |
| | 426925 | NM_001196 | Hs.315689 | Homo sapiens cDNA: FLJ22373 fs, clone H | 4.6 |
| 15 | 409041 | AB033025 | Hs.50081 | Hypothetical protein, XP_051860 (KIAA119 | 4.6 |
| | 428832 | AA578229 | Hs.324239 | ESTs, Moderately similar to ZN91_HUMAN Z | 4.6 |
| | 423770 | AW976766 | Hs.132776 | Homo sapiens cDNA FLJ10077 fs, clone HE | 4.6 |
| | 410264 | AK001853 | Hs.61508 | Homo sapiens cDNA FLJ10991 fs, clone PL | 4.6 |
| 20 | 429149 | AW193360 | Hs.197962 | ESTs, Weakly similar to I38022 hypothe | 4.6 |
| | 437762 | T78028 | Hs.154679 | synaptotagmin I | 4.6 |
| | 439249 | AF086060 | Hs.170053 | G-protein coupled receptor 88 | 4.6 |
| | 416426 | AA180256 | Hs.210473 | Homo sapiens cDNA FLJ14872 fs, clone PL | 4.6 |
| | 425256 | BE297611 | Hs.155392 | collapsin response mediator protein 1 | 4.6 |
| 25 | 415257 | F03016 | Hs.27513 | ESTs | 4.6 |
| | 428186 | AW504300 | Hs.295605 | mannosidase, alpha, class 2A, member 2 | 4.6 |
| | 458814 | AI498957 | Hs.170861 | ESTs, Weakly similar to Z195_HUMAN ZINC | 4.6 |
| | 451320 | AW118072 | | diacylglycerol kinase, zeta (104kD) | 4.5 |
| | 424998 | U58515 | Hs.154138 | chitinase 3-like 2 | 4.5 |
| 30 | 422709 | AA315331 | Hs.153485 | ESTs | 4.5 |
| | 420578 | AA813546 | Hs.99034 | GTP-binding protein Rho7 | 4.5 |
| | 421977 | W94197 | Hs.110165 | ribosomal protein L26 homolog | 4.5 |
| | 457465 | AW301344 | Hs.122908 | DNA replication factor | 4.5 |
| | 427712 | AI368024 | Hs.283696 | ESTs | 4.5 |
| 35 | 444656 | AI277924 | Hs.145199 | ESTs | 4.5 |
| | 413409 | AI638418 | Hs.1440 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypep | 4.5 |
| | 429399 | AA452244 | Hs.16727 | ESTs | 4.5 |
| | 450639 | AI703186 | Hs.277174 | ESTs | 4.5 |
| | 452106 | AI141031 | Hs.21342 | ESTs | 4.5 |
| 40 | 424240 | AB023185 | Hs.143535 | calcium/calmodulin-dependent protein kin | 4.5 |
| | 433009 | AA761668 | | gb:nz24c08.s1 NCI_CGAP_GCB1 Homo sapiens | 4.5 |
| | 446657 | AI335191 | Hs.260702 | ESTs, Weakly similar to 2109260A B cell | 4.5 |
| | 428189 | AA424030 | Hs.46627 | ESTs | 4.5 |
| | 423178 | AI033140 | Hs.124983 | Homo sapiens mRNA; cDNA DKFZp564C142 (fr | 4.5 |
| 45 | 445133 | AW157646 | Hs.198689 | ESTs | 4.5 |
| | 418771 | AA807881 | Hs.25329 | ESTs | 4.4 |
| | 438456 | AA913381 | Hs.20594 | ESTs | 4.4 |
| | 410386 | W26187 | Hs.3327 | Homo sapiens cDNA: FLJ22219 fs, clone H | 4.4 |
| | 413834 | BE296896 | Hs.224179 | ESTs, Weakly similar to I38022 hypothe | 4.4 |
| 50 | 419103 | Z40229 | Hs.96423 | hypothetical protein FLJ23033 | 4.4 |
| | 420560 | AW207748 | Hs.59115 | ESTs | 4.4 |
| | 439662 | H97552 | Hs.269060 | ESTs | 4.4 |
| | 408577 | H50572 | Hs.19515 | ESTs, Highly similar to NRG3_HUMAN PRO-N | 4.4 |
| | 445034 | AW293376 | Hs.143659 | ESTs | 4.4 |
| 55 | 402605 | | | Target Exon | 4.4 |
| | 426271 | AF026547 | Hs.169047 | chondroitin sulfate proteoglycan 3 (neur | 4.4 |
| | 457561 | AA331517 | Hs.285055 | chimerin (chimaerin) 2 | 4.4 |
| | 430676 | AF084866 | | gb:Homo sapiens envelope protein RIC-3 (| 4.4 |
| | 439570 | T79925 | Hs.269165 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 4.4 |
| 60 | 452752 | AW044058 | Hs.33578 | KIAA0820 protein | 4.4 |
| | 439108 | AW163034 | Hs.6467 | synaptogyrin 3 | 4.4 |
| | 405819 | | | NM_002578:Homo sapiens p21 (CDKN1A)-acti | 4.4 |
| | 446544 | AI631932 | Hs.7047 | ESTs, Weakly similar to Unknown [H.sapie | 4.4 |
| | 412530 | AA766268 | Hs.266273 | hypothetical protein FLJ13346 | 4.4 |
| 65 | 420871 | AA702972 | Hs.65300 | ESTs | 4.4 |
| | 408622 | AA056060 | Hs.202577 | Homo sapiens cDNA FLJ12166 fs, clone MA | 4.4 |
| | 429269 | AA449013 | Hs.99203 | ESTs | 4.4 |
| | 427463 | AA442224 | Hs.97900 | ESTs | 4.3 |
| | 425402 | AI215881 | Hs.24970 | ESTs, Weakly similar to B34323 GTP-bindi | 4.3 |
| 70 | 412046 | Y07847 | Hs.73088 | RAS-related on chromosome 22 | 4.3 |
| | 427194 | AA399018 | Hs.250835 | ESTs | 4.3 |
| | 437834 | AA769294 | Hs.283854 | gb:nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens | 4.3 |
| | 409172 | Z99399 | Hs.122593 | ESTs | 4.3 |
| | 409953 | AA332277 | Hs.57691 | cadherin 18, type 2 | 4.3 |
| 75 | 426968 | U07616 | Hs.173034 | amphiphysin (Stiff-Mann syndrome with br | 4.3 |
| | 452092 | BE245374 | Hs.27842 | hypothetical protein FLJ11210 | 4.3 |
| | 438458 | AW975186 | | gb:EST387294 MAGE resequences, MAGN Homo | 4.3 |
| | 446936 | H10207 | Hs.47314 | ESTs | 4.3 |
| | 433932 | AW954599 | Hs.169330 | neuronal protein | 4.3 |
| 80 | 424800 | AL035588 | Hs.153203 | MyoD family inhibitor | 4.3 |
| | 421988 | AW450481 | Hs.161333 | ESTs | 4.3 |
| | 442632 | AW206560 | Hs.253569 | ESTs | 4.3 |
| | 416586 | D44643 | Hs.14144 | secreted modular calcium-binding protein | 4.2 |
| | 408369 | R38438 | Hs.182575 | solute carrier family 15 (H???) transport | 4.2 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 450530 | NM_006668 | Hs.25121 | cytochrome P450, subfamily 46 (cholester | 4.2 |
| | 449318 | AW236021 | Hs.78531 | Homo sapiens, Similar to RIKEN cDNA 5730 | 4.2 |
| | 438624 | AA889055 | Hs.123468 | ESTs | 4.2 |
| | 421027 | AA761198 | Hs.55254 | ESTs | 4.2 |
| 5 | 417632 | R20855 | Hs.5422 | glycoprotein M6B | 4.2 |
| | 419412 | AW161058 | Hs.90297 | synuclein, beta | 4.2 |
| | 430228 | AW950939 | Hs.6382 | ESTs, Highly similar to T00391 hypotheti | 4.2 |
| | 450813 | AI739625 | Hs.203376 | ESTs | 4.2 |
| | 412505 | AA974491 | Hs.21734 | ESTs | 4.2 |
| 10 | 440168 | AA868507 | Hs.126141 | ESTs | 4.2 |
| | 441707 | R42637 | Hs.21963 | hypothetical protein DKFZp761B0514 | 4.2 |
| | 438703 | AI803373 | Hs.31599 | ESTs | 4.2 |
| | 444127 | N63620 | Hs.13281 | ESTs | 4.2 |
| | 447397 | BE247676 | Hs.18442 | E-1 enzyme | 4.2 |
| 15 | 445523 | Z30118 | Hs.293788 | ESTs, Moderately similar to unnamed prot | 4.2 |
| | 415079 | R43179 | Hs.22895 | hypothetical protein FLJ23548 | 4.2 |
| | 416871 | H98716 | | gb:yx13d08.s1 Soares melanocyte 2NbHM Ho | 4.2 |
| | 408838 | AI669535 | Hs.40369 | ESTs | 4.2 |
| 20 | 425287 | R88249 | Hs.155524 | peanut (Drosophila)-like 2 | 4.2 |
| | 404584 | | | Target Exon | 4.2 |
| | 436035 | AA703679 | Hs.106999 | ESTs, Weakly similar to SYT5_HUMAN SYNAP | 4.2 |
| | 409091 | AW970386 | Hs.269423 | ESTs | 4.2 |
| | 437117 | AL049256 | Hs.122593 | ESTs | 4.2 |
| 25 | 429643 | AA455889 | Hs.167279 | FYVE-finger-containing Rab5 effector pro | 4.2 |
| | 439231 | AW581935 | Hs.141480 | Homo sapiens mRNA; cDNA DKFZp434N079 (fr | 4.2 |
| | 408177 | AI241733 | Hs.43871 | ESTs | 4.2 |
| | 438875 | AA827640 | Hs.189059 | ESTs | 4.2 |
| | 447877 | AI435184 | Hs.164252 | ESTs | 4.2 |
| 30 | 415402 | AA164687 | Hs.177576 | mannosyl (alpha-1,3)-glycoprotein beta- | 4.2 |
| | 434859 | BE255080 | Hs.299315 | collapsin response mediator protein-5; C | 4.2 |
| | 449714 | AB033015 | Hs.23941 | KIAA1189 protein | 4.2 |
| | 427315 | AA179949 | Hs.175563 | Homo sapiens mRNA; cDNA DKFZp564N0763 (f | 4.2 |
| | 404541 | | | NM_030795:Homo sapiens stathmin-like 4 (| 4.1 |
| 35 | 449969 | AW295142 | Hs.180187 | Homo sapiens cDNA FLJ14337 fis, clone PL | 4.1 |
| | 422374 | AW732869 | Hs.1519 | protein kinase, cAMP-dependent, regulato | 4.1 |
| | 422253 | WB1526 | Hs.118329 | ESTs, Moderately similar to GAD_HUMAN GA | 4.1 |
| | 440483 | AI200836 | Hs.150386 | ESTs | 4.1 |
| | 429421 | AL031658 | | Human DNA sequence from clone RP1-310013 | 4.1 |
| 40 | 432882 | NM_013257 | Hs.279696 | serum/glucocorticoid regulated kinase-li | 4.1 |
| | 424001 | W67883 | Hs.137476 | paternally expressed 10 | 4.1 |
| | 422170 | AI791949 | Hs.112432 | anti-Mullerian hormone | 4.1 |
| | 445292 | AV653264 | Hs.13982 | Homo sapiens cDNA FLJ14666 fis, clone NT | 4.1 |
| | 450407 | NM_000810 | Hs.24969 | gamma-aminobutyric acid (GABA) A recepto | 4.1 |
| 45 | 429401 | AW296102 | Hs.99272 | ESTs, Weakly similar to S32567 A4 protei | 4.1 |
| | 408950 | AA707814 | Hs.14945 | long fatty acyl-CoA synthetase 2 gene | 4.1 |
| | 415796 | R87548 | Hs.78854 | ATPase, Na ⁺ transporting, beta 2 polypep | 4.1 |
| | 446619 | AU076643 | Hs.313 | secreted phosphoprotein 1 (osteopontin, | 4.1 |
| | 457211 | AW972565 | Hs.32399 | ESTs, Weakly similar to S51797 vasodilat | 4.1 |
| | 416547 | H62914 | Hs.268946 | ESTs, Weakly similar to PC4259 ferritin | 4.1 |
| 50 | 412777 | AI335773 | Hs.270123 | ESTs | 4.1 |
| | 445225 | AI216555 | Hs.202398 | ESTs | 4.1 |
| | 408926 | AF217525 | Hs.49002 | Down syndrome cell adhesion molecule | 4.1 |
| | 417873 | BE266659 | Hs.293659 | Homo sapiens, Similar to RIKEN cDNA A430 | 4.1 |
| 55 | 443301 | AI733614 | Hs.220587 | ESTs, Moderately similar to ALU5_HUMAN A | 4.1 |
| | 429281 | AA830856 | Hs.29808 | Homo sapiens cDNA: FLJ21122 fis, clone C | 4.1 |
| | 448966 | AW372914 | Hs.86149 | phosphoinositol 3-phosphate-binding prot | 4.1 |
| | 453857 | AL080235 | Hs.35861 | DKFZP586E1621 protein | 4.1 |
| | 417355 | D13168 | Hs.82002 | endothelin receptor type B | 4.1 |
| 60 | 410359 | R38624 | Hs.106313 | ESTs | 4.1 |
| | 426529 | AF090100 | Hs.170241 | Homo sapiens clone IMAGE 23915 | 4.1 |
| | 433323 | AA805132 | Hs.159142 | ESTs | 4.1 |
| | 434933 | R91095 | Hs.4276 | KIAA1701 protein | 4.1 |
| | 453331 | AI240665 | | ESTs | 4.1 |
| 65 | 422661 | NM_014700 | Hs.119004 | KIAA0665 gene product | 4.1 |
| | 424726 | AK001007 | Hs.138760 | Homo sapiens cDNA FLJ10145 fis, clone HE | 4.0 |
| | 416805 | F13271 | Hs.79981 | Human clone 23560 mRNA sequence | 4.0 |
| | 441797 | AI936933 | Hs.214635 | ESTs | 4.0 |
| | 424282 | R76421 | Hs.135694 | ESTs | 4.0 |
| 70 | 407792 | AI077715 | Hs.39384 | putative secreted ligand homologous to l | 4.0 |
| | 425390 | AI092634 | Hs.156114 | protein tyrosine phosphatase, non-recept | 4.0 |
| | 453312 | AJ243396 | Hs.4865 | voltage-gated sodium channel beta-3 subu | 4.0 |
| | 424635 | AA420687 | Hs.115455 | Homo sapiens cDNA FLJ14259 fis, clone PL | 4.0 |
| | 423279 | AW959861 | Hs.290943 | ESTs | 4.0 |
| | 444001 | AI095087 | Hs.152299 | ESTs, Moderately similar to S65657 alpha | 4.0 |
| 75 | 410768 | AF038185 | Hs.66187 | Homo sapiens clone 23700 mRNA sequence | 4.0 |
| | 426413 | AA377823 | | gb:EST90805 Synovial sarcoma Homo sapien | 4.0 |
| | 450581 | AF081513 | Hs.25195 | TGF-beta 4 | 4.0 |
| | 435854 | AJ278120 | Hs.4996 | putative ankyrin-repeat containing prote | 4.0 |
| 80 | 433615 | AA732982 | Hs.269607 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 4.0 |
| | 432058 | AW665996 | Hs.130729 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 4.0 |
| | 439774 | AL360257 | Hs.213493 | Homo sapiens mRNA full length insert cDN | 4.0 |
| | 445666 | R59960 | Hs.282386 | ESTs | 4.0 |
| | 450582 | AI339732 | | G-rich RNA sequence binding factor 1 | 4.0 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 437814 | AI088192 | Hs.135474 | ESTs, Weakly similar to DDX9_HUMAN ATP-D | 4.0 |
| | 451468 | AW503398 | Hs.293663 | ESTs, Moderately similar to I38022 hypot | 4.0 |
| | 449277 | AA001064 | Hs.43670 | ESTs | 4.0 |
| 5 | 440553 | AA889416 | Hs.344043 | Homo sapiens cDNA FLJ14459 fis, clone HE | 4.0 |
| | 445888 | AF070564 | Hs.13415 | Homo sapiens clone 24571 mRNA sequence | 4.0 |
| | 420111 | AA255652 | | gb:z521h11.1 NCI_CGAP_GC81 Homo sapiens | 4.0 |
| | 407198 | H91679 | | gb:yy04a07.s1 Soares fetal liver spleen | 4.0 |
| | 422564 | AI148006 | Hs.222120 | ESTs | 4.0 |
| 10 | 443992 | AW022228 | Hs.322922 | ESTs | 4.0 |
| | 435542 | AA687376 | | ESTs | 4.0 |
| | 444153 | AK001610 | Hs.10414 | hypothetical protein FLJ10748 | 4.0 |
| | 437748 | AF234882 | Hs.5814 | suppression of tumorigenicity 7 | 4.0 |
| | 439285 | AL133916 | | hypothetical protein FLJ20093 | 4.0 |
| 15 | 449655 | AI021987 | Hs.59970 | ESTs | 4.0 |
| | 458435 | AI418718 | Hs.144121 | ESTs, Weakly similar to T46916 hypotheti | 4.0 |
| | 412659 | AW753865 | Hs.74376 | olfactomedin related ER localized protei | 4.0 |
| | 423905 | AW579960 | Hs.135150 | lung type-I cell membrane-associated gly | 4.0 |
| | 432683 | AW995441 | Hs.10475 | ESTs | 4.0 |
| 20 | 410765 | AI694972 | Hs.66180 | nucleosome assembly protein 1-like 2 | 4.0 |
| | 420649 | AI866964 | Hs.124704 | ESTs, Moderately similar to S65657 alpha | 4.0 |
| | 450927 | AI807804 | Hs.134342 | TASP for testis-specific adriamycin sens | 4.0 |
| | 448985 | AA324885 | Hs.22777 | carbonic anhydrase XI | 4.0 |
| | 416406 | D86961 | Hs.79299 | tipoma HMGC fusion partner-like 2 | 4.0 |
| 25 | 412754 | AW160375 | Hs.74565 | amyloid beta (A4) precursor-like protein | 3.9 |
| | 416340 | N31772 | Hs.79226 | fasciculation and elongation protein zet | 3.9 |
| | 428862 | NM_000346 | Hs.2316 | SRY (sex determining region Y)-box 9 (ca | 3.9 |
| | 413554 | AA319146 | Hs.75426 | secretogranin II (chromogranin C) | 3.9 |
| | 419687 | AI638859 | Hs.227699 | ESTs, Weakly similar to T2D3_HUMAN TRANS | 3.9 |
| 30 | 453438 | AI469935 | Hs.22792 | ESTs | 3.9 |
| | 410082 | AA081594 | Hs.158311 | Musashi (Drosophila) homolog 1 | 3.9 |
| | 424736 | AF230877 | Hs.152701 | microtubule-interacting protein that ass | 3.9 |
| | 412326 | R07566 | Hs.73817 | small inducible cytokine A3 (homologous | 3.9 |
| | 411666 | AF106564 | Hs.71346 | neurofilament 3 (150kD medium) | 3.9 |
| 35 | 439935 | S75105 | Hs.8358 | glutamate receptor, ionotropic, kainate | 3.9 |
| | 459278 | AW294659 | Hs.34054 | Homo sapiens cDNA: FLJ22488 fis, clone H | 3.9 |
| | 432809 | AA565509 | Hs.131703 | ESTs | 3.9 |
| | 450568 | AL050078 | Hs.25159 | Homo sapiens cDNA FLJ10784 fis, clone NT | 3.9 |
| | 413951 | AW051200 | Hs.75640 | natriuretic peptide precursor A | 3.9 |
| 40 | 435743 | T66861 | Hs.12962 | ESTs | 3.9 |
| | 447937 | AL109716 | Hs.20034 | Homo sapiens mRNA full length insert cDN | 3.9 |
| | 417576 | AA339449 | Hs.82285 | phosphoribosylglycinamide formyltransfer | 3.9 |
| | 448526 | AB028946 | Hs.21361 | KIAA1023 protein | 3.9 |
| | 445890 | AF055019 | Hs.21906 | Homo sapiens clone 24670 mRNA sequence | 3.9 |
| 45 | 425241 | AA324624 | Hs.155247 | aldolase C, fructose-bisphosphate | 3.8 |
| | 417333 | AL157545 | Hs.173179 | bromodomain and PHD finger containing, 3 | 3.8 |
| | 435832 | AA425688 | Hs.41641 | Bruno (Drosophila) -like 4, RNA binding | 3.8 |
| | 410592 | R94088 | Hs.43569 | ESTs | 3.8 |
| | 443361 | AI792628 | Hs.133273 | ESTs | 3.8 |
| 50 | 403696 | | | C4001100*:gil5852342[gb]AAD54015.1] (AF0 | 3.8 |
| | 437756 | AA767537 | Hs.197096 | ESTs | 3.8 |
| | 433675 | AW977653 | Hs.75319 | ribonucleotide reductase M2 polypeptide | 3.8 |
| | 414998 | NM_002543 | Hs.77729 | oxidised low density lipoprotein (lectin | 3.8 |
| | 425652 | AB021742 | Hs.322431 | neurogenic differentiation 2 | 3.8 |
| 55 | 437449 | AL390153 | Hs.208339 | Homo sapiens mRNA; cDNA DKFZp762G113 (fr | 3.8 |
| | 421040 | AA715026 | Hs.135280 | ESTs | 3.8 |
| | 454171 | AW854832 | | gb:QV2-CT0261-201099-011-405 CT0261 Homo | 3.8 |
| | 443740 | R56434 | Hs.21062 | ESTs | 3.8 |
| | 441668 | AI611973 | Hs.136313 | ESTs | 3.8 |
| 60 | 423175 | W27595 | Hs.347310 | hypothetical protein FLJ14627 | 3.8 |
| | 457183 | H91882 | Hs.118569 | Dvl-binding protein IDAX (inhibition of | 3.8 |
| | 438142 | T90309 | Hs.269651 | ESTs | 3.8 |
| | 408875 | NM_015434 | Hs.48604 | DKFZP434B168 protein | 3.8 |
| | 436899 | AA764852 | Hs.291567 | ESTs | 3.8 |
| 65 | 456497 | AW967956 | Hs.123648 | ESTs, Weakly similar to AF108460 1 ubinu | 3.8 |
| | 416892 | L24498 | Hs.80409 | growth arrest and DNA-damage-inducible, | 3.8 |
| | 413199 | M62843 | Hs.75236 | ELAV (embryonic lethal, abnormal vision, | 3.8 |
| | 410711 | AB002316 | Hs.65746 | KIAA0318 protein | 3.8 |
| | 454117 | BE410100 | Hs.40368 | adaptor-related protein complex 1, sigma | 3.8 |
| 70 | 438944 | AA302517 | Hs.92732 | KIAA1444 protein | 3.8 |
| | 445078 | AI869975 | Hs.4775 | junctional protein 3 | 3.8 |
| | 424330 | AW073953 | Hs.333396 | Homo sapiens cDNA FLJ13596 fis, clone PL | 3.8 |
| | 439099 | AB037800 | Hs.6462 | protein kinase C and casein kinase subst | 3.8 |
| | 449444 | AW818436 | Hs.23590 | solute carrier family 16 (monocarboxylic | 3.8 |
| 75 | 411252 | AB018549 | Hs.69328 | MD-2 protein | 3.7 |
| | 448275 | BE514434 | Hs.20830 | kinesin-like 2 | 3.7 |
| | 434269 | AK001991 | Hs.3781 | similar to murine leucine-rich repeat pr | 3.7 |
| | 400777 | | | NM_007325*:Homo sapiens glutamate recept | 3.7 |
| | 419586 | AI088485 | Hs.144759 | ESTs, Weakly similar to I38022 hypotheti | 3.7 |
| 80 | 458072 | AI890347 | Hs.271923 | Homo sapiens cDNA: FLJ22785 fis, clone K | 3.7 |
| | 445908 | R13580 | Hs.13436 | Homo sapiens clone 24425 mRNA sequence | 3.7 |
| | 448451 | AW015994 | Hs.345433 | gb:UH-B10p-abh-g-09-0-ULs1 NCI_CGAP_S | 3.7 |
| | 430183 | BE010038 | | gb:PM3-BN0176-100400-001-g04 BN0176 Homo | 3.7 |
| | 430147 | R60704 | Hs.234434 | hairly/enhancer-of-split related with YRP | 3.7 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 458912 | AJ911066 | Hs. | ESTs | 3.7 |
| | 428110 | AI312485 | Hs.138294 | ESTs, Moderately similar to Z195_HUMAN Z | 3.7 |
| | 448048 | BE281291 | Hs.170408 | ESTs, Moderately similar to A47582 B-cel | 3.7 |
| | 442326 | H92962 | Hs.124813 | hypothetical protein MGC14817 | 3.7 |
| 5 | 422798 | R92347 | Hs.34574 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.7 |
| | 428873 | AI701609 | Hs.98908 | ESTs | 3.7 |
| | 438208 | AL041224 | Hs.65379 | ESTs | 3.7 |
| | 414040 | N58513 | Hs.32171 | ESTs | 3.7 |
| 10 | 407846 | AA426202 | Hs.40403 | Cbp/p300-interacting transactivator, wit | 3.7 |
| | 408829 | NM_006042 | Hs.48384 | heparan sulfate (glucosamine) 3-O-sulfot | 3.7 |
| | 425010 | T16837 | Hs.4241 | ESTs | 3.7 |
| | 427209 | H06509 | Hs.92423 | KIAA1566 protein | 3.7 |
| | 407603 | AW955705 | Hs.62604 | Homo sapiens, clone IMAGE:4299322, mRNA, | 3.6 |
| | 410126 | BE169274 | | KIAA0036 gene product | 3.6 |
| 15 | 426646 | AA382787 | Hs.122713 | ESTs | 3.6 |
| | 418329 | AW247430 | Hs.84152 | cystathionine-beta-synthase | 3.6 |
| | 419390 | AI701162 | Hs.90207 | hypothetical protein MGC11138 | 3.6 |
| | 441703 | AW390054 | Hs.192843 | leucine zipper protein FKSG14 | 3.6 |
| | 431725 | X65724 | Hs.2839 | Norrie disease (pseudoglioma) | 3.6 |
| 20 | 448425 | AI500359 | Hs.346112 | ESTs | 3.6 |
| | 423611 | AB011163 | Hs.129908 | KIAA0591 protein | 3.6 |
| | 438831 | BE263273 | Hs.6439 | synapsin II | 3.6 |
| | 419235 | AW470411 | Hs.288433 | neurotrimin | 3.6 |
| | 451027 | AW519204 | Hs.40808 | ESTs | 3.6 |
| 25 | 428483 | AI908539 | Hs.184592 | KIAA0344 gene product | 3.6 |
| | 424947 | R77952 | | ESTs, Weakly similar to alternatively sp | 3.6 |
| | 404150 | | | Target Exon | 3.6 |
| | 450297 | AW901347 | Hs.38592 | hypothetical protein FLJ23342 | 3.6 |
| | 443715 | AI583187 | Hs.9700 | cyclin E1 | 3.6 |
| 30 | 435910 | AI084152 | Hs.21782 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 3.6 |
| | 418064 | BE387287 | Hs.83384 | S100 calcium-binding protein, beta (neur | 3.6 |
| | 432488 | AA551010 | Hs.216640 | ESTs | 3.6 |
| | 431342 | AW971018 | Hs.21659 | ESTs | 3.6 |
| | 437916 | BE566249 | Hs.20999 | hypothetical protein FLJ23142 | 3.6 |
| 35 | 412043 | BE156622 | Hs.333371 | Homo sapiens clone TA40 untranslated mRNA | 3.6 |
| | 448448 | NM_014954 | Hs.21239 | KIAA0985 protein | 3.6 |
| | 447818 | W79940 | Hs.21906 | Homo sapiens clone 24670 mRNA sequence | 3.6 |
| | 445105 | AF238869 | Hs.283955 | Homo sapiens clone GLSH-2 similar to gli | 3.6 |
| | 409557 | BE182896 | Hs.211193 | ESTs | 3.6 |
| 40 | 425202 | AW962282 | Hs.152049 | ESTs, Weakly similar to I38022 hypotheti | 3.6 |
| | 451734 | NM_006176 | Hs.26944 | neurogranin (protein kinase C substrate, | 3.6 |
| | 425331 | AW962128 | | gb:EST374201 MAGE resequences, MAGG Homo | 3.6 |
| | 412799 | AI267606 | | gb:aq91h03.x1 Stanley Frontal S8 pool 1 | 3.6 |
| | 435040 | AI932350 | Hs.152825 | ESTs | 3.6 |
| 45 | 434149 | Z43829 | Hs.244624 | hypothetical protein MGC5469 | 3.6 |
| | 415709 | AA649850 | Hs.278558 | ESTs | 3.6 |
| | 424051 | AL110203 | Hs.138411 | Homo sapiens mRNA; cDNA DKFZp586J1922 (f | 3.6 |
| | 437640 | AA764893 | Hs.272155 | ESTs, Weakly similar to I38022 hypotheti | 3.6 |
| | 445953 | AI612775 | Hs.145710 | ESTs | 3.6 |
| 50 | 449256 | AA059050 | Hs.59847 | ESTs | 3.6 |
| | 424687 | J05070 | Hs.151738 | matrix metalloproteinase 9 (gelatinase B | 3.6 |
| | 409327 | L41162 | Hs.53563 | collagen, type IX, alpha 3 | 3.6 |
| | 417675 | AI808607 | Hs.3781 | similar to murine leucine-rich repeat pr | 3.6 |
| | 423641 | AL137256 | Hs.130489 | ATPase, aminophospholipid transporter-li | 3.6 |
| 55 | 443912 | R37257 | Hs.184780 | ESTs | 3.6 |
| | 424572 | M19650 | | 2',3'-cyclic nucleotide 3' phosphodiester | 3.5 |
| | 424899 | AL119387 | Hs.119062 | ESTs | 3.5 |
| | 439726 | AW449893 | Hs.293707 | ESTs, Weakly similar to I38598 zinc fing | 3.5 |
| | 416490 | AF090116 | Hs.79348 | regulator of G-protein signalling 7 | 3.5 |
| 60 | 458809 | AW972512 | Hs.20985 | sin3-associated polypeptide, 30kD | 3.5 |
| | 429084 | AJ001443 | Hs.195614 | splicing factor 3b, subunit 3, 130kD | 3.5 |
| | 407624 | AW157431 | Hs.248941 | ESTs | 3.5 |
| | 419038 | AW134924 | Hs.190325 | ESTs | 3.5 |
| 65 | 451489 | NM_005503 | Hs.26468 | amyloid beta (A4) precursor protein-bind | 3.5 |
| | 428242 | H55709 | Hs.2250 | leukemia inhibitory factor (cholinergic | 3.5 |
| | 411048 | AK001742 | Hs.67991 | hypothetical protein DKFZp434G0522 | 3.5 |
| | 435575 | AF213457 | Hs.44234 | triggering receptor expressed on myeloid | 3.5 |
| | 424340 | AA339036 | Hs.7033 | ESTs | 3.5 |
| | 425790 | AW136286 | Hs.288446 | ESTs | 3.5 |
| 70 | 432188 | AI362952 | Hs.2928 | solute carrier family 7 (cationic amino | 3.5 |
| | 453896 | AW293483 | Hs.255205 | KIAA1853 protein | 3.5 |
| | 434784 | AA649051 | Hs.164007 | ESTs | 3.5 |
| | 452449 | AW068658 | Hs.20943 | ESTs | 3.5 |
| | 425212 | AW962253 | Hs.171618 | ESTs | 3.5 |
| 75 | 407253 | AA411175 | Hs.141939 | ESTs, Moderately similar to S65657 alpha | 3.5 |
| | 418049 | AA211467 | Hs.190488 | Homo sapiens, Similar to nuclear localiz | 3.5 |
| | 421247 | BE391727 | Hs.102910 | general transcription factor IIH, polype | 3.5 |
| | 459311 | R40192 | Hs.21527 | Human DNA sequence from clone GS1-115M3 | 3.5 |
| 80 | 439450 | R51613 | Hs.125304 | ESTs | 3.5 |
| | 435545 | AA687415 | Hs.28107 | ESTs | 3.5 |
| | 445729 | H21066 | Hs.13223 | Homo sapiens mRNA full length insert cDN | 3.5 |
| | 448999 | AF179274 | Hs.22791 | transmembrane protein with EGF-like and | 3.5 |
| | 412590 | AL134388 | Hs.135033 | ESTs, Weakly similar to I38022 hypotheti | 3.5 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 438527 | AI969251 | Hs.115325 | RAB7, member RAS oncogene family-like 1 | 3.5 |
| | 441111 | AI806887 | Hs.126594 | ESTs | 3.5 |
| | 418630 | AI351311 | Hs.251946 | poly(A)-binding protein, cytoplasmic 1-J | 3.5 |
| | 439920 | H05430 | Hs.288433 | neurotrophin | 3.5 |
| 5 | 421268 | AI126821 | Hs.30514 | ESTs | 3.5 |
| | 432022 | AL162042 | Hs.272348 | Homo sapiens mRNA; cDNA DKFZp761L1212 (I | 3.5 |
| | 412719 | AWD16610 | Hs.816 | ESTs | 3.5 |
| | 435092 | AL137310 | Hs.4749 | Homo sapiens mRNA; cDNA DKFZp761E13121 (| 3.5 |
| 10 | 414178 | AW957372 | Hs.46791 | ESTs, Weakly similar to I38022 hypothe | 3.5 |
| | 437252 | AI433833 | Hs.164159 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.5 |
| | 452108 | AW135982 | Hs.203013 | hypothetical protein FLJ12748 | 3.4 |
| | 421183 | AL135740 | Hs.102447 | TSC-22-like | 3.4 |
| | 441834 | AL138034 | Hs.7979 | KIAA0736 gene product | 3.4 |
| | 413812 | AW188687 | Hs.44748 | ESTs | 3.4 |
| 15 | 449932 | AI675444 | Hs.263024 | ESTs | 3.4 |
| | 447067 | RA2098 | Hs.21964 | ESTs | 3.4 |
| | 408296 | AL117452 | Hs.44155 | DKFZP586G1517 protein | 3.4 |
| | 447028 | AI973128 | Hs.167257 | brain link protein-1 | 3.4 |
| 20 | 432715 | AA247152 | Hs.200483 | ESTs, Weakly similar to KIAA1074 protein | 3.4 |
| | 418358 | L02840 | Hs.84244 | potassium voltage-gated channel, Shab-re | 3.4 |
| | 417084 | H08370 | Hs.33067 | ESTs | 3.4 |
| | 444534 | AW271626 | Hs.42294 | ESTs | 3.4 |
| | 440700 | AW952281 | Hs.296184 | guanine nucleotide binding protein (G pr | 3.4 |
| 25 | 436637 | AI783629 | Hs.26765 | ESTs | 3.4 |
| | 412820 | BE001236 | | gb:CM3-BN0075-240200-101-d11 BN0075 Homo | 3.4 |
| | 428138 | AA773842 | Hs.293799 | ESTs | 3.4 |
| | 453033 | AA325869 | Hs.31463 | KIAA0281 gene product | 3.4 |
| | 453305 | R39224 | Hs.267997 | EHM2 gene | 3.4 |
| 30 | 459660 | M79082 | | ESTs | 3.4 |
| | 418821 | AA436002 | Hs.183161 | ESTs | 3.4 |
| | 439518 | W76326 | | gb:zd60d04.r1 Soares_fetal_heart_NbHH19W | 3.4 |
| | 400379 | NM_018432 | | Homo sapiens ovarian cancer related prot | 3.4 |
| | 437085 | AA743935 | Hs.202329 | ESTs | 3.4 |
| 35 | 419852 | AW503756 | Hs.286184 | hypothetical protein dJ55102.5 | 3.4 |
| | 430694 | AA810624 | Hs.30936 | ESTs, Weakly similar to H2BH_HUMAN HISTO | 3.4 |
| | 441287 | AW293132 | Hs.131373 | ESTs | 3.4 |
| | 425870 | R13406 | Hs.56782 | ESTs | 3.4 |
| | 443672 | AA323362 | Hs.9667 | butyrobetaine (gamma), 2-oxoglutarate di | 3.4 |
| 40 | 448044 | AI458682 | | gb:tk13e01.x1 NCI_CGAP_Lu24 Homo sapiens | 3.4 |
| | 405238 | | | Target Exon | 3.4 |
| | 440404 | AI015881 | Hs.324527 | mitochondrial ribosomal protein S5 | 3.4 |
| | 453990 | AF150278 | Hs.33578 | KIAA0820 protein | 3.4 |
| | 450756 | AI733488 | Hs.144062 | ESTs | 3.4 |
| 45 | 404283 | | | ENSP00000244751: Copine-like protein KIA | 3.4 |
| | 423257 | AW161039 | Hs.125878 | synapsin III | 3.4 |
| | 432149 | AW614326 | Hs.133483 | ESTs, Weakly similar to T34549 probable | 3.4 |
| | 412986 | X81120 | Hs.75110 | cannabinoid receptor 1 (brain) | 3.4 |
| | 422809 | AK001379 | Hs.121028 | hypothetical protein FLJ10549 | 3.4 |
| 50 | 420050 | AL118615 | Hs.94653 | neurochondrin | 3.4 |
| | 431789 | H19500 | Hs.269222 | mitogen-activated protein kinase 4 | 3.4 |
| | 408601 | U47928 | Hs.86122 | protein A | 3.4 |
| | 453740 | AL120295 | Hs.311809 | ESTs, Moderately similar to PC4259 ferri | 3.4 |
| | 449919 | AI674685 | Hs.200141 | ESTs | 3.4 |
| 55 | 426380 | AI291267 | Hs.149990 | ESTs | 3.4 |
| | 408554 | AA836381 | Hs.315111 | nuclear receptor co-repressor/HDAC3 comp | 3.3 |
| | 443257 | AI334040 | Hs.11614 | HSPC065 protein | 3.3 |
| | 432731 | R31178 | Hs.287820 | fibronectin 1 | 3.3 |
| | 421679 | AI475110 | Hs.203933 | ESTs | 3.3 |
| 60 | 453169 | AB037815 | Hs.32156 | KIAA1394 protein | 3.3 |
| | 437397 | AA349847 | Hs.4221 | hypothetical protein DKFZp761H039 | 3.3 |
| | 443310 | BE552018 | Hs.133152 | ESTs | 3.3 |
| | 423169 | BE047009 | Hs.21837 | ESTs, Weakly similar to KIAA0927 protein | 3.3 |
| | 433657 | AI244368 | Hs.8124 | PH domain containing protein in retina 1 | 3.3 |
| 65 | 408449 | NM_004408 | Hs.166161 | dynamitin 1 | 3.3 |
| | 417402 | BE503227 | Hs.134759 | ESTs | 3.3 |
| | 416677 | T83470 | Hs.334840 | ESTs, Moderately similar to I76885 serin | 3.3 |
| | 439753 | BE262233 | Hs.7423 | hypothetical protein from EUROIMAGE 2168 | 3.3 |
| | 455646 | BE064420 | | gb:RC4-BT0311-241199-012-c08 BT0311 Homo | 3.3 |
| 70 | 450337 | AI693256 | Hs.202427 | ESTs | 3.3 |
| | 423420 | AI571364 | Hs.128382 | Homo sapiens mRNA; cDNA DKFZp761I1224 (I | 3.3 |
| | 433236 | NM_004296 | Hs.3221 | regulator of G-protein signalling 6 | 3.3 |
| | 417868 | AI078534 | Hs.122592 | ESTs | 3.3 |
| | 436207 | AA334774 | Hs.12845 | hypothetical protein MGC13159 | 3.3 |
| 75 | 441607 | NM_005010 | Hs.7912 | neuronal cell adhesion molecule | 3.3 |
| | 449249 | T52285 | Hs.193115 | Homo sapiens mRNA for KIAA1764 protein, | 3.3 |
| | 418216 | AA662240 | Hs.283099 | AF15q14 protein | 3.3 |
| | 458060 | C14904 | Hs.45184 | Homo sapiens cDNA FLJ12284 fis, clone MA | 3.3 |
| | 449145 | AI632122 | Hs.198408 | ESTs | 3.3 |
| 80 | 415101 | RA5531 | Hs.144534 | ESTs | 3.3 |
| | 401272 | | | C9000559:gij12314195jmbjCAB99338.1j(A | 3.3 |
| | 420297 | AI628272 | Hs.88323 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.3 |
| | 419991 | AI000098 | Hs.94210 | eyes absent (Drosophila) homolog 1 | 3.3 |
| | 443761 | AI525743 | Hs.345187 | ESTs | 3.3 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 427317 | AB028955 | Hs.175780 | KIAA1032 protein | 3.3 |
| | 426920 | AA393351 | Hs.132121 | ESTs | 3.3 |
| | 433894 | AI907682 | Hs.243293 | ESTs | 3.3 |
| 5 | 454253 | AV660717 | Hs.47144 | DKFZP586N0819 protein | 3.3 |
| | 419647 | AA348947 | Hs.91816 | hypothetical protein | 3.3 |
| | 439978 | BE139460 | Hs.124673 | Homo sapiens cDNA FLJ11477 fis, clone HE | 3.3 |
| | 407881 | AW072003 | Hs.40968 | heparan sulfate (glucosamine) 3-O-sulfot | 3.3 |
| | 428670 | AA431682 | Hs.134832 | ESTs | 3.3 |
| 10 | 435375 | AI733610 | Hs.187832 | ESTs | 3.3 |
| | 419043 | T19167 | Hs.89566 | ets variant gene 1 | 3.3 |
| | 403341 | | | Target Exon | 3.3 |
| | 436282 | R91913 | Hs.272104 | ESTs, Moderately similar to ALU1_HUMAN A | 3.3 |
| | 439627 | BE621702 | Hs.29076 | hypothetical protein FLJ21841 | 3.3 |
| 15 | 456209 | W60633 | Hs.297792 | ESTs | 3.3 |
| | 438810 | AW897846 | Hs.6421 | hypothetical protein DKFZp761N09121 | 3.3 |
| | 411565 | AW851728 | | gb:MR2-CT0222-011199-007-d06 CT0222 Homo | 3.3 |
| | 418203 | X54942 | Hs.83758 | CDC28 protein kinase 2 | 3.3 |
| | 451254 | AI571016 | Hs.172967 | ESTs | 3.3 |
| 20 | 435056 | AW023337 | Hs.5422 | glycoprotein M6B | 3.3 |
| | 433842 | AI652156 | Hs.26346 | ESTs | 3.3 |
| | 433325 | AW206986 | Hs.143905 | ESTs | 3.3 |
| | 451066 | AI758660 | Hs.206132 | ESTs | 3.3 |
| | 436114 | AA778232 | Hs.19515 | ESTs, Highly similar to NRG3_HUMAN PRO-N | 3.3 |
| 25 | 421586 | AB011156 | Hs.106794 | KIAA0584 protein | 3.3 |
| | 429228 | AI553633 | Hs.326447 | ESTs | 3.3 |
| | 450325 | AI935962 | Hs.26289 | ESTs | 3.3 |
| | 412350 | AI659306 | Hs.73826 | protein tyrosine phosphatase, non-recept | 3.3 |
| | 451778 | AI826131 | Hs.62954 | ESTs, Weakly similar to zinc finger prot | 3.3 |
| 30 | 435977 | AL138079 | Hs.5012 | brain-specific membrane-anchored protein | 3.2 |
| | 450475 | AW805634 | Hs.205015 | ESTs | 3.2 |
| | 418661 | NM_001949 | Hs.1189 | E2F transcription factor 3 | 3.2 |
| | 436480 | AJ271643 | Hs.87469 | putative acid-sensing ion channel | 3.2 |
| | 407332 | AI801565 | Hs.200113 | Homo sapiens cDNA FLJ11379 fis, clone HE | 3.2 |
| 35 | 415131 | D61119 | | gb:HUM158C118 Clontech human fetal brain | 3.2 |
| | 409248 | AB033035 | Hs.51965 | KIAA1209 protein | 3.2 |
| | 431462 | AW583672 | Hs.256311 | granin-like neuroendocrine peptide precu | 3.2 |
| | 434834 | AF156774 | Hs.324020 | 1-acylglycerol-3-phosphate O-acyltransfe | 3.2 |
| | 450358 | AB010098 | Hs.24907 | coronin, actin-binding protein, 2B | 3.2 |
| 40 | 438461 | AW075485 | Hs.286049 | phosphoserine aminotransferase | 3.2 |
| | 405239 | U89281 | | oxidative 3 alpha hydroxysteroid dehydro | 3.2 |
| | 407304 | AA565832 | Hs.271649 | gb:nj32b03.s1 NCI_CGAP_AA1 Homo sapiens | 3.2 |
| | 451697 | AW449774 | Hs.296380 | POM (POM121 rat homolog) and ZP3 fusion | 3.2 |
| | 435071 | D60683 | Hs.35495 | ESTs | 3.2 |
| 45 | 420352 | BE258835 | | gb:601117374F1 NIH_MGC_16 Homo sapiens c | 3.2 |
| | 412193 | AI684467 | Hs.144057 | ESTs | 3.2 |
| | 442320 | AI287817 | Hs.129636 | ESTs | 3.2 |
| | 407378 | AA299264 | Hs.57776 | ESTs, Moderately similar to I38022 hypot | 3.2 |
| | 414528 | AA148950 | Hs.188836 | ESTs | 3.2 |
| 50 | 439764 | T26535 | Hs.22744 | hypothetical protein MGC13105 | 3.2 |
| | 410425 | BE278367 | Hs.63510 | KIAA0141 gene product | 3.2 |
| | 429876 | AB028977 | Hs.225974 | KIAA1054 protein | 3.2 |
| | 427627 | R87582 | Hs.179915 | guanine nucleotide binding protein (G pr | 3.2 |
| | 439039 | AI656707 | Hs.48713 | ESTs | 3.2 |
| 55 | 447925 | AW292271 | Hs.250718 | ESTs | 3.2 |
| | 447714 | AW296313 | Hs.255537 | ESTs | 3.2 |
| | 434574 | AI424458 | Hs.33470 | ESTs | 3.2 |
| | 437269 | AA334384 | Hs.149420 | ESTs | 3.2 |
| | 416845 | H95279 | Hs.293788 | gb:yu20h02.s1 Soares fetal liver spleen | 3.2 |
| 60 | 452234 | AW084176 | Hs.223296 | ESTs, Weakly similar to I38022 hypotheti | 3.2 |
| | 440274 | R24595 | Hs.7122 | scrapie responsive protein 1 | 3.2 |
| | 437698 | R61837 | Hs.7990 | ESTs, Moderately similar to I84505 calci | 3.2 |
| | 414761 | AU077228 | Hs.77256 | enhancer of zeste (Drosophila) homolog 2 | 3.2 |
| | 445828 | F05802 | Hs.81907 | ESTs | 3.2 |
| 65 | 423779 | AW071837 | Hs.57971 | ESTs | 3.2 |
| | 403790 | | | NM_001334*:Homo sapiens cathepsin O (CTS | 3.2 |
| | 453792 | AL134539 | Hs.254129 | KIAA1678 | 3.2 |
| | 428167 | AA770021 | Hs.16332 | ESTs | 3.2 |
| 70 | 445413 | AA151342 | Hs.12677 | CGI-147 protein | 3.2 |
| | 415314 | N88802 | Hs.5422 | glycoprotein M6B | 3.2 |
| | 425115 | R44664 | Hs.123956 | ESTs | 3.2 |
| | 432625 | AJ243596 | Hs.94830 | ESTs, Moderately similar to T03094 A-kin | 3.2 |
| | 412420 | AL035668 | Hs.73853 | bone morphogenetic protein 2 | 3.1 |
| | 422772 | AL119585 | Hs.120228 | KIAA0749 protein | 3.1 |
| 75 | 437414 | AW894071 | Hs.48448 | hypothetical protein DKFZp547C176 | 3.1 |
| | 427951 | AW293165 | Hs.143134 | ESTs | 3.1 |
| | 435256 | AF193766 | Hs.13872 | cytokine-like protein C17 | 3.1 |
| | 428966 | AF059214 | Hs.194687 | cholesterol 25-hydroxylase | 3.1 |
| | 413995 | BE048146 | Hs.75671 | syntxin 1A (brain) | 3.1 |
| 80 | 443431 | AI056847 | Hs.20654 | ESTs | 3.1 |
| | 414217 | AI309298 | Hs.279898 | Homo sapiens cDNA: FLJ23165 fis, clone L | 3.1 |
| | 419617 | AL008583 | Hs.91622 | neuronal pentraxin receptor | 3.1 |
| | 444326 | AI939357 | Hs.270710 | ESTs | 3.1 |
| | 436315 | BE390513 | Hs.27935 | hypothetical protein MGC4837 | 3.1 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 446131 | NM_000929 | Hs.290 | phospholipase A2, group V | 3.1 |
| | 423858 | AL137326 | Hs.133483 | Homo sapiens mRNA; cDNA DKFZp434B0650 (f | 3.1 |
| | 448475 | BE613134 | Hs.247474 | hypothetical protein FLJ21032 | 3.1 |
| | 432682 | AI376400 | Hs.159588 | ESTs | 3.1 |
| 5 | 450661 | AW952160 | Hs.83849 | ESTs | 3.1 |
| | 417636 | R08916 | Hs.191212 | ESTs | 3.1 |
| | 417918 | AA209205 | Hs.163754 | hypothetical protein FLJ12606 | 3.1 |
| | 454032 | W31790 | Hs.194293 | ESTs, Weakly similar to IS4374 gene NF2 | 3.1 |
| | 443150 | AI034487 | Hs.34650 | ESTs | 3.1 |
| 10 | 404632 | | | NM_022490:Homo sapiens hypothetical prot | 3.1 |
| | 425537 | AB007913 | Hs.158291 | KIAA0444 protein | 3.1 |
| | 437162 | AW005505 | Hs.5464 | thyroid hormone receptor coactivating pr | 3.1 |
| | 400090 | | | Eos Control | 3.1 |
| | 445424 | AB028945 | Hs.12696 | cortactin SH3 domain-binding protein | 3.1 |
| 15 | 422949 | AA319435 | | gb:EST21657 Adrenal gland tumor Homo sap | 3.1 |
| | 448750 | U95020 | Hs.21903 | calcium channel, voltage-dependent, beta | 3.1 |
| | 433560 | AI925195 | Hs.130891 | hypothetical protein MGC4400 | 3.1 |
| | 433042 | AW193534 | Hs.281895 | Homo sapiens cDNA FLJ11660 fis, clone HE | 3.1 |
| | 449722 | BE280074 | Hs.23960 | cyclin B1 | 3.1 |
| 20 | 425480 | AB023198 | Hs.158135 | KIAA0981 protein | 3.1 |
| | 449670 | F07693 | Hs.85603 | Homo sapiens mRNA; cDNA DKFZp434K2172 (f | 3.1 |
| | 452619 | AW298597 | Hs.61884 | Homo sapiens, clone IMAGE:4298026, mRNA, | 3.1 |
| | 428722 | U76456 | Hs.190787 | tissue inhibitor of metalloproteinase 4 | 3.1 |
| | 405605 | | | C2001342.gi127814 sp P26434 NAH4_RAT SO | 3.1 |
| 25 | 417565 | AI203405 | Hs.47831 | ESTs | 3.1 |
| | 439538 | AA837323 | Hs.56407 | ESTs | 3.1 |
| | 414117 | W88559 | Hs.1787 | proteolipid protein 1 (Pelizaeus-Merzbac | 3.1 |
| | 430818 | AI311928 | Hs.348156 | gb:qo89h04.x1 NCI_CGAP_Kid5 Homo sapiens | 3.1 |
| | 408508 | AI806109 | Hs.135736 | KIAA1580 protein | 3.1 |
| 30 | 414884 | R54418 | Hs.183745 | hypothetical protein FLJ13456 | 3.1 |
| | 439963 | AW247529 | Hs.6793 | platelet-activating factor acetylhydrola | 3.1 |
| | 446636 | AC002563 | Hs.15767 | citron (rho-interacting, serine/threonin | 3.1 |
| | 417169 | R13550 | Hs.246773 | ESTs | 3.1 |
| | 450202 | AW969756 | Hs.34145 | ESTs, Weakly similar to B49647 GTP-bindi | 3.1 |
| 35 | 428060 | AA420616 | Hs.249483 | ESTs | 3.1 |
| | 430526 | AF181862 | Hs.242407 | G protein-coupled receptor, family C, gr | 3.1 |
| | 421458 | NM_003654 | Hs.104576 | carbohydrate (keratan sulfate Gal-6) sul | 3.0 |
| | 429163 | AA884768 | | gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s | 3.0 |
| | 428180 | AI129767 | Hs.182874 | guanine nucleotide binding protein (G pr | 3.0 |
| 40 | 422631 | BE218919 | Hs.118793 | hypothetical protein FLJ10688 | 3.0 |
| | 433290 | R20077 | Hs.302185 | Homo sapiens clone 23618 mRNA sequence | 3.0 |
| | 412507 | L36645 | Hs.73964 | EphA4 | 3.0 |
| | 415827 | H17462 | Hs.23079 | ESTs | 3.0 |
| | 429609 | AF002246 | Hs.210863 | cell adhesion molecule with homology to | 3.0 |
| 45 | 457358 | AI479755 | Hs.129010 | ESTs | 3.0 |
| | 441732 | AW298818 | Hs.127341 | ESTs | 3.0 |
| | 459318 | NM_000038 | | gb:Homo sapiens adenomatosis polyposis c | 3.0 |
| | 426384 | AI472078 | Hs.203662 | hypothetical protein FLJ13189 (FLJ13189) | 3.0 |
| 50 | 436267 | AW450938 | Hs.180115 | ESTs | 3.0 |
| | 450650 | T65617 | Hs.101257 | hypothetical protein MGC3295 | 3.0 |
| | 414865 | AA157155 | Hs.274414 | hypothetical protein FLJ14457 | 3.0 |
| | 459080 | AW192083 | Hs.290855 | ESTs | 3.0 |
| | 412783 | BE276738 | Hs.74578 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypep | 3.0 |
| 55 | 432593 | AW301003 | Hs.51483 | ESTs, Weakly similar to hypothetical pro | 3.0 |
| | 443753 | AW367578 | Hs.134749 | ESTs | 3.0 |
| | 445921 | AW015211 | Hs.146181 | ESTs | 3.0 |
| | 427695 | R88483 | Hs.172862 | ESTs | 3.0 |
| | 438283 | AI458931 | Hs.37282 | ESTs | 3.0 |
| 60 | 453324 | W26592 | Hs.232089 | ESTs | 3.0 |
| | 421094 | AW978202 | Hs.289064 | hypothetical protein FLJ22251 | 3.0 |
| | 433434 | AA588429 | | gb:no22b03.s1 NCI_CGAP_Pr22 Homo sapiens | 3.0 |
| | 452850 | H23230 | Hs.22481 | ESTs, Moderately similar to A46010 X-fin | 3.0 |
| | 416658 | U03272 | Hs.79432 | fibrillin 2 (congenital contractual ara | 3.0 |
| 65 | 429569 | AA454993 | Hs.138343 | ESTs, Weakly similar to I78885 serine/th | 3.0 |
| | 428600 | AW863261 | Hs.242413 | hypothetical protein DKFZp434K1421 | 3.0 |
| | 443633 | AL031290 | Hs.9654 | similar to pregnancy-associated plasma p | 3.0 |
| | 433229 | AB040925 | Hs.91625 | KIAA1492 protein | 3.0 |
| | 429046 | X57436 | Hs.194772 | oligodendrocyte myelin glycoprotein | 3.0 |
| | 431431 | AL096711 | Hs.252953 | Human DNA sequence from clone RP3-403A15 | 3.0 |
| 70 | 414430 | AI346201 | Hs.76118 | ubiquitin carboxyl-terminal esterase L1 | 3.0 |
| | 423165 | AI937547 | Hs.124915 | hypothetical protein MGC2601 | 3.0 |
| | 440261 | M81886 | Hs.7117 | glutamate receptor, ionotropic, AMPA 1 | 3.0 |
| | 441364 | AW450466 | Hs.126830 | ESTs, Weakly similar to Y038_YEAST HYPOT | 3.0 |
| | 437056 | AI147061 | | gb:ok33a11.s1 Soares_NSIF_F8_9W_OT_PA_P_S | 3.0 |
| 75 | 429168 | AA984682 | Hs.146589 | ESTs, Weakly similar to JC5238 galactosy | 3.0 |
| | 453739 | AL120266 | | ESTs | 3.0 |

TABLE 158:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey CAT Number Accession

| | | | |
|----|--------|-----------|--|
| 5 | 410099 | 117647_1 | AA081630 T08671 A1174254 D83874 AW959843 AA364503 AA693467 AW993370 BE327037 AA167714 N79906 AW901977 AW901980 W52882 T07735 AA484549 W60090 D52685 T23811 BE327043 AW901768 BE551237 AA917004 AA716027 A1439658 AA283724 A1805992 A1457096 AA084618 BE467736 A1092635 A1887863 A1697593 AA436618 A1167419 A1418634 T31586 AA436630 AA706191 A1041169 A1422304 T03534 AA211402 A1204899 A1366472 AW827081 AA788593 T32736 A1767935 AA167791 AA747914 AA663870 A1865504 BE169274 AW893230 AA210998 H24222 AA081774 BE000935 BE000834 AA334880 |
| 10 | 410126 | 117761_1 | AW851728 AW851607 AW851621 AW851702 AW851647 AW851727 AW851658 AW851617 AW851628 |
| 15 | 411565 | 1249756_1 | A1267606 AA121045 AA126521 |
| 20 | 412799 | 132817_1 | H06382 AW957730 AA352014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 A1424991 A1693507 A1863108 AA599060 A1091148 AA598689 R39887 AA813482 AW016452 H06383 R41807 A1364268 AA620528 A1241940 AW089149 AW090733 AW088875 Z38240 AA121202 R17734 |
| 25 | 412820 | 1330039_1 | BE001236 BE001177 BE001180 BE001234 |
| 30 | 414372 | 143909_1 | AA143654 AW753140 AA213770 AW970865 AA569075 AA492132 |
| 35 | 415131 | 1523680_1 | D61119 D81508 D81734 |
| 40 | 416871 | 1626761_1 | H98716 N90792 N24283 |
| 45 | 418512 | 176394_1 | AW498974 T09332 R58460 AA350990 T33786 T30936 AA350905 T08592 T09274 AA224297 D54678 T08951 R15346 AW953188 AA350074 AW890649 |
| 50 | 419544 | 185760_2 | A1909154 AA526337 AA244193 A1909153 |
| 55 | 420111 | 190755_1 | AA255652 AA280911 AW967920 AA262684 |
| 60 | 420352 | 192979_1 | BE258835 AW958316 AA258918 AW843305 R14744 A1580388 BE071923 R36280 |
| 65 | 422949 | 223184_1 | AA319435 N56456 AA319377 AW961532 T48452 AA894424 |
| 70 | 423476 | 22861_1 | AL035633 F11794 F11783 H18042 T66089 H29379 R19493 AW134660 A1299437 AL133995 AA057405 N78357 AA917450 A1002692 T09262 T65008 H29290 A1200874 AA894415 A1732887 A1791768 A1733447 AA988785 N62128 T09261 AW956936 |
| 75 | 424572 | 24097_1 | M19650 R18810 R18721 AW896146 AW889520 AA192362 AA176814 F12085 BE255264 BE251393 T65248 AA380585 AA380465 BE408684 AA459037 AW498869 AA776107 BE274289 D45269 M61958 AA378818 AW663180 AW672958 H08611 M78164 BE393721 AA348660 R36303 |
| 80 | | | AW498662 AA019090 AA001087 AA054302 AA019775 AA018808 AA019132 A1858240 R73218 H30477 H17776 AA659570 BE276750 AL118657 AA375861 AA352427 AW581695 A1141188 N63474 AA654162 H17659 A120696 T28867 AW498868 A1355918 AA902349 AA569098 A1088231 A1042604 AA555133 A1183611 A1068822 A1275941 AW316805 AA349486 A1355233 R85117 AW613626 R49234 AA458846 N20669 H18693 AA977567 T15423 AW002084 A1824721 N36242 A1417281 A1018212 AA912337 F09722 AA749449 AW879172 AA885427 AA916639 A1872560 F00482 H45184 A1217251 AA775807 BE390071 AA303517 AA001050 BE515169 N44066 AL133684 A1807085 AA808009 AA915914 F00007 AA019749 AL121560 |
| | | | AW675544 AW090233 AW072071 A1810932 A1089733 AW026222 AA770155 A1089647 A1085733 AW516061 AL037636 AL037635 A1863947 H50420 R11203 AA019133 N94772 N71842 N29047 AA778138 AA554336 AA179865 N59453 T65212 AA054270 AW806630 AA533375 D13146 AA349487 AU077160 BE255671 BE276795 BE250823 AL120301 BE311390 BE252483 |
| | 424945 | 245223_1 | A1221919 Z19967 AA348780 AW964077 AW166028 BE540193 N94800 AA452368 N99604 A1341345 AW298800 AA724961 AA931158 A1741227 A1806660 A1982626 D81263 D53937 D52496 AA974487 AW043854 N50483 Z39997 A1492961 A1361526 F04002 AA452141 T23551 A1472655 A193667 A1341984 N92658 T32870 R52664 N50428 AW089291 A1934175 A1423737 D60665 |
| | 424947 | 245247_1 | R77952 AA348809 AW959960 AW959962 A1565552 AW070702 AA973910 R85973 |
| | 425331 | 250199_1 | AW962128 AA355353 AA427363 |
| | 426413 | 266650_1 | AA377823 AW954494 A1022688 |
| | 426503 | 268283_1 | AA380153 AA380233 AW963529 |
| | 426919 | 273507_1 | AL041228 D82004 D61361 A1203314 A1990307 AW900295 A1018308 AW087473 AW183530 AA393346 H50055 AA935601 |
| | 428342 | 290035_2 | A1739168 AA426249 A1199636 AW505198 AW977291 AA824583 AA883419 AA724079 A1015524 A1377728 AW293682 A1928140 AA731438 A1092404 A1085630 AA731340 |
| | 429007 | 298301_1 | D80642 AA443145 AL119015 AW904500 |
| | 429163 | 300543_1 | AA884766 AW974271 AA592975 AA447312 |
| | 429421 | 30431_1 | AL031658 A1693758 AL040619 AW977914 AA811957 A1352198 AW104364 AA648367 AA897604 AW341668 A1201382 AL040620 |
| | 430183 | 31412_2 | BE010038 AA676833 A1311783 T86895 W68032 BE064393 BE064394 BE157228 BE183282 A1936370 AA552514 T67280 AA039909 |
| | 430676 | 32168_1 | AF084866 AF084870 AF084864 AF084867 AF084869 AF084865 AF084868 AW818206 AW812038 BE144813 BE144812 AW812041 AW812040 AW812067 BE061583 BE061604 T05808 A1352469 AA580921 BE141783 BE141782 BE061601 AW814393 AW885029 |
| | 430968 | 326269_1 | AW972830 AA527647 AA489820 AA570362 |
| | 433009 | 357371_1 | AA761668 AA573621 R92814 R09670 |
| | 433434 | 366095_1 | AA588429 A1972567 AW504832 A1298694 |
| | 433523 | 368873_1 | H29882 AW665533 AW149901 A1572917 AA598500 A1686466 A1336390 AW864390 AW864320 |
| | 435542 | 407744_1 | AA687376 H74234 AW975503 |
| | 437034 | 431713_1 | AA742643 AA808575 AW976668 |
| | 437056 | 432262_1 | A1147061 AA743380 AA765523 AW976398 A1803927 |
| | 438458 | 457837_1 | AW975186 AA807807 D29548 |
| | 439285 | 47065_1 | AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 A1346341 A1867454 N54784 A1655270 A1421279 AW014882 AA775552 N62351 N59253 AA626243 A1341407 BE175639 AA456968 A1358918 AA457077 |
| | 439518 | 47334_1 | W76326 AF086341 W72300 |
| | 439566 | 47387_1 | AF086387 W77884 W72711 |
| | 441102 | 509504_1 | AA973905 A1299888 AA917019 H63235 T90771 |
| | 446692 | 689623_1 | Z44514 A1352097 A1803984 AW235923 AW196558 A1954637 A1336983 |
| | 447197 | 711623_1 | R36075 A1366546 R36167 |
| | 448044 | 747196_1 | A1458682 H24240 R14537 R18426 AW867082 |
| | 449625 | 8113_1 | NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 A1375997 R45432 D59344 A1203107 F07491 R35360 R25094 A1913631 A1498402 T61382 A1016320 N45526 T61415 AA331486 |
| | 450375 | 83327_1 | AA009547 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 A1161014 AA099554 R69067 |
| | 450582 | 83933_1 | A1339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878 |
| | 451320 | 86576_1 | AW118072 A1631982 T15734 AA224195 A1701458 W20198 F26326 AA890570 N90552 AW071907 A1671352 A1375892 T03517 R88265 A1124088 AA224388 A1084316 A1354686 T33652 A1140719 A1720211 T03490 A1372637 T15415 AW205836 AA630384 T03515 T33230 AA017131 AA443303 T33623 A1222556 T33511 T33785 A1419606 D55612 |
| | 453331 | 96214_1 | A1240665 T53681 N77468 H51833 AA147247 R75732 C18450 R73999 A1095755 T49904 H03868 AA411580 R33395 AA410586 T48869 D63292 R31981 H12498 H02668 AA035018 R75957 A1803329 R27528 R36203 A1809932 A1808765 R78948 AA411449 AA976929 A1378760 A1378620 T48870 R73906 R75632 H03612 AA909684 N50695 H02580 H12839 N58781 AA742532 A1360919 H03502 BE208298 R68588 A1350463 R31935 AW069127 AA411621 R25671 R36105 H12451 H03869 H51263 AA035486 R25109 R25110 AA147933 |
| | 453739 | 979419_1 | AL120266 AW269469 AW890114 |
| | 454171 | 1049240_1 | AW854832 AW854798 AW854857 AW854816 AW854834 AW854817 |
| | 455646 | 1348557_1 | BE064420 BE064435 BE064429 BE064414 BE064400 BE064517 |
| | 458912 | 823104_1 | A1911066 A1933734 A1680888 A1003599 |

TABLE 15C:

Pkey:

Unique number corresponding to an Eos probe set.

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

| Pkey | Ref | Strand | Nt_position |
|--------|---------|--------|---|
| 400533 | 6981826 | Minus | 277132-277595 |
| 400777 | 8131663 | Plus | 70745-71121 |
| 401272 | 9797373 | Minus | 98374-98509 |
| 402145 | 8018280 | Plus | 113086-114800 |
| 402604 | 9909420 | Plus | 20393-20767 |
| 402605 | 9909420 | Minus | 47680-47973 |
| 402855 | 9662953 | Minus | 59763-59909 |
| 403142 | 9444521 | Plus | 89285-90131 |
| 403341 | 8569175 | Plus | 30699-30910 |
| 403696 | 3135242 | Minus | 143467-143634 |
| 403790 | 8084957 | Minus | 87826-87947,89835-90002 |
| 404150 | 7534008 | Plus | 165811-165943 |
| 404283 | 2276311 | Minus | 99460-99564 |
| 404541 | 8318559 | Plus | 103456-103664 |
| 404584 | 9857511 | Plus | 138651-139153 |
| 404632 | 9796668 | Plus | 45096-45229 |
| 404819 | 4678240 | Plus | 16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578 |
| 405238 | 7249119 | Minus | 51728-51836 |
| 405239 | 7249119 | Plus | 144345-144464,144690-144836,151750-151883,152407-152484 |
| 405348 | 2914717 | Minus | 43310-43462 |
| 405605 | 5836195 | Minus | 117070-117270 |
| 405819 | 4007557 | Plus | 2830-2967 |

TABLE 16A: ABOUT 859 GENES UP-REGULATED IN GLIOBLASTOMA MULTIFORMA COMPARED TO NORMAL CENTRAL NERVOUS SYSTEM
 Table 16A lists about 859 genes up-regulated in glioblastoma multiforma (GBM) compared to normal central nervous system (CNS). These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" LGG to "average" CNS tissues was greater than or equal to 3.0. The "average" GBM level was set to the 85th percentile amongst various GBM tumors. The "average" normal CNS tissue level was set to the 85th percentile amongst various CNS tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of GLIOBLASTOMA MULTIFORMA to CNS

| Pkey | ExAccn | UnigenelD | Unigene Title | R1 |
|--------|-----------|-----------|--|------|
| 414555 | N98569 | Hs.76422 | phospholipase A2, group IIA (platelets, | 47.2 |
| 422737 | M26939 | Hs.119571 | collagen, type III, alpha 1 (Ehlers-Danl | 44.9 |
| 423961 | D13666 | Hs.136348 | periostin (OSF-2os) | 33.3 |
| 433001 | AF217513 | Hs.279905 | clone HQ0310 PRO0310p1 | 25.9 |
| 449539 | W80363 | Hs.58446 | ESTs | 25.8 |
| 417308 | H60720 | Hs.81892 | KIAA0101 gene product | 23.3 |
| 424800 | AL035588 | Hs.153203 | MyoD family inhibitor | 23.0 |
| 414825 | X06370 | Hs.77432 | epidermal growth factor receptor (avian | 19.6 |
| 431941 | AK000106 | Hs.272227 | Homo sapiens cDNA FLJ20099 fis, clone CO | 18.7 |
| 453392 | U23752 | Hs.32964 | SRY (sex determining region Y)-box 11 | 17.8 |
| 444190 | AI878918 | Hs.10526 | cysteine and glycine-rich protein 2 | 17.8 |
| 428330 | L22524 | Hs.2256 | matrix metalloproteinase 7 (matrilysin, | 17.7 |
| 417130 | AW276858 | Hs.81256 | S100 calcium-binding protein A4 (calcium | 17.5 |
| 414217 | AI309298 | Hs.279898 | Homo sapiens cDNA: FLJ23165 fis, clone L | 17.0 |
| 428242 | H55709 | Hs.2250 | leukemia inhibitory factor (cholinergic | 15.9 |
| 425397 | J04088 | Hs.156346 | topoisomerase (DNA) II alpha (170kD) | 15.6 |
| 424635 | AA420687 | Hs.115455 | Homo sapiens cDNA FLJ14259 fis, clone PL | 15.2 |
| 408243 | Y00787 | Hs.624 | interleukin 8 | 14.7 |
| 422672 | X12784 | Hs.119129 | collagen, type IV, alpha 1 | 14.7 |
| 434078 | AW880709 | Hs.283683 | chromosome 8 open reading frame 4 | 14.6 |
| 409799 | D11928 | Hs.76845 | phosphoserine phosphatase-like | 14.2 |
| 414761 | AU077228 | Hs.77256 | enhancer of zeste (Drosophila) homolog 2 | 14.2 |
| 442432 | BE093589 | Hs.38178 | hypothetical protein FLJ23468 | 14.1 |
| 446584 | U53445 | Hs.15432 | downregulated in ovarian cancer 1 | 14.0 |
| 444969 | AI203334 | Hs.160628 | ESTs | 13.5 |
| 430691 | C14187 | Hs.103538 | ESTs | 12.9 |
| 426075 | AW513691 | Hs.270149 | ESTs, Weakly similar to 2109260A B cell | 12.4 |
| 445101 | T75202 | Hs.12314 | Homo sapiens mRNA; cDNA DKFZp586C1019 (f | 12.1 |
| 441269 | AW015206 | Hs.178784 | ESTs | 11.9 |
| 417426 | NM_002291 | Hs.82124 | laminin, beta 1 | 11.9 |
| 430132 | AA204686 | Hs.234149 | hypothetical protein FLJ20647 | 11.8 |
| 422163 | AF027208 | Hs.112360 | prominin (mouse)-like 1 | 11.3 |
| 411411 | AA345241 | Hs.55950 | ESTs, Weakly similar to KIAA1330 protein | 11.3 |
| 449722 | BE280074 | Hs.23960 | cyclin B1 | 11.2 |
| 436291 | BE568452 | Hs.344037 | protein regulator of cytokinesis 1 | 11.0 |
| 435020 | AW505076 | Hs.301855 | DiGeorge syndrome critical region gene 8 | 10.9 |
| 412140 | AA219691 | Hs.73625 | RAB6 interacting, kinesin-like (rabkines | 10.9 |
| 419239 | AA468183 | Hs.184598 | Homo sapiens cDNA: FLJ23241 fis, clone C | 10.6 |
| 417043 | NM_004369 | Hs.80988 | collagen, type VI, alpha 3 | 10.6 |
| 413929 | BE501689 | Hs.75617 | collagen, type IV, alpha 2 | 10.6 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 420602 | AF060877 | Hs.99236 | regulator of G-protein signaling 20 | 10.6 |
| | 409142 | AL136877 | Hs.50758 | SMC4 (structural maintenance of chromoso | 10.4 |
| | 406972 | M32053 | | gb:Human H19 RNA gene, complete cds. | 10.4 |
| 5 | 412986 | X81120 | Hs.75110 | cannabinoid receptor 1 (brain) | 10.3 |
| | 419508 | AW997938 | Hs.90786 | ATP-binding cassette, sub-family C (CFTR | 10.3 |
| | 449611 | AI970394 | Hs.197075 | ESTs | 10.1 |
| | 427581 | NM_014788 | Hs.179703 | KIAA0129 gene product | 10.1 |
| | 431512 | BE270734 | Hs.2795 | lactate dehydrogenase A | 9.9 |
| 10 | 429183 | AB014604 | Hs.197955 | KIAA0704 protein | 9.8 |
| | 433437 | U20536 | Hs.3280 | caspase 6, apoptosis-related cysteine pr | 9.7 |
| | 424840 | D79987 | Hs.153479 | extra spindle poles, S. cerevisiae, homo | 9.7 |
| | 433800 | AI034361 | Hs.135150 | lung type-I cell membrane-associated gly | 9.7 |
| | 433647 | AA603367 | Hs.222294 | ESTs | 9.7 |
| | 414622 | AI752666 | Hs.76669 | nicotinamide N-methyltransferase | 9.5 |
| 15 | 413719 | BE439580 | Hs.75498 | small inducible cytokine subfamily A (Cy | 9.3 |
| | 409461 | AA382169 | Hs.54483 | N-myc (and STAT) interactor | 9.3 |
| | 409902 | AI337658 | Hs.156351 | ESTs | 9.3 |
| | 450375 | AA009647 | | a disintegrin and metalloproteinase doma | 9.2 |
| | 445873 | AA250970 | Hs.251946 | poly(A)-binding protein, cytoplasmic 14 | 9.1 |
| 20 | 442802 | AL133035 | Hs.8728 | hypothetical protein DKFZp434G171 | 9.1 |
| | 452461 | N78223 | Hs.108106 | transcription factor | 9.1 |
| | 434846 | AW295389 | Hs.119768 | ESTs | 9.1 |
| | 422158 | L10343 | Hs.112341 | protease inhibitor 3, skin-derived (SKAL | 9.0 |
| 25 | 425187 | AW014486 | Hs.22509 | ESTs | 9.0 |
| | 443247 | BE614387 | Hs.333893 | c-Myc target JPO1 | 8.7 |
| | 458079 | AI796870 | Hs.54277 | DNA segment on chromosome X (unique) 992 | 8.7 |
| | 410276 | AI554545 | Hs.68301 | angiotensin-2 | 8.6 |
| | 402855 | | | NM_001839: Homo sapiens calponin 3, acid | 8.6 |
| 30 | 439710 | AF086543 | | gb:Homo sapiens full length insert cDNA | 8.6 |
| | 411968 | AI207410 | Hs.69280 | Homo sapiens, clone IMAGE:3636299, mRNA, | 8.6 |
| | 410102 | AW248508 | Hs.279727 | ESTs; homologue of PEM-3 (Ciona savignyi | 8.6 |
| | 436895 | AF037335 | Hs.5338 | carbonic anhydrase XII | 8.6 |
| | 418203 | X54942 | Hs.83758 | CDC28 protein kinase 2 | 8.6 |
| 35 | 416892 | L24498 | Hs.80409 | growth arrest and DNA-damage-inducible, | 8.5 |
| | 425234 | AW152225 | Hs.165909 | ESTs, Weakly similar to I38022 hypotheti | 8.5 |
| | 449961 | AW265634 | Hs.133100 | ESTs | 8.5 |
| | 449444 | AW818436 | Hs.23590 | solute carrier family 16 (monocarboxylic | 8.4 |
| | 417061 | AI675944 | Hs.188691 | Homo sapiens cDNA FLJ12033 fis, clone HE | 8.3 |
| 40 | 453884 | AA355925 | Hs.36232 | KIAA0186 gene product | 8.3 |
| | 424085 | NM_002914 | Hs.139226 | replication factor C (activator 1) 2 (40 | 8.2 |
| | 419938 | AU076772 | Hs.1279 | complement component 1, r subcomponent | 8.1 |
| | 411078 | AI222020 | Hs.182364 | CocoaCrisp | 8.1 |
| | 406850 | AI624300 | Hs.172928 | collagen, type I, alpha 1 | 8.0 |
| 45 | 447726 | AL137638 | Hs.19368 | matrilin 2 | 8.0 |
| | 439999 | AA115811 | Hs.6838 | ras homolog gene family, member E | 8.0 |
| | 416658 | U03272 | Hs.79432 | fibrillin 2 (congenital contractural ara | 7.9 |
| | 439451 | AF086270 | Hs.278554 | heterochromatin-like protein 1 | 7.9 |
| | 458814 | AI498957 | Hs.170861 | ESTs, Weakly similar to Z195_HUMAN ZINC | 7.9 |
| 50 | 447004 | AW296968 | Hs.157539 | ESTs | 7.9 |
| | 436140 | W87355 | Hs.269587 | ESTs | 7.9 |
| | 436607 | AW661783 | Hs.211061 | ESTs | 7.8 |
| | 422809 | AK001379 | Hs.121028 | hypothetical protein FLJ10549 | 7.7 |
| | 440052 | AI633744 | Hs.195648 | ESTs, Weakly similar to I38022 hypotheti | 7.7 |
| 55 | 422106 | D84239 | Hs.111732 | Fc fragment of IgG binding protein | 7.7 |
| | 418113 | AI272141 | Hs.83484 | SRY (sex determining region Y)-box 4 | 7.7 |
| | 410286 | AI739159 | Hs.61898 | DKFZP586N2124 protein | 7.7 |
| | 424587 | J05070 | Hs.151738 | matrix metalloproteinase 9 (gelatinase B | 7.6 |
| | 422048 | NM_012445 | Hs.288126 | spondin 2, extracellular matrix protein | 7.6 |
| 60 | 421988 | AW450481 | Hs.161333 | ESTs | 7.6 |
| | 452620 | AA436504 | Hs.119286 | ESTs | 7.6 |
| | 453941 | U39817 | Hs.36820 | Bloom syndrome | 7.5 |
| | 416737 | AF154335 | Hs.79691 | LIM domain protein | 7.5 |
| | 425289 | AW139342 | Hs.155530 | interferon, gamma-inducible protein 16 | 7.5 |
| 65 | 418400 | BE243026 | Hs.301989 | KIAA0246 protein | 7.5 |
| | 437036 | AI571514 | Hs.133022 | ESTs | 7.5 |
| | 421899 | AJ011895 | Hs.109281 | Nef-associated factor 1 | 7.4 |
| | 409731 | AA125985 | Hs.56145 | thymosin, beta, identified in neuroblast | 7.4 |
| | 427528 | AJ077143 | Hs.179565 | minichromosome maintenance deficient (S. | 7.4 |
| 70 | 427871 | AW992405 | Hs.59622 | Homo sapiens, clone IMAGE:3507281, mRNA, | 7.3 |
| | 448935 | AL078596 | Hs.22591 | nuclear receptor subfamily 2, group E, m | 7.3 |
| | 415079 | R43179 | Hs.22895 | hypothetical protein FLJ23548 | 7.3 |
| | 449571 | AW016812 | Hs.200266 | ESTs | 7.3 |
| | 427899 | AA829286 | Hs.332053 | serum amyloid A1 | 7.3 |
| 75 | 447458 | AI741082 | Hs.158961 | ESTs | 7.3 |
| | 430630 | AW269920 | Hs.2621 | cystatin A (stefin A) | 7.2 |
| | 411252 | AB018549 | Hs.69328 | MD-2 protein | 7.2 |
| | 432731 | R31178 | Hs.287820 | fibronectin 1 | 7.2 |
| | 454117 | BE410100 | Hs.40368 | adaptor-related protein complex 1, sigma | 7.2 |
| 80 | 407881 | AW072003 | Hs.40968 | heparan sulfate (glucosamine) 3-O-sulfot | 7.2 |
| | 428728 | NM_016625 | Hs.191381 | hypothetical protein | 7.1 |
| | 416111 | AA033813 | Hs.79018 | chromatin assembly factor 1, subunit A (| 7.1 |
| | 432281 | AK001239 | Hs.274263 | hypothetical protein FLJ10377 | 7.1 |
| | 410434 | AF051152 | Hs.63668 | tol-like receptor 2 | 7.1 |

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|----|--------|-----------|-----------|--|-----|
| | 420018 | U56387 | Hs.94376 | proprotein convertase subtilisin/kexin 1 | 7.1 |
| | 418293 | AI224483 | Hs.16063 | hypothetical protein FLJ21877 | 7.1 |
| | 424954 | NM_000546 | Hs.1846 | tumor protein p53 (Li-Fraumeni syndrome) | 7.0 |
| 5 | 445800 | AF070526 | Hs.125036 | Homo sapiens clone 24787 mRNA sequence | 7.0 |
| | 419741 | NM_007019 | Hs.93002 | ubiquitin carrier protein E2-C | 7.0 |
| | 422283 | AW411307 | Hs.114311 | CDC45 (cell division cycle 45, S.cerevis | 7.0 |
| | 434808 | AF155108 | Hs.256150 | Homo sapiens, Similar to RIKEN cDNA 2810 | 6.9 |
| | 416847 | L43821 | Hs.80261 | enhancer of filamentation 1 (cas-like do | 6.9 |
| 10 | 424381 | AA285249 | Hs.145329 | protein kinase Chk2 | 6.9 |
| | 410064 | X53416 | Hs.195464 | filamin A, alpha (actin-binding protein- | 6.9 |
| | 415682 | AI347128 | Hs.191870 | ESTs | 6.9 |
| | 421977 | W94197 | Hs.110165 | ribosomal protein L26 homolog | 6.8 |
| | 429447 | AW812452 | Hs.83286 | ESTs, Weakly similar to S14747 sphingomy | 6.8 |
| 15 | 423198 | M81933 | Hs.1634 | cell division cycle 25A | 6.8 |
| | 413627 | BE182082 | Hs.246973 | ESTs | 6.8 |
| | 412777 | AI335773 | Hs.270123 | ESTs | 6.8 |
| | 409829 | M33552 | Hs.56729 | lymphocyte-specific protein 1 | 6.8 |
| | 451129 | BE072881 | | gb:RC2-BT0548-200300-012-e09 BT0548 Homo | 6.8 |
| 20 | 444381 | BE387335 | Hs.283713 | ESTs, Weakly similar to S64054 hypotheti | 6.7 |
| | 446131 | NM_000929 | Hs.290 | phospholipase A2, group V | 6.7 |
| | 441703 | AW390054 | Hs.192843 | leucine zipper protein FKSG14 | 6.7 |
| | 420311 | AW445044 | Hs.38207 | Human DNA sequence from clone RP4-530115 | 6.7 |
| | 425202 | AW962282 | Hs.152049 | ESTs, Weakly similar to I38022 hypotheti | 6.7 |
| 25 | 408161 | AW952912 | Hs.300383 | hypothetical protein MGC3032 | 6.7 |
| | 440704 | M69241 | Hs.162 | insulin-like growth factor binding prote | 6.7 |
| | 407182 | AA312551 | Hs.230157 | ESTs | 6.7 |
| | 445837 | AI261700 | Hs.145544 | ESTs | 6.7 |
| | 433376 | AI249361 | Hs.74122 | caspase 4, apoptosis-related cysteine pr | 6.6 |
| 30 | 431211 | M86849 | Hs.323733 | gap junction protein, beta 2, 26kD (conn | 6.6 |
| | 447439 | AA313565 | Hs.145020 | ESTs, Weakly similar to KIAA1205 protein | 6.6 |
| | 407235 | D20569 | Hs.169407 | SAC2 (suppressor of actin mutations 2, y | 6.5 |
| | 450506 | NM_004460 | | fibroblast activation protein, alpha | 6.5 |
| 35 | 432593 | AW301003 | Hs.51483 | ESTs, Weakly similar to hypothetical pro | 6.5 |
| | 418054 | NM_002318 | Hs.83354 | lysyl oxidase-like 2 | 6.5 |
| | 452799 | AI948829 | Hs.213786 | ESTs | 6.5 |
| | 446657 | AI335191 | Hs.260702 | ESTs, Weakly similar to 2109260A B cell | 6.4 |
| | 424247 | X14008 | Hs.234734 | lysozyme (renal amyloidosis) | 6.4 |
| | 443884 | N20617 | Hs.194397 | leptin receptor | 6.4 |
| 40 | 420560 | AW207748 | Hs.59115 | ESTs | 6.4 |
| | 419485 | AA489023 | Hs.99807 | ESTs, Weakly similar to unnamed protein | 6.3 |
| | 420649 | AI866964 | Hs.124704 | ESTs, Moderately similar to S65657 alpha | 6.3 |
| | 457465 | AW301344 | Hs.122908 | DNA replication factor | 6.3 |
| | 440332 | AI218517 | Hs.188051 | ESTs | 6.3 |
| 45 | 449246 | AW411209 | Hs.23363 | hypothetical protein FLJ10983 | 6.3 |
| | 413063 | AL035737 | Hs.75184 | chitinase 3-like 1 (cartilage glycoprote | 6.2 |
| | 448275 | BE514434 | Hs.20830 | kinesin-like 2 | 6.2 |
| | 440286 | U29589 | Hs.7138 | cholinergic receptor, muscarinic 3 | 6.2 |
| 50 | 439518 | W76326 | | gb:zd60d04.r1 Soares_fetal_heart_NbH19W | 6.1 |
| | 412567 | AI750979 | Hs.74034 | Homo sapiens clone 24651 mRNA sequence | 6.1 |
| | 426935 | NM_000088 | Hs.172928 | collagen, type I, alpha 1 | 6.1 |
| | 456977 | AK000252 | Hs.169758 | hypothetical protein FLJ20245 | 6.1 |
| | 428450 | NM_014791 | Hs.184339 | KIAA0175 gene product | 6.0 |
| | 412125 | Y17114 | Hs.73393 | eyes absent (Drosophila) homolog 4 | 6.0 |
| 55 | 413786 | AW613780 | Hs.13500 | ESTs | 6.0 |
| | 410555 | U92649 | Hs.64311 | a disintegrin and metalloproteinase doma | 5.9 |
| | 400419 | AF084545 | | Target | 5.9 |
| | 408380 | AF123050 | Hs.44532 | diubiquitin | 5.9 |
| 60 | 426108 | AA622037 | Hs.166468 | programmed cell death 5 | 5.9 |
| | 414774 | X02419 | Hs.77274 | plasminogen activator, urokinase | 5.9 |
| | 437695 | AA769202 | Hs.192142 | ESTs | 5.8 |
| | 409463 | AI458165 | Hs.17296 | hypothetical protein MGC2376 | 5.8 |
| | 411048 | AK001742 | Hs.67991 | hypothetical protein DKFZp434G0522 | 5.8 |
| | 443731 | AI083928 | Hs.145418 | ESTs | 5.8 |
| 65 | 405558 | | | Target Exon | 5.8 |
| | 422094 | AF129535 | Hs.272027 | F-box only protein 5 | 5.8 |
| | 429113 | D28235 | Hs.196384 | prostaglandin-endoperoxide synthase 2 (p | 5.8 |
| | 425882 | U83115 | Hs.161002 | absent in melanoma 1 | 5.8 |
| | 412471 | M83193 | Hs.73946 | endothelial cell growth factor 1 (platelet | 5.8 |
| 70 | 429149 | AW193360 | Hs.197962 | ESTs, Weakly similar to I38022 hypotheti | 5.8 |
| | 436827 | H72187 | Hs.5322 | guanine nucleotide binding protein (G pr | 5.7 |
| | 425905 | AB032959 | Hs.318584 | novel C3HC4 type Zinc finger (ring finge | 5.7 |
| | 414053 | BE391635 | Hs.75725 | transgelin 2 | 5.7 |
| | 436805 | AA731533 | Hs.270751 | ESTs | 5.7 |
| 75 | 442201 | AW516704 | Hs.208726 | ESTs | 5.7 |
| | 453361 | AA035197 | Hs.107375 | ESTs | 5.7 |
| | 429083 | Y09397 | Hs.227817 | BCL2-related protein A1 | 5.6 |
| | 426490 | NM_001621 | Hs.170087 | aryl hydrocarbon receptor | 5.6 |
| | 423081 | AF262992 | Hs.123159 | sperm associated antigen 4 | 5.6 |
| 80 | 407013 | U35637 | | gb:Human nebulin mRNA, partial cds | 5.5 |
| | 406478 | | | Target Exon | 5.5 |
| | 435937 | AA830893 | Hs.119769 | ESTs | 5.5 |
| | 453362 | H14988 | Hs.107375 | ESTs | 5.5 |
| | 449969 | AW295142 | Hs.180187 | Homo sapiens cDNA FLJ14337 fs, clone PL | 5.5 |

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|----|--------|-----------|-----------|---|-----|
| 5 | 442547 | AA306997 | Hs.217484 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 5.5 |
| | 443883 | AA114212 | Hs.9930 | serine (or cysteine) proteinase inhibitor | 5.5 |
| | 429643 | AA455889 | Hs.167279 | FYVE-finger-containing Rab5 effector pro | 5.5 |
| | 407862 | BE548267 | Hs.337986 | Homo sapiens cDNA FLJ10934 fis, clone OV | 5.4 |
| | 407624 | AW157431 | Hs.248941 | ESTs | 5.4 |
| 10 | 448769 | N56037 | Hs.38173 | ESTs | 5.4 |
| | 417124 | BE122762 | Hs.25338 | ESTs | 5.4 |
| | 422493 | AW474183 | Hs.250173 | hypothetical protein FLJ13158 | 5.4 |
| | 457292 | AI921270 | Hs.281462 | hypothetical protein FLJ14251 | 5.3 |
| | 418596 | AW976721 | Hs.293327 | ESTs | 5.3 |
| 15 | 410295 | AA741357 | Hs.5174 | nidogen (enactin) | 5.3 |
| | 433323 | AA805132 | Hs.159142 | ESTs | 5.3 |
| | 412326 | R07566 | Hs.73817 | small inducible cytokine A3 (homologous | 5.3 |
| | 418630 | AI351311 | Hs.251946 | poly(A)-binding protein, cytoplasmic 1-4 | 5.3 |
| | 420075 | AF142482 | Hs.203846 | TEA domain family member 3 | 5.2 |
| 20 | 427676 | AA394062 | Hs.300772 | tropomyosin 2 (beta) | 5.2 |
| | 407729 | T40707 | Hs.270862 | ESTs | 5.2 |
| | 416908 | AA333990 | Hs.80424 | coagulation factor XIII, A1 polypeptide | 5.2 |
| | 414372 | AA143654 | | gb:z065a02.r1 Stratagene pancreas (93720 | 5.2 |
| | 433556 | W56321 | Hs.111460 | calcium/calmodulin-dependent protein kin | 5.2 |
| 25 | 424998 | U58515 | Hs.154138 | chitinase 3-like 2 | 5.2 |
| | 407603 | AW955705 | Hs.62604 | Homo sapiens, clone IMAGE:4299322, mRNA, | 5.2 |
| | 445118 | AI208762 | Hs.345572 | ESTs | 5.2 |
| | 408523 | AW833259 | Hs.314287 | ESTs | 5.2 |
| | 412530 | AA766268 | Hs.266273 | hypothetical protein FLJ13346 | 5.2 |
| 30 | 449300 | AI656959 | Hs.346514 | ESTs | 5.2 |
| | 429732 | U20158 | Hs.2488 | lymphocyte cytosolic protein 2 (SH2 doma | 5.2 |
| | 423757 | AL049337 | Hs.132571 | Homo sapiens mRNA; cDNA DKFZp564P016 (fr | 5.1 |
| | 439570 | T79925 | Hs.269165 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 5.1 |
| | 415323 | BE269352 | Hs.949 | neutrophil cytosolic factor 2 (65kD, chr | 5.1 |
| 35 | 443604 | C03577 | Hs.9615 | myosin regulatory light chain 2, smooth | 5.1 |
| | 421247 | BE391727 | Hs.102910 | general transcription factor IIH, polype | 5.1 |
| | 416913 | AW934714 | | gb:RC1-DT0001-031299-011-a11 DT0001 Homo | 5.1 |
| | 419968 | X04430 | Hs.93913 | interleukin 6 (interferon, beta 2) | 5.0 |
| | 424009 | F11690 | | gb:HSC3D041 normalized infant brain cDN | 5.0 |
| 40 | 418283 | S79895 | Hs.83942 | cathepsin K (pseudosclerosis) | 5.0 |
| | 429469 | M54590 | Hs.27 | glycine dehydrogenase (decarboxylating; | 5.0 |
| | 417404 | NM_007350 | Hs.82101 | pleckstrin homology-like domain, family | 5.0 |
| | 408829 | NM_006042 | Hs.48384 | heparan sulfate (glucosamine) 3-O-sulfot | 5.0 |
| | 418097 | R45137 | Hs.21868 | ESTs | 5.0 |
| 45 | 453331 | AI240665 | | ESTs | 4.9 |
| | 429433 | AA452899 | Hs.213586 | ESTs, Weakly similar to KIAA1353 protein | 4.9 |
| | 426044 | AA502490 | Hs.170290 | ESTs | 4.9 |
| | 444161 | NS2543 | Hs.142940 | ESTs | 4.9 |
| | 428227 | AA321649 | Hs.2248 | small inducible cytokine subfamily B (Cy | 4.9 |
| 50 | 432242 | AW022715 | Hs.162160 | ESTs, Weakly similar to ALU4_HUMAN ALU S | 4.9 |
| | 447752 | M73700 | Hs.105938 | factotransferrin | 4.9 |
| | 439627 | BE621702 | Hs.29076 | hypothetical protein FLJ21841 | 4.9 |
| | 402274 | | | C19000498:gi 4567179 gb AAD23607.1 AC00 | 4.9 |
| | 444656 | AI277924 | Hs.145199 | ESTs | 4.9 |
| 55 | 422087 | X58968 | Hs.111301 | matrix metalloproteinase 2 (gelatinase A | 4.9 |
| | 443744 | AI084326 | Hs.271548 | ESTs, Weakly similar to I78885 serine/th | 4.9 |
| | 416871 | H98716 | | gb:yx13d08.s1 Soares melanocyte 2NbHM Ho | 4.9 |
| | 409112 | BE243971 | Hs.50649 | quinone oxidoreductase homolog | 4.8 |
| | 403481 | | | Target Exon | 4.8 |
| 60 | 443740 | R56434 | Hs.21062 | ESTs | 4.8 |
| | 435005 | U80743 | Hs.306094 | trinucleotide repeat containing 12 | 4.8 |
| | 429163 | AA884766 | | gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s | 4.8 |
| | 451418 | BE387790 | Hs.26369 | hypothetical protein FLJ20287 | 4.8 |
| | 428403 | AI393048 | Hs.326159 | leucine rich repeat (in FLJ) interactin | 4.8 |
| 65 | 430968 | AW972830 | | gb:EST384925 MAGE resequences, MAGL Homo | 4.8 |
| | 425212 | AW962253 | Hs.171618 | ESTs | 4.8 |
| | 409205 | AI952884 | Hs.14832 | ESTs, Moderately similar to unnamed prot | 4.8 |
| | 431176 | AI026984 | Hs.293662 | ESTs | 4.8 |
| | 420092 | AA814043 | Hs.88045 | ESTs | 4.8 |
| 70 | 437834 | AA769294 | Hs.283854 | gb:nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens | 4.8 |
| | 432363 | AA534489 | | gb:nf76g11.s1 NCI_CGAP_Co3 Homo sapiens | 4.8 |
| | 403011 | | | ENSP00000215330:Probable serine/threoni | 4.7 |
| | 405348 | | | C7001664:gi 12698061 dbj BAB21849.1 (AB | 4.7 |
| | 447072 | D61594 | Hs.17279 | tyrosylprotein sulfotransferase 1 | 4.7 |
| 75 | 443318 | AI051603 | Hs.133141 | ESTs | 4.7 |
| | 421027 | AA761198 | Hs.55254 | ESTs | 4.7 |
| | 449318 | AW236021 | Hs.78531 | Homo sapiens, Similar to RIKEN cDNA 5730 | 4.7 |
| | 429170 | NM_001394 | Hs.2359 | dual specificity phosphatase 4 | 4.7 |
| | 411852 | AA528140 | Hs.107515 | ESTs, Weakly similar to T00329 hypotheti | 4.7 |
| 80 | 450166 | AA429504 | | ESTs | 4.7 |
| | 438456 | AA913381 | Hs.20594 | ESTs | 4.7 |
| | 446839 | BE091926 | Hs.16244 | mitotic spindle coiled-coil related prot | 4.7 |
| | 438527 | AI969251 | Hs.115325 | RAB7, member RAS oncogene family-like 1 | 4.7 |
| | 458946 | AA009716 | Hs.42311 | ESTs | 4.7 |
| | 454860 | AW835767 | | gb:OV4-LT0016-240200-110-b08 LT0016 Homo | 4.7 |
| | 424736 | AF230877 | Hs.152701 | microtubule-interacting protein that ass | 4.7 |
| | 443426 | AF098158 | Hs.9329 | chromosome 20 open reading frame 1 | 4.6 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 422648 | D86983 | Hs.118893 | Melanoma associated gene | 4.6 |
| | 431319 | AA873350 | Hs.302232 | ESTs | 4.6 |
| | 445666 | R59960 | Hs.282386 | ESTs | 4.6 |
| 5 | 416406 | D86961 | Hs.79299 | lipoma HMGIC fusion partner-like 2 | 4.6 |
| | 422887 | AJ751848 | Hs.49215 | ESTs | 4.6 |
| | 422938 | NM_001809 | Hs.1594 | centromere protein A (17kD) | 4.6 |
| | 405141 | Y14443 | | zinc finger protein 200 | 4.6 |
| | 440210 | AW674562 | Hs.125296 | ESTs | 4.6 |
| 10 | 432527 | AW975028 | Hs.102754 | ESTs | 4.6 |
| | 439726 | AW449893 | Hs.293707 | ESTs, Weakly similar to I38598 zinc fing | 4.6 |
| | 435143 | R12375 | Hs.194600 | ESTs | 4.6 |
| | 422170 | AJ791949 | Hs.112432 | an6-Mullerian hormone | 4.6 |
| | 452874 | AK001061 | Hs.30925 | hypothetical protein FLJ10199 | 4.6 |
| 15 | 408996 | AJ979168 | Hs.344096 | glycoprotein (transmembrane) nmb | 4.6 |
| | 412568 | A878826 | Hs.74034 | caveolin 1, caveolae protein, ZkD | 4.5 |
| | 426215 | AW963419 | Hs.155223 | stanniocalcin 2 | 4.5 |
| | 413076 | U10564 | Hs.75188 | wee1 (S. pombe) homolog | 4.5 |
| | 456759 | BE259150 | Hs.127792 | delta (Drosophila)-like 3 | 4.5 |
| 20 | 419735 | AW750056 | Hs.169577 | Homo sapiens cDNA FLJ14743 fis, clone NT | 4.5 |
| | 433675 | AW977653 | Hs.75319 | ribonucleotide reductase M2 polypeptide | 4.5 |
| | 441217 | AJ922183 | Hs.213246 | ESTs | 4.5 |
| | 435542 | AA687376 | | ESTs | 4.5 |
| | 440435 | AL042201 | Hs.21273 | transcription factor NYD-sp10 | 4.5 |
| 25 | 400288 | X06256 | Hs.149609 | integrin, alpha 5 (fibronectin receptor, | 4.5 |
| | 416114 | AJ695549 | Hs.183868 | glucuronidase, beta | 4.5 |
| | 437323 | AA371145 | Hs.194397 | leptin receptor | 4.5 |
| | 425139 | AW630488 | Hs.25338 | protease, serine, 23 | 4.5 |
| | 423678 | AW963357 | Hs.7847 | ESTs | 4.5 |
| 30 | 403961 | | | Target Exon | 4.5 |
| | 443462 | AJ064690 | Hs.171176 | ESTs | 4.5 |
| | 418483 | W26076 | Hs.221847 | ESTs | 4.5 |
| | 428873 | AJ701609 | Hs.98908 | ESTs | 4.5 |
| | 410268 | AA316181 | Hs.61635 | six transmembrane epithelial antigen of | 4.5 |
| 35 | 408298 | AJ745325 | Hs.271923 | Homo sapiens cDNA: FLJ22785 fis, clone K | 4.5 |
| | 449145 | AJ632122 | Hs.198408 | ESTs | 4.4 |
| | 439574 | AJ69788 | Hs.165190 | ESTs | 4.4 |
| | 423905 | AW579960 | Hs.135150 | lung type-I cell membrane-associated gly | 4.4 |
| | 453387 | AJ990741 | Hs.252809 | ESTs | 4.4 |
| 40 | 447444 | AK000318 | Hs.18616 | hypothetical protein FLJ20311 | 4.4 |
| | 433507 | AJ817336 | Hs.191791 | ESTs | 4.4 |
| | 448048 | BE281291 | Hs.170408 | ESTs, Moderately similar to A47582 B-cel | 4.4 |
| | 421064 | AJ245432 | Hs.101382 | tumor necrosis factor, alpha-induced pro | 4.4 |
| | 402604 | | | Target Exon | 4.4 |
| 45 | 446291 | BE397753 | Hs.14623 | interferon, gamma-inducible protein 30 | 4.4 |
| | 424503 | NM_002205 | Hs.149609 | integrin, alpha 5 (fibronectin receptor, | 4.4 |
| | 423600 | AJ633559 | Hs.310359 | ESTs | 4.4 |
| | 403361 | | | NM_002210*:Homo sapiens integrin, alpha | 4.4 |
| | 408432 | AW195262 | | gb:xn67b05.x1 NCL CGAP_CML1 Homo sapiens | 4.4 |
| 50 | 424489 | T48851 | Hs.274470 | D-siglec precursor, | 4.3 |
| | 442264 | AJ278777 | Hs.263455 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 4.3 |
| | 447247 | AW369351 | Hs.287955 | Homo sapiens cDNA FLJ13090 fis, clone NT | 4.3 |
| | 417018 | M16038 | Hs.80887 | v-yes-1 Yamaguchi sarcoma viral related | 4.3 |
| | 414020 | NM_002984 | Hs.75703 | small inducible cytokine A4 (homologous | 4.3 |
| 55 | 439566 | AF086387 | | gb:Homo sapiens full length insert cDNA | 4.3 |
| | 425242 | D13635 | Hs.155287 | KIAA0010 gene product | 4.3 |
| | 423529 | T87318 | Hs.120411 | ESTs | 4.3 |
| | 439538 | AA837323 | Hs.56407 | ESTs | 4.3 |
| | 453682 | T79703 | | gb:yd71e08.r1 Soares fetal liver spleen | 4.3 |
| 60 | 425259 | AL049280 | Hs.155397 | Homo sapiens mRNA; cDNA DKFZp564K143 (fr | 4.3 |
| | 417918 | AA209205 | Hs.163754 | hypothetical protein FLJ12606 | 4.3 |
| | 426649 | AJ914936 | Hs.97152 | ESTs | 4.3 |
| | 438875 | AA827640 | Hs.189059 | ESTs | 4.3 |
| | 445868 | BE169357 | Hs.207428 | ESTs | 4.3 |
| 65 | 426509 | M31166 | Hs.2050 | pentaxin-related gene, rapidly induced b | 4.3 |
| | 408893 | AW247090 | Hs.57101 | minichromosome maintenance deficient (S. | 4.3 |
| | 432058 | AW665996 | Hs.130729 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 4.3 |
| | 430694 | AA810624 | Hs.30936 | ESTs, Weakly similar to H2BH_HUMAN HISTO | 4.3 |
| | 441523 | AW514263 | Hs.301771 | ESTs, Weakly similar to ALUF_HUMAN !!! | 4.2 |
| 70 | 443950 | NM_001425 | Hs.9999 | epithelial membrane protein 3 | 4.2 |
| | 419896 | Z99362 | | gb:HSZ99362 DKFZphamy1 Homo sapiens cDNA | 4.2 |
| | 452994 | AW962597 | Hs.31305 | KIAA1547 protein | 4.2 |
| | 420841 | AJ625251 | Hs.94037 | hypothetical protein FLJ23053 | 4.2 |
| | 441255 | RO6350 | Hs.171635 | ESTs | 4.2 |
| 75 | 416426 | AA180256 | Hs.210473 | Homo sapiens cDNA FLJ14872 fis, clone PL | 4.2 |
| | 411789 | AF245505 | Hs.72157 | Adican | 4.2 |
| | 409638 | AW450420 | Hs.21335 | ESTs | 4.2 |
| | 439192 | AW970536 | Hs.105413 | ESTs | 4.2 |
| | 440684 | AJ253123 | Hs.127356 | ESTs, Highly similar to S21424 nestin (H | 4.2 |
| 80 | 437470 | AL390147 | Hs.134742 | hypothetical protein DKFZp547D065 | 4.2 |
| | 432343 | NM_002960 | Hs.2961 | S100 calcium-binding protein A3 | 4.2 |
| | 401454 | | | NM_014226*:Homo sapiens renal tumor anti | 4.2 |
| | 431770 | BE221880 | Hs.268555 | 5'-3' exonuclease 2 | 4.2 |
| | 442326 | H92962 | Hs.124813 | hypothetical protein MGC14817 | 4.2 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 419402 | Z68155 | Hs.90291 | laminin, beta 2 (laminin S) | 4.2 |
| | 435703 | AW630133 | Hs.83313 | GK003 protein | 4.2 |
| | 444609 | AW571659 | Hs.278081 | ESTs | 4.2 |
| 5 | 404407 | | | Target Exon | 4.2 |
| | 450581 | AF081513 | Hs.25195 | TGF-beta 4 | 4.2 |
| | 407838 | BE146411 | Hs.40342 | putative nuclear protein | 4.1 |
| | 410407 | X66839 | Hs.63287 | carbonic anhydrase IX | 4.1 |
| | 418883 | BE387036 | Hs.1211 | acid phosphatase 5, tartrate resistant | 4.1 |
| 10 | 438898 | AJ819863 | Hs.106243 | ESTs | 4.1 |
| | 421674 | T10707 | Hs.296355 | hypothetical protein FLJ23138 | 4.1 |
| | 445921 | AW015211 | Hs.146181 | ESTs | 4.1 |
| | 453055 | AW291436 | Hs.31917 | Homo sapiens, clone MGC:9658, mRNA, comp | 4.1 |
| | 413450 | Z99716 | Hs.75372 | N-acetylgalactosaminidase, alpha- | 4.1 |
| 15 | 427463 | AA442224 | Hs.97900 | ESTs | 4.1 |
| | 450639 | AJ703186 | Hs.277174 | ESTs | 4.1 |
| | 417576 | AA339449 | Hs.82285 | phosphonobosylglycinamide formyltransfer | 4.1 |
| | 437269 | AA334384 | Hs.149420 | ESTs | 4.1 |
| | 415688 | AA166963 | | gb:zo86d01.s1 Stratagene ovarian cancer | 4.1 |
| 20 | 414300 | AI304870 | Hs.188680 | ESTs | 4.1 |
| | 413278 | BE563085 | Hs.833 | interferon-stimulated protein, 15 kDa | 4.1 |
| | 415024 | AJ983981 | Hs.189114 | ESTs | 4.1 |
| | 408102 | U46351 | Hs.621 | lectin, galactoside-binding, soluble, 3 | 4.1 |
| | 448019 | AW947164 | Hs.195641 | ESTs, Moderately similar to I38022 hypot | 4.1 |
| 25 | 451433 | AA021140 | Hs.269265 | ESTs, Weakly similar to A46010 X-linked | 4.1 |
| | 446523 | NM_003063 | Hs.334629 | sarcolipin | 4.1 |
| | 427700 | AA262294 | Hs.180383 | dual specificity phosphatase 6 | 4.1 |
| | 402239 | | | Target Exon | 4.1 |
| | 423713 | AW754182 | | gb:RC2-CT0321-131199-011-c01 CT0321 Homo | 4.1 |
| 30 | 437814 | AJ088192 | Hs.135474 | ESTs, Weakly similar to DDX9_HUMAN ATP-D | 4.1 |
| | 414948 | C15240 | Hs.182155 | ESTs | 4.0 |
| | 421307 | BE539976 | Hs.103305 | Homo sapiens mRNA; cDNA DKFZp43B0425 (f | 4.0 |
| | 427375 | AL035460 | Hs.177536 | metallocarboxypeptidase CPX-1 | 4.0 |
| | 450297 | AW901347 | Hs.38592 | hypothetical protein FLJ23342 | 4.0 |
| 35 | 449655 | AJ021987 | Hs.59970 | ESTs | 4.0 |
| | 439978 | BE139460 | Hs.124673 | Homo sapiens cDNA FLJ11477 fis, clone HE | 4.0 |
| | 432842 | AW674093 | Hs.334822 | hypothetical protein MGC4485 | 4.0 |
| | 422282 | AF019225 | Hs.114309 | apolipoprotein L | 4.0 |
| | 452574 | AF127481 | Hs.301946 | lymphoid blast crisis oncogene | 4.0 |
| 40 | 449256 | AA059050 | Hs.59847 | ESTs | 4.0 |
| | 453385 | AW296101 | Hs.252806 | ESTs | 4.0 |
| | 443715 | AJ583187 | Hs.9700 | cyclin E1 | 4.0 |
| | 451778 | AJ826131 | Hs.62954 | ESTs, Weakly similar to zinc finger prot | 4.0 |
| | 441287 | AW293132 | Hs.131373 | ESTs | 4.0 |
| 45 | 418661 | NM_001949 | Hs.1189 | E2F transcription factor 3 | 4.0 |
| | 420894 | AA744597 | Hs.88854 | ESTs | 4.0 |
| | 454120 | AB032990 | Hs.40719 | hypothetical protein KIAA1164 | 4.0 |
| | 441627 | AA947552 | Hs.58086 | branched chain aminotransferase 1, cytos | 4.0 |
| | 453948 | AI970797 | Hs.64859 | ESTs | 4.0 |
| 50 | 444170 | AW613879 | Hs.102408 | ESTs | 4.0 |
| | 427221 | L15409 | Hs.174007 | von Hippel-Lindau syndrome | 4.0 |
| | 418821 | AA436002 | Hs.183161 | ESTs | 4.0 |
| | 418216 | AA662240 | Hs.283099 | AF15q14 protein | 4.0 |
| | 435106 | AA100847 | Hs.5978 | ESTs, Highly similar to AF174600 1 F-box | 4.0 |
| 55 | 430890 | X54232 | Hs.2699 | glypican 1 | 3.9 |
| | 429490 | AI971131 | Hs.23889 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 3.9 |
| | 425292 | NM_005824 | Hs.155545 | 37 kDa leucine-rich repeat (LRR) protein | 3.9 |
| | 436265 | AA731331 | Hs.190668 | ESTs | 3.9 |
| | 407304 | AA565832 | Hs.271649 | gb:nj32b03.s1 NCI_CGAP_AA1 Homo sapiens | 3.9 |
| 60 | 433244 | AB040943 | Hs.271285 | KIAA1510 protein | 3.9 |
| | 446960 | AW294936 | Hs.156762 | ESTs | 3.9 |
| | 406627 | T64904 | Hs.163780 | ESTs | 3.9 |
| | 420552 | AK000492 | Hs.98806 | hypothetical protein | 3.9 |
| | 402082 | | | C18000743:gi16678363[ref]NP_033416.1[t | 3.9 |
| 65 | 419594 | AA013051 | Hs.91417 | topoisomerase (DNA) II binding protein | 3.9 |
| | 448966 | AW372914 | Hs.86149 | phosphoinositol 3-phosphate-binding prot | 3.9 |
| | 427527 | AI809057 | Hs.293441 | immunoglobulin heavy constant mu | 3.9 |
| | 422564 | AJ148006 | Hs.222120 | ESTs | 3.9 |
| | 418781 | T41160 | Hs.8404 | ESTs | 3.9 |
| 70 | 431820 | AW410408 | Hs.271167 | L-pipecolic acid oxidase | 3.9 |
| | 413095 | AA494359 | Hs.30715 | potassium voltage-gated channel, Isk-rel | 3.9 |
| | 430637 | BE160081 | Hs.256290 | S100 calcium-binding protein A11 (calgiz | 3.9 |
| | 443539 | AJ076182 | Hs.134074 | ESTs, Moderately similar to ALU6_HUMAN A | 3.9 |
| | 422173 | BE385828 | Hs.250619 | phorbol-like protein MDS019 | 3.9 |
| 75 | 433388 | AJ432672 | Hs.288539 | hypothetical protein FLJ22191 | 3.8 |
| | 403849 | | | Target Exon | 3.8 |
| | 406646 | M33600 | Hs.308026 | major histocompatibility complex, class | 3.8 |
| | 445075 | AI651827 | Hs.344767 | ESTs | 3.8 |
| | 420004 | AW975532 | Hs.164039 | ESTs, Moderately similar to I38022 hypot | 3.8 |
| 80 | 449670 | F07693 | Hs.85603 | Homo sapiens mRNA; cDNA DKFZp434K2172 (f | 3.8 |
| | 424479 | AF064238 | Hs.149098 | smoothelin | 3.8 |
| | 449625 | NM_014253 | | odz (odd Oz/ten-m, Drosophila) homolog 1 | 3.8 |
| | 418641 | BE243136 | Hs.86947 | a disintegrin and metalloproteinase doma | 3.8 |
| | 439979 | AW600291 | Hs.6823 | hypothetical protein FLJ10430 | 3.8 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 427286 | AW732802 | Hs.2132 | epidermal growth factor receptor pathway | 3.8 |
| | 453920 | AI133148 | Hs.36602 | I factor (complement) | 3.8 |
| | 453857 | AL080235 | Hs.35861 | DKFZP586E1621 protein | 3.8 |
| 5 | 406872 | AI760903 | | gbwi09h08.x1 NCI_CGAP_CLL1 Homo sapiens | 3.8 |
| | 403696 | | | C4001100:gi 5852342 gb AAD54015.1 (AF0 | 3.8 |
| | 417791 | AW965339 | Hs.111471 | ESTs | 3.8 |
| | 418036 | Z37976 | Hs.83337 | latent transforming growth factor beta b | 3.8 |
| | 404209 | | | Target Exon | 3.8 |
| 10 | 431454 | AW975980 | Hs.292918 | ESTs | 3.8 |
| | 410422 | AL042014 | Hs.63348 | Homo sapiens, clone MGC:15203, mRNA, com | 3.8 |
| | 406739 | AI566709 | Hs.182426 | ribosomal protein S2 | 3.8 |
| | 450810 | BE207588 | Hs.334360 | transforming growth factor beta 1 induce | 3.8 |
| | 457876 | AI821940 | | ESTs, Moderately similar to ALU8_HUMAN A | 3.8 |
| 15 | 435718 | R06569 | Hs.269534 | ESTs | 3.8 |
| | 429716 | R25685 | Hs.211933 | collagen, type XIII, alpha 1 | 3.8 |
| | 442710 | AI015631 | Hs.23210 | ESTs | 3.8 |
| | 456534 | X91195 | Hs.100623 | phospholipase C, beta 3, neighbor pseudo | 3.8 |
| | 419764 | BE262524 | Hs.93183 | vasodilator-stimulated phosphoprotein | 3.8 |
| 20 | 436674 | AA725002 | Hs.272018 | low molecular mass ubiquinone-binding pr | 3.8 |
| | 408896 | AI610447 | Hs.48778 | niban protein | 3.8 |
| | 425300 | AW601773 | Hs.270259 | ESTs | 3.8 |
| | 432886 | BE159028 | Hs.279704 | chromatin accessibility complex 1 | 3.8 |
| | 424090 | X99699 | Hs.139262 | XIAP associated factor-1 | 3.7 |
| 25 | 420202 | AL036557 | Hs.95910 | putative lymphocyte G0/G1 switch gene | 3.7 |
| | 427584 | BE410293 | Hs.179718 | v-myb avian myeloblastosis viral oncogen | 3.7 |
| | 420579 | AA278449 | Hs.137429 | ESTs | 3.7 |
| | 406038 | Y14443 | | zinc finger protein 200 | 3.7 |
| | 412590 | AL134388 | Hs.135033 | ESTs, Weakly similar to I38022 hypotheri | 3.7 |
| 30 | 406714 | AI219304 | Hs.266959 | hemoglobin, gamma G | 3.7 |
| | 412014 | AI620650 | Hs.43761 | ESTs, Weakly similar to A46010 X-linked | 3.7 |
| | 419713 | AW968058 | Hs.92381 | nudix (nucleoside diphosphate linked moi | 3.7 |
| | 449115 | AW959952 | Hs.37528 | ESTs, Weakly similar to AF090944 1 PRO06 | 3.7 |
| | 408955 | BE315170 | Hs.8087 | Target CAT | 3.7 |
| 35 | 441362 | BE614410 | Hs.23044 | RAD51 (S. cerevisiae) homolog (E coli Re | 3.7 |
| | 413774 | AA131782 | Hs.182314 | ESTs | 3.7 |
| | 440225 | BE295782 | Hs.159 | tumor necrosis factor receptor superfam | 3.7 |
| | 414528 | AA148950 | Hs.188836 | ESTs | 3.7 |
| | 436137 | AI056769 | Hs.133512 | ESTs | 3.7 |
| 40 | 414733 | BE514535 | Hs.77171 | minichromosome maintenance deficient (S. | 3.7 |
| | 406785 | AA588061 | | gbnk10d03.s1 NCI_CGAP_Co2 Homo sapiens | 3.7 |
| | 443361 | AI792628 | Hs.133273 | ESTs | 3.7 |
| | 434868 | R50032 | Hs.159263 | collagen, type VI, alpha 2 | 3.7 |
| | 409557 | BE182896 | Hs.211193 | ESTs | 3.7 |
| 45 | 420300 | AA258245 | Hs.127573 | Homo sapiens FKSG41 (FKSG41) mRNA, compl | 3.7 |
| | 427695 | R88483 | Hs.127862 | ESTs | 3.7 |
| | 407756 | AA116021 | Hs.38260 | ubiquitin specific protease 18 | 3.6 |
| | 437916 | BE566249 | Hs.20999 | hypothetical protein FLJ23142 | 3.6 |
| | 434563 | AW083994 | Hs.9469 | pleckstrin homology domain-containing, f | 3.6 |
| 50 | 444371 | BE540274 | Hs.239 | forkhead box M1 | 3.6 |
| | 437816 | AI823445 | Hs.280699 | ESTs | 3.6 |
| | 405605 | | | C2001342:gi 127814 sp P26434 NAH4_RAT SO | 3.6 |
| | 444794 | AI419991 | Hs.145225 | ESTs | 3.6 |
| | 430540 | AW245422 | Hs.106357 | Homo sapiens cDNA: FLJ22105 fis, clone H | 3.6 |
| 55 | 429747 | M87507 | Hs.2490 | caspase 1, apoptosis-related cysteine pr | 3.6 |
| | 453785 | AI368236 | Hs.283732 | ESTs, Moderately similar to ALU1_HUMAN A | 3.6 |
| | 403267 | | | Target Exon | 3.6 |
| | 440370 | AA884000 | Hs.8173 | hypothetical protein FLJ10803 | 3.6 |
| | 447497 | AW167254 | Hs.205722 | ESTs | 3.6 |
| 60 | 428600 | AW863261 | Hs.242413 | hypothetical protein DKFZp434K1421 | 3.6 |
| | 428715 | AW293716 | Hs.53126 | ESTs | 3.6 |
| | 416097 | BE387371 | Hs.118964 | hypothetical protein FLJ20085 | 3.6 |
| | 453438 | AI469935 | Hs.22792 | ESTs | 3.6 |
| | 427299 | AA830210 | Hs.214263 | ESTs, Moderately similar to ALU1_HUMAN A | 3.6 |
| 65 | 434577 | R37316 | Hs.179769 | Homo sapiens cDNA: FLJ22487 fis, clone H | 3.6 |
| | 452785 | AL359942 | Hs.296434 | erythroid differentiation and denucleati | 3.6 |
| | 434467 | BE552368 | Hs.231853 | Homo sapiens cDNA FLJ13445 fis, clone PL | 3.6 |
| | 435523 | T62849 | Hs.11080 | membrane-spanning 4-domains, subfamily A | 3.6 |
| | 418287 | AI872319 | Hs.78935 | methionine aminopeptidase; eIF-2-associa | 3.6 |
| 70 | 422156 | N34524 | | gb:yy56d10.s1 Soares_multiple_sclerosis_ | 3.6 |
| | 441224 | AI076964 | Hs.7753 | calumenin | 3.6 |
| | 458072 | AI890347 | Hs.271923 | Homo sapiens cDNA: FLJ22785 fis, clone K | 3.6 |
| | 435677 | AA694142 | Hs.293726 | ESTs, Weakly similar to TSGA RAT TESTIS | 3.6 |
| | 433325 | AW206986 | Hs.143905 | ESTs | 3.6 |
| | 420683 | AA830168 | Hs.271305 | ESTs | 3.6 |
| 75 | 443206 | AB011420 | Hs.9075 | serine/threonine kinase 17a (apoptosis-i | 3.6 |
| | 454078 | AA601518 | Hs.22209 | secreted modular calcium-binding protein | 3.6 |
| | 404584 | | | Target Exon | 3.5 |
| | 428311 | NM_005651 | Hs.183671 | tryptophan 2,3-dioxygenase | 3.5 |
| 80 | 425922 | AL157466 | Hs.162751 | Homo sapiens mRNA: cDNA DKFZp761E2423 (f | 3.5 |
| | 415131 | D61119 | | gb:HUM158C118 Clontech human fetal brain | 3.5 |
| | 412971 | AA889628 | Hs.35125 | ESTs | 3.5 |
| | 451593 | AF151879 | Hs.26706 | CGI-121 protein | 3.5 |
| | 416427 | BE244050 | Hs.79307 | Rac/Cdc42 guanine exchange factor (GEF) | 3.5 |

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|----|--------|-----------|-----------|--|-----|
| | 427809 | M26380 | Hs.180878 | lipoprotein lipase | 3.5 |
| | 443303 | U67319 | Hs.9216 | caspase 7, apoptosis-related cysteine pr | 3.5 |
| | 42765 | AW409701 | Hs.1578 | baculoviral IAP repeat-containing 5 (sur | 3.5 |
| | 445936 | BE543594 | Hs.61478 | hypothetical protein FLJ22329 | 3.5 |
| 5 | 411537 | BE073250 | | gb:MR0-BT0551-060300-102-e05 BT0551 Homo | 3.5 |
| | 432250 | AA452088 | Hs.274170 | Ops-interacting protein 2 | 3.5 |
| | 458438 | AI141520 | Hs.151464 | ESTs, Weakly similar to ALUC_HUMAN !!!! | 3.5 |
| | 407253 | AA411175 | Hs.141939 | ESTs, Moderately similar to S65657 alpha | 3.5 |
| | 410507 | AA355288 | Hs.76064 | transitional epithelia response protein | 3.5 |
| 10 | 412436 | AA665089 | | gb:nu76d01.s1 NCI_CGAP_Alv1 Homo sapiens | 3.5 |
| | 416933 | BE561850 | Hs.80506 | small nuclear ribonucleoprotein polypept | 3.5 |
| | 437681 | AI207958 | Hs.166556 | Homo sapiens, Similar to TEA domain fami | 3.5 |
| | 408247 | AA053451 | Hs.225632 | leucine zipper protein 3 | 3.5 |
| | 440074 | AA863045 | Hs.10669 | ESTs, Weakly similar to T00050 hypotheti | 3.5 |
| 15 | 422448 | AW372922 | Hs.116774 | integrin, alpha 1 | 3.5 |
| | 420676 | AA434780 | Hs.4248 | vav 2 oncogene | 3.5 |
| | 417663 | R07483 | Hs.180461 | ESTs | 3.5 |
| | 451089 | AA903705 | Hs.4190 | Homo sapiens cDNA: FLJ23269 fs, clone C | 3.5 |
| | 451446 | AI826288 | Hs.171637 | hypothetical protein MGC2628 | 3.5 |
| 20 | 414727 | BE466904 | Hs.190162 | gb:hz28f03.x1 NCI_CGAP_GC6 Homo sapiens | 3.5 |
| | 421778 | AA428000 | Hs.283072 | actin related protein 2/3 complex, subun | 3.5 |
| | 427413 | BE547647 | Hs.177781 | hypothetical protein MGC5618 | 3.5 |
| | 414039 | M83221 | Hs.858 | v-rel avian reticuloendotheliosis viral | 3.5 |
| | 456304 | AI820973 | | gb:nc21c02.y5 NCI_CGAP_Prl1 Homo sapiens | 3.5 |
| 25 | 449162 | AI632740 | Hs.10476 | ESTs | 3.5 |
| | 437774 | AW978199 | Hs.291648 | ESTs, Weakly similar to i38022 hypotheti | 3.5 |
| | 426827 | AW067805 | Hs.172665 | methyleneetetrahydrofolate dehydrogenase | 3.4 |
| | 452203 | X57522 | | transporter 1, ATP-binding cassette, sub | 3.4 |
| | 450325 | AI935962 | Hs.26289 | ESTs | 3.4 |
| 30 | 457211 | AW972565 | Hs.32399 | ESTs, Weakly similar to S51797 vasodilat | 3.4 |
| | 419726 | U50330 | Hs.1274 | bone morphogenetic protein 1 | 3.4 |
| | 417409 | BE272506 | Hs.82109 | syndecan 1 | 3.4 |
| | 412811 | H06382 | | ESTs | 3.4 |
| | 430758 | T91568 | Hs.270616 | ESTs, Moderately similar to A34087 hypot | 3.4 |
| 35 | 425769 | U72513 | Hs.159486 | Human RPL13-2 pseudogene mRNA, complete | 3.4 |
| | 452682 | AA456193 | Hs.9071 | progesterone membrane binding protein | 3.4 |
| | 429500 | X78565 | Hs.289114 | hexabrachion (tenascin C, cytotoxicity) | 3.4 |
| | 447674 | BE270640 | Hs.19192 | cyclin-dependent kinase 2 | 3.4 |
| | 443378 | AW392550 | Hs.9280 | proteasome (prosome, macropain) subunit, | 3.4 |
| 40 | 446134 | AW161234 | Hs.13993 | TBP-like 1 | 3.4 |
| | 418669 | U85992 | Hs.87197 | Human clone IMAGE:35527 unknown protein | 3.4 |
| | 425006 | R38685 | Hs.222746 | ESTs | 3.4 |
| | 435256 | AF193766 | Hs.13872 | cytokine-like protein C17 | 3.4 |
| | 453379 | AA035261 | Hs.61753 | ESTs | 3.4 |
| 45 | 448224 | R48700 | Hs.20733 | Homo sapiens cDNA: FLJ22356 fs, clone H | 3.4 |
| | 455899 | BE155112 | | gb:PM1-HT0350-151299-003-a03 HT0350 Homo | 3.4 |
| | 422017 | NM_003877 | Hs.110776 | STAT induced STAT inhibitor-2 | 3.4 |
| | 417395 | BE564245 | Hs.82084 | integrin beta 3 binding protein (beta3-e | 3.4 |
| | 405046 | | | C3000978:gi9280045:dbj BAB01579.1 (AB0 | 3.4 |
| 50 | 423178 | AI033140 | Hs.124983 | Homo sapiens mRNA; cDNA DKFZp564C142 (fr | 3.4 |
| | 455142 | AW861840 | | gb:CMO-CT0337-250200-243-g01 CT0337 Homo | 3.4 |
| | 418819 | AA228776 | Hs.191721 | ESTs | 3.4 |
| | 428289 | M26301 | Hs.2253 | complement component 2 | 3.4 |
| | 412799 | AI267606 | | gb:aq91h03.x1 Stanley Frontal S8 pool 1 | 3.4 |
| 55 | 403108 | | | ENSP00000241415: Hypothetical 67.7 kDa p | 3.4 |
| | 421637 | AF035290 | Hs.106300 | Homo sapiens clone 23556 mRNA sequence | 3.4 |
| | 419373 | NM_003244 | Hs.90077 | TG-interacting factor (TALE family homeo | 3.4 |
| | 424408 | AI754813 | Hs.146428 | collagen, type V, alpha 1 | 3.4 |
| | 451061 | AW291487 | Hs.213659 | ESTs, Weakly similar to KIAA1357 protein | 3.4 |
| 60 | 433578 | BE336886 | Hs.3416 | adipose differentiation-related protein | 3.4 |
| | 439867 | AA847510 | Hs.161292 | ESTs | 3.4 |
| | 449249 | T52285 | Hs.193115 | Homo sapiens mRNA for KIAA1764 protein, | 3.4 |
| | 420982 | AW576160 | Hs.100729 | KIAA0692 protein | 3.4 |
| | 440826 | AW383618 | Hs.346256 | ESTs, Moderately similar to ALU2_HUMAN A | 3.4 |
| 65 | 427687 | AW003867 | Hs.1570 | histamine receptor H1 | 3.4 |
| | 400533 | | | ENSP00000209376: PRED65 protein (Fragmen | 3.3 |
| | 436314 | AI983409 | Hs.189226 | ESTs | 3.3 |
| | 418110 | R43523 | Hs.217754 | hypothetical protein FLJ22202 | 3.3 |
| 70 | 448140 | AF146761 | Hs.20450 | BCM-like membrane protein precursor | 3.3 |
| | 402229 | BE262804 | | mitochondrial ribosomal protein S2 | 3.3 |
| | 410687 | U24389 | Hs.65436 | lysyl oxidase-like 1 | 3.3 |
| | 424614 | X54486 | Hs.151242 | serine (or cysteine) proteinase inhibito | 3.3 |
| | 443338 | R99575 | Hs.302908 | ESTs | 3.3 |
| 75 | 433062 | AK001757 | Hs.281348 | hypothetical protein FLJ10895 | 3.3 |
| | 405303 | | | Target Exon | 3.3 |
| | 410889 | X91662 | Hs.66744 | twist (Drosophila) homolog (acrocephalos | 3.3 |
| | 406673 | M34996 | Hs.198253 | major histocompatibility complex, class | 3.3 |
| | 431721 | AB032996 | Hs.268044 | KIAA1170 protein | 3.3 |
| 80 | 426746 | J03626 | Hs.2057 | uridine monophosphate synthetase (orotat | 3.3 |
| | 425262 | D87119 | Hs.155418 | GS3955 protein | 3.3 |
| | 424947 | R77952 | | ESTs, Weakly similar to alternatively sp | 3.3 |
| | 437634 | AW293046 | Hs.255158 | ESTs | 3.3 |
| | 437014 | AA808757 | Hs.222531 | ESTs, Weakly similar to S59501 interfero | 3.3 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 411688 | AW953440 | | gb:EST365510 MAGE resequences, MAGB Homo | 3.3 |
| | 447499 | AW262580 | Hs.147674 | protocadherin beta 16 | 3.3 |
| | 432625 | AI243596 | Hs.94830 | ESTs, Moderately similar to T03094 A-kin | 3.3 |
| 5 | 435644 | AA700867 | Hs.269659 | ESTs | 3.3 |
| | 406060 | | | Target Exon | 3.3 |
| | 425018 | BE245277 | Hs.154196 | E4F transcription factor 1 | 3.3 |
| | 450728 | AW162923 | Hs.25363 | presenilin 2 (Alzheimer disease 4) | 3.3 |
| | 443105 | X96753 | Hs.9004 | chondroitin sulfate proteoglycan 4 (mela | 3.3 |
| 10 | 414799 | AI752416 | Hs.77326 | insulin-like growth factor binding prote | 3.3 |
| | 435375 | AI733610 | Hs.187832 | ESTs | 3.3 |
| | 432693 | AW449630 | Hs.293790 | ESTs | 3.3 |
| | 449340 | AW235786 | Hs.195359 | hypothetical protein MGC10954 | 3.3 |
| | 422530 | AW972300 | Hs.118110 | bone marrow stromal cell antigen 2 | 3.3 |
| 15 | 448002 | Y15227 | Hs.20149 | deleted in lymphocytic leukemia, 1 | 3.3 |
| | 433160 | AW207002 | Hs.134342 | TASP for testis-specific adriamycin sens | 3.3 |
| | 429125 | AA446854 | Hs.271004 | ESTs, Weakly similar to I38022 hypotheri | 3.3 |
| | 452526 | W38537 | Hs.280740 | hypothetical protein MGC3040 | 3.3 |
| | 416664 | H77780 | Hs.20289 | ESTs | 3.3 |
| 20 | 444911 | U06117 | Hs.250 | xanthene dehydrogenase | 3.3 |
| | 453544 | AA831785 | Hs.171914 | Homo sapiens cDNA FLJ14209 fis, clone NT | 3.3 |
| | 433042 | AW193534 | Hs.281895 | Homo sapiens cDNA FLJ11660 fis, clone HE | 3.3 |
| | 444046 | AI360834 | Hs.135094 | ESTs | 3.3 |
| | 411373 | BE326276 | Hs.8861 | ESTs | 3.3 |
| 25 | 431865 | AA521106 | Hs.136375 | ESTs, Weakly similar to S65824 reverse t | 3.3 |
| | 408116 | AA251393 | Hs.289052 | Homo sapiens, Similar to RIKEN cDNA 5430 | 3.3 |
| | 410006 | AW732308 | Hs.57783 | eukaryotic translation initiation factor | 3.3 |
| | 442485 | BE092285 | Hs.29724 | hypothetical protein FLJ13187 | 3.3 |
| | 416379 | N38857 | Hs.203933 | ESTs | 3.3 |
| 30 | 416308 | AW291942 | Hs.23628 | 3 beta-hydroxy-delta 5-C27-steroid oxido | 3.3 |
| | 427954 | J03060 | Hs.247551 | metaxin 1 | 3.3 |
| | 459660 | M79082 | | ESTs | 3.3 |
| | 419829 | AI924228 | Hs.115185 | ESTs, Moderately similar to PC4259 ferri | 3.3 |
| | 437945 | T78519 | | gb:yd68c08.r1 Soares fetal liver spleen | 3.3 |
| 35 | 400850 | | | Target Exon | 3.3 |
| | 457244 | AA581385 | Hs.162473 | ESTs, Weakly similar to I38022 hypotheri | 3.3 |
| | 430462 | AI584156 | Hs.105640 | Homo sapiens, clone IMAGE:4139775, mRNA, | 3.3 |
| | 457653 | AI820719 | Hs.154662 | DnaJ (Hsp40) homolog, subfamily A, membe | 3.3 |
| | 431836 | AF178532 | Hs.271411 | beta-site APP-cleaving enzyme 2 | 3.2 |
| 40 | 440933 | AI208217 | Hs.142879 | ESTs | 3.2 |
| | 418079 | R40058 | Hs.6911 | ESTs | 3.2 |
| | 414280 | BE410769 | Hs.75873 | zyxin | 3.2 |
| | 425295 | AA431366 | Hs.37251 | ESTs | 3.2 |
| | 408872 | AI476139 | Hs.13291 | ESTs | 3.2 |
| 45 | 416857 | AA188775 | Hs.292453 | ESTs | 3.2 |
| | 429599 | AA806106 | Hs.123664 | ESTs | 3.2 |
| | 437437 | AA226869 | | hypothetical protein DKFZp762L0311 | 3.2 |
| | 434274 | AA628539 | Hs.116252 | ESTs, Moderately similar to ALU1_HUMAN A | 3.2 |
| | 403349 | NM_001406 | | ephrin-B3 | 3.2 |
| 50 | 449385 | AI650471 | Hs.347290 | ESTs | 3.2 |
| | 431421 | AW969118 | Hs.108144 | ESTs, Weakly similar to unnamed protein | 3.2 |
| | 419865 | NM_007020 | Hs.93502 | U1-snRNP binding protein homolog (70kD) | 3.2 |
| | 410700 | AA352335 | Hs.65641 | hypothetical protein FLJ20073 | 3.2 |
| 55 | 432044 | AW972727 | | gb:EST384819 MAGE resequences, MAGL Homo | 3.2 |
| | 412490 | AW803564 | Hs.288850 | Homo sapiens cDNA: FLJ22528 fis, clone H | 3.2 |
| | 408431 | AI338631 | Hs.43266 | Homo sapiens cDNA: FLJ22536 fis, clone H | 3.2 |
| | 430413 | AW842182 | Hs.241392 | small inducible cytokine A5 (RANTES) | 3.2 |
| | 448789 | BE539108 | Hs.22051 | hypothetical protein MGC15548 | 3.2 |
| | 439332 | AW842747 | Hs.300870 | Homo sapiens mRNA; cDNA DKFZp547M072 (fr | 3.2 |
| 60 | 418030 | BE207573 | Hs.83321 | neuromedin B | 3.2 |
| | 428878 | AA436884 | Hs.48926 | ESTs | 3.2 |
| | 451527 | AF022813 | Hs.26518 | transmembrane 4 superfamily member 7 | 3.2 |
| | 426406 | AI742501 | Hs.169756 | complement component 1, s subcomponent | 3.2 |
| | 448432 | AI783586 | Hs.208575 | ESTs | 3.2 |
| 65 | 433894 | AI907682 | Hs.243293 | ESTs | 3.2 |
| | 436210 | AI825420 | Hs.197824 | ESTs | 3.2 |
| | 433791 | AA719352 | Hs.112718 | ESTs | 3.2 |
| | 450150 | AI754391 | Hs.23510 | Kruppel-like factor 12 | 3.2 |
| | 427513 | AI476318 | Hs.192480 | ESTs | 3.2 |
| 70 | 423789 | AK002084 | Hs.132851 | hypothetical protein FLJ11222 | 3.2 |
| | 451350 | AI791447 | | gb:ni13a05.y5 NCL_CGAP_Co4 Homo sapiens | 3.2 |
| | 429065 | AI753247 | Hs.29643 | Homo sapiens cDNA FLJ13103 fis, clone NT | 3.2 |
| | 416784 | AA334592 | Hs.79914 | lumican | 3.2 |
| | 406851 | AA609784 | | major histocompatibility complex, class | 3.2 |
| 75 | 428032 | AW997704 | Hs.11493 | Homo sapiens cDNA FLJ13536 fis, clone PL | 3.2 |
| | 412646 | NM_006825 | Hs.74368 | transmembrane protein (63kD), endoplasmic | 3.2 |
| | 432065 | AA401039 | Hs.2903 | protein phosphatase 4 (formerly X), cata | 3.2 |
| | 415709 | AA649850 | Hs.278558 | ESTs | 3.2 |
| | 422798 | R92347 | Hs.34574 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.2 |
| 80 | 437807 | AI017875 | Hs.136829 | ESTs | 3.2 |
| | 425171 | AW732240 | Hs.16365 | ESTs | 3.2 |
| | 448108 | AW300021 | Hs.170685 | ESTs | 3.2 |
| | 402523 | | | C1001173:gi9743439[gb]AAAF79932.2[AF2 | 3.2 |
| | 440146 | AW014231 | Hs.90790 | Homo sapiens cDNA: FLJ22930 fis, clone K | 3.2 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 429415 | NM_002593 | Hs.202097 | procollagen C-endopeptidase enhancer | 3.2 |
| | 422081 | AW136820 | Hs.196011 | ESTs | 3.2 |
| | 436258 | AW867491 | Hs.107125 | plasmalemma vesicle associated protein | 3.2 |
| 5 | 410886 | AW809324 | | gb:MR4-ST0121-141099-010-G06_1 ST0121 Ho | 3.2 |
| | 442609 | AL020996 | Hs.8518 | selenoprotein N | 3.2 |
| | 416188 | BE157260 | Hs.79070 | v-myc avian myelocytomatosis viral oncog | 3.2 |
| | 441544 | AW300043 | Hs.127137 | ESTs | 3.2 |
| | 437860 | AA333063 | Hs.279898 | Homo sapiens cDNA: FLJ23165 fis, clone L | 3.2 |
| | 419652 | AL157485 | Hs.91973 | hypothetical protein | 3.2 |
| 10 | 443623 | AA345519 | Hs.9641 | complement component 1, q subcomponent, | 3.2 |
| | 415198 | AW009480 | Hs.943 | natural killer cell transcript 4 | 3.2 |
| | 441701 | AW339828 | Hs.127497 | ESTs | 3.2 |
| | 426384 | AI472078 | Hs.303662 | hypothetical protein FLJ13189 (FLJ13189) | 3.2 |
| | 420886 | AA805453 | | ESTs, Weakly similar to T29012 hypotheti | 3.2 |
| 15 | 428896 | AW291932 | Hs.98936 | ESTs | 3.2 |
| | 458253 | AW296952 | Hs.196802 | ESTs | 3.2 |
| | 456895 | AA354771 | Hs.43047 | Homo sapiens cDNA FLJ13585 fis, clone PL | 3.2 |
| | 434818 | AA650097 | Hs.5996 | ESTs | 3.2 |
| | 424278 | AK000723 | Hs.144517 | hypothetical protein FLJ20716 | 3.2 |
| 20 | 434131 | AI858275 | Hs.143659 | ESTs | 3.2 |
| | 447111 | AI017574 | Hs.17409 | cysteine-rich protein 1 (intestinal) | 3.1 |
| | 443021 | AA368546 | Hs.8904 | Ig superfamily protein | 3.1 |
| | 416677 | T83470 | Hs.334840 | ESTs, Moderately similar to I78885 serin | 3.1 |
| | 429973 | AI423317 | Hs.164580 | ESTs | 3.1 |
| 25 | 422545 | X02761 | Hs.287820 | fibronectin 1 | 3.1 |
| | 444006 | BE395085 | Hs.10086 | type I transmembrane protein Fn14 | 3.1 |
| | 420116 | NM_013241 | Hs.95231 | FH1/FH2 domain-containing protein | 3.1 |
| | 401841 | | | NM_015113:Homo sapiens KIAA0399 protein | 3.1 |
| 30 | 414416 | AW409985 | Hs.76084 | hypothetical protein MGC2721 | 3.1 |
| | 431019 | NM_005249 | Hs.2714 | forkhead box G1B | 3.1 |
| | 453707 | AW003879 | Hs.126522 | Homo sapiens, clone MGC:16722, mRNA, com | 3.1 |
| | 432188 | AI362952 | Hs.2928 | solute carrier family 7 (cationic amino | 3.1 |
| | 407378 | AA299264 | Hs.57776 | ESTs, Moderately similar to I38022 hypot | 3.1 |
| | 430701 | AI760833 | Hs.293971 | ESTs | 3.1 |
| 35 | 429569 | AA454993 | Hs.138343 | ESTs, Weakly similar to I78885 serine/th | 3.1 |
| | 458918 | H56499 | Hs.252692 | ESTs, Weakly similar to I38022 hypotheti | 3.1 |
| | 439764 | T26535 | Hs.22744 | hypothetical protein MGC13105 | 3.1 |
| | 452221 | C21322 | Hs.288057 | hypothetical protein FLJ22242 | 3.1 |
| 40 | 403969 | | | ENSP0000034663:Zinc finger protein 131 | 3.1 |
| | 427359 | AW020782 | Hs.79881 | Homo sapiens cDNA: FLJ23006 fis, clone L | 3.1 |
| | 414396 | BE548266 | Hs.76057 | galactose-4-epimerase, UDP- | 3.1 |
| | 444153 | AK001610 | Hs.10414 | hypothetical protein FLJ10748 | 3.1 |
| | 414403 | AW969551 | Hs.76064 | ribosomal protein L27a | 3.1 |
| | 444168 | AW379879 | | gb:RC1-HT0256-081199-011-01 HT0256 Homo | 3.1 |
| 45 | 410595 | AW629223 | Hs.64794 | zinc finger protein 183 (RING finger, C3 | 3.1 |
| | 444881 | AI623288 | Hs.192805 | ESTs | 3.1 |
| | 440381 | AA917808 | Hs.190495 | ESTs | 3.1 |
| | 416207 | NM_014745 | Hs.79077 | Homo sapiens, clone MGC:2908, mRNA, comp | 3.1 |
| | 439130 | AA306090 | Hs.124707 | ESTs | 3.1 |
| 50 | 457579 | AB030816 | Hs.36761 | HRAS-like suppressor | 3.1 |
| | 406736 | AI254733 | Hs.182426 | ribosomal protein S2 | 3.1 |
| | 420172 | AA601122 | Hs.95655 | secreted and transmembrane 1 | 3.1 |
| | 428060 | AA420616 | Hs.249483 | ESTs | 3.1 |
| | 444143 | AW747996 | Hs.160999 | ESTs, Moderately similar to A56194 throm | 3.1 |
| 55 | 409154 | U72882 | Hs.50842 | interferon-induced protein 35 | 3.1 |
| | 449426 | T92251 | Hs.196882 | ESTs | 3.1 |
| | 458760 | AI498631 | Hs.111334 | ferritin, light polypeptide | 3.1 |
| | 450811 | AI739486 | Hs.245497 | ESTs | 3.1 |
| | 425331 | AW962128 | | gb:EST374201 MAGE resequences, MAGG Homo | 3.1 |
| 60 | 445211 | BE045601 | Hs.118248 | ESTs, Weakly similar to YC18_HUMAN HYPOT | 3.1 |
| | 441318 | AI078234 | Hs.176130 | ESTs | 3.1 |
| | 450625 | AW970107 | | gb:EST382188 MAGE resequences, MAGK Homo | 3.1 |
| | 437640 | AA764893 | Hs.272155 | ESTs, Weakly similar to I38022 hypotheti | 3.1 |
| | 444672 | Z95636 | Hs.11669 | laminin, alpha 5 | 3.1 |
| 65 | 407047 | X65965 | | gb:H.sapiens SOD-2 gene for manganese su | 3.1 |
| | 413834 | BE296896 | Hs.224179 | ESTs, Weakly similar to I38022 hypotheti | 3.1 |
| | 439755 | AW748482 | Hs.77873 | B7 homolog 3 | 3.1 |
| | 435520 | AA297990 | Hs.9315 | HNOEL-iso protein | 3.1 |
| | 414598 | AI094221 | Hs.135150 | lung type-I cell membrane-associated gly | 3.1 |
| 70 | 440948 | AW188311 | Hs.128619 | ESTs | 3.1 |
| | 412851 | AI826502 | Hs.106149 | ESTs | 3.1 |
| | 417336 | R70429 | Hs.81988 | disabled (Drosophila) homolog 2 (mitogen | 3.1 |
| | 417944 | AU077196 | Hs.82985 | collagen, type V, alpha 2 | 3.1 |
| | 411671 | BE049094 | | ESTs | 3.1 |
| 75 | 430444 | AW296421 | Hs.121035 | ESTs | 3.1 |
| | 425843 | BE313280 | Hs.159627 | death associated protein 3 | 3.1 |
| | 407721 | Y12735 | Hs.38018 | dual-specificity tyrosine-[Y]-phosphoryl | 3.1 |
| | 439093 | AA534163 | Hs.5476 | Homo sapiens, clone IMAGE:3530123, mRNA, | 3.1 |
| | 449523 | NM_000579 | Hs.54443 | chemokine (C-C motif) receptor 5 | 3.1 |
| 80 | 435664 | AI032087 | Hs.269819 | ESTs | 3.1 |
| | 453085 | AW954243 | | KIAA0251 protein | 3.1 |
| | 430314 | AA369601 | Hs.239138 | pre-B-cell colony-enhancing factor | 3.0 |
| | 447527 | AI702896 | Hs.42091 | ESTs | 3.0 |

| | | | | | |
|------------|-------------|---------------------------------------|--|---|-----|
| 5 | 432682 | AI376400 | Hs.159588 | ESTs | 3.0 |
| | 416941 | BE000150 | Hs.48778 | niban protein | 3.0 |
| | 455481 | AW948317 | | gb:RC0-MT0015-280300-021-a09 MT0015 Homo | 3.0 |
| | 445906 | N28939 | Hs.13434 | Homo sapiens clone 24418 mRNA sequence | 3.0 |
| | 408716 | AI567839 | Hs.151714 | Homo sapiens mRNA for KIAA1769 protein, | 3.0 |
| 10 | 424308 | AW975531 | Hs.154443 | minichromosome maintenance deficient (S. | 3.0 |
| | 436443 | AW138211 | Hs.128746 | ESTs | 3.0 |
| | 425421 | L11669 | Hs.157145 | tetracycline transporter-like protein | 3.0 |
| | 427725 | U66839 | Hs.180533 | mitogen-activated protein kinase kinase | 3.0 |
| | 456816 | AK001509 | Hs.144391 | hypothetical protein FLJ10647 | 3.0 |
| 15 | 404632 | | | NM_022490:Homo sapiens hypothetical prot | 3.0 |
| | 411565 | AW851728 | | gb:MR2-CT0222-011199-007-d06 CT0222 Homo | 3.0 |
| | 428917 | AA437337 | Hs.16689 | ESTs | 3.0 |
| | 424584 | H10692 | Hs.13310 | ESTs | 3.0 |
| | 452483 | AI903731 | Hs.106357 | valosin-containing protein | 3.0 |
| 20 | 404453 | | | C8000963*:gq6329915jdbjBAA86452.1 (AB | 3.0 |
| | 426931 | NM_003416 | Hs.2076 | zinc finger protein 7 (K0X 4, clone HF.1 | 3.0 |
| | 455646 | BE064420 | | gb:RC4-BT0311-241199-012-c08 BT0311 Homo | 3.0 |
| | 452188 | AI864208 | Hs.176275 | ESTs | 3.0 |
| | 409703 | NM_006187 | Hs.56009 | 2'-5'-oligoadenylate synthetase 3 (100 k | 3.0 |
| 25 | 413922 | AI535895 | Hs.221024 | ESTs | 3.0 |
| | 452367 | U71207 | Hs.29279 | eyes absent (Drosophila) homolog 2 | 3.0 |
| | 434070 | AF116652 | Hs.270087 | hypothetical protein PRO0813 | 3.0 |
| | 406679 | AA070786 | | gb:zm66b07.r1 Stratagene neuroepithelium | 3.0 |
| | 414747 | U30872 | Hs.77204 | centromere protein F (350/400kD, mitotin | 3.0 |
| 30 | 435472 | AW972330 | Hs.283022 | triggering receptor expressed on myeloid | 3.0 |
| | 429612 | AF062649 | Hs.252587 | pituitary tumor-transforming 1 | 3.0 |
| | 408989 | AW361666 | Hs.49500 | KIAA0746 protein | 3.0 |
| | 418365 | AW014345 | Hs.161690 | ESTs | 3.0 |
| | 418677 | S83308 | Hs.87224 | SRY (sex determining region Y)-box 5 | 3.0 |
| 35 | 426765 | AA743603 | Hs.172108 | nucleoporin 88kD | 3.0 |
| | 400295 | W72838 | | AI905687:IL-BT095-190199-019 BT095 Homo | 3.0 |
| | 429751 | M55210 | Hs.214982 | laminin, gamma 1 (formerly LAMB2) | 3.0 |
| | 429940 | W25215 | | gb:zb87a09.r1 Soares_senescent_fibroblas | 3.0 |
| | 412281 | AI810054 | Hs.14119 | ESTs | 3.0 |
| 40 | 434898 | AW500458 | Hs.29956 | KIAA0460 protein | 3.0 |
| | 424830 | AW270580 | Hs.189311 | ESTs, Weakly similar to putative p150 [H | 3.0 |
| | 459727 | AI906494 | | gb:RC-BT113-060499-024 BT113 Homo sapien | 3.0 |
| | 453900 | AW003582 | Hs.226414 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 3.0 |
| | 458729 | AI364504 | Hs.93967 | ESTs, Weakly similar to NBHUC8 decorin p | 3.0 |
| 45 | 402105 | | | C18000230*:gq12585552[sp]Q9Y2Q1[Z257_HU | 3.0 |
| | 425248 | AW957442 | Hs.252766 | ESTs | 3.0 |
| | 440995 | T57773 | Hs.10263 | ESTs | 3.0 |
| | 441360 | AI091713 | Hs.106597 | Homo sapiens, Similar to RUKEN cDNA 1110 | 3.0 |
| | 432692 | AW974944 | Hs.200577 | ESTs | 3.0 |
| 50 | 428899 | AA744610 | Hs.194431 | palladin | 3.0 |
| | 452811 | AA937079 | Hs.118983 | hypothetical protein FLJ12150 | 3.0 |
| | 447183 | AI554733 | Hs.173182 | ESTs | 3.0 |
| | 429679 | NM_006290 | Hs.211600 | tumor necrosis factor, alpha-induced pro | 3.0 |
| | 416505 | H66470 | Hs.16004 | ESTs | 3.0 |
| 55 | 420144 | AA811813 | Hs.119421 | ESTs | 3.0 |
| | 439184 | AW021842 | Hs.16533 | myosin phosphatase, target subunit 1 | 3.0 |
| | 438033 | T26483 | Hs.6059 | EGF-containing fibulin-like extracellular | 3.0 |
| | 442476 | AF069475 | | gb:AF069475 Homo sapiens astrocytoma lib | 3.0 |
| | 441035 | AI694309 | Hs.126458 | ESTs | 3.0 |
| 60 | 458810 | BE407125 | Hs.231510 | ESTs | 3.0 |
| | 435046 | AA662772 | Hs.174330 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.0 |
| | 414271 | AK000275 | Hs.75871 | protein kinase C binding protein 1 | 3.0 |
| | 450879 | AI742685 | Hs.210347 | ESTs | 3.0 |
| | 454036 | AA374756 | Hs.93560 | Homo sapiens mRNA for KIAA1771 protein, | 3.0 |
| 65 | 403780 | | | C4001759:gq1133250[sp]P19474[RO52_HUMAN | 3.0 |
| | 411543 | AW851248 | | gb:IL3-CT0220-160200-066-F01 CT0220 Homo | 3.0 |
| | 440351 | AF030933 | Hs.7179 | RAD1 (S. pombe) homolog | 3.0 |
| | 452139 | AA099969 | Hs.16331 | Homo sapiens cDNA: FLJ21482 fls, clone C | 3.0 |
| | 449433 | AI672096 | Hs.9012 | ESTs, Weakly similar to S26650 DNA-bind | 3.0 |
| 70 | 413945 | NM_000591 | Hs.75627 | CD14 antigen | 3.0 |
| | 433681 | AI004377 | Hs.200360 | Homo sapiens cDNA FLJ13027 fls, clone NT | 3.0 |
| | 422605 | H16646 | Hs.118666 | hypothetical protein PP591 | 3.0 |
| | 443502 | AI074528 | Hs.133949 | ESTs | 3.0 |
| | 410781 | AI375672 | Hs.165028 | ESTs | 3.0 |
| 75 | 449428 | AI651280 | Hs.195685 | ESTs | 3.0 |
| | 436671 | AW137159 | Hs.146151 | ESTs | 3.0 |
| TABLE 16B: | | | | | |
| 80 | Pkey: | Unique Eos probeset identifier number | | | |
| | CAT number: | Gene cluster number | | | |
| | Accession: | Genbank accession numbers | | | |
| 80 | Pkey | CAT Number | Accession | | |
| | 408432 | 1058667_1 | AW195262 R27868 AW811262 | | |
| | 410886 | 1225822_1 | AW809324 BE144977 BE144956 | | |
| | 411537 | 1248899_1 | BE073250 BE073378 BE073379 AW850533 AW850529 | | |
| | 411543 | 1249127_1 | AW851248 AW851425 AW850805 AW851021 AW850905 | | |

| | | | |
|----|--------|-----------|---|
| 5 | 411565 | 1249756_1 | AW851728 AW851607 AW851621 AW851702 AW851647 AW851727 AW851658 AW851617 AW851628 |
| | 411671 | 125369_1 | BE049094 AA700765 H86770 AA094646 R02483 C03868 N56170 |
| | 411688 | 1254076_1 | AW953440 T08189 AW857085 |
| | 412436 | 129439_1 | AA665089 AA135130 AA484059 AA102419 AW877755 |
| | 412799 | 132817_1 | A1267606 AA121045 AA126521 |
| | 412811 | 132943_1 | H06382 AW957730 AA352014 R13591 AA121201 D60420 BE263253 BE047862 Z41952 A1424991 A1693507 A1863108 AA599060 A1091148 AA598689 |
| | 414372 | 143909_1 | R39887 AA813482 AWO16452 H06383 R41807 A1364268 AA620528 A1241940 AW089149 AW090733 AW088875 Z38240 AA121202 R17734 |
| 10 | 415131 | 1523680_1 | AA143654 AW753140 AA213770 AW970865 AA569075 AA492132 |
| | 415688 | 154643_1 | D61119 D81508 D81734 |
| | 416871 | 1626761_1 | AA166963 AW971218 AA493942 |
| | 416913 | 163001_1 | H98716 N90792 N24283 |
| | 419896 | 1888662_1 | AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499 |
| | 420886 | 197344_1 | Z99362 Z99363 |
| 15 | 422156 | 212379_1 | AA805453 AA281379 |
| | 423713 | 231290_1 | N34524 AA305071 AW954803 AA502335 A1433430 A1203597 AW026670 AW265323 AW850787 AA317554 AW993643 AW835572 AW385512 |
| | 424009 | 234177_1 | A1334966 W32951 H62656 H53902 R88904 AW835732 |
| | 424947 | 245247_1 | AW754182 AW754198 AA329983 |
| 20 | 425331 | 250199_1 | F11690 AW965370 AA333586 D30830 |
| | 429163 | 300543_1 | R77952 AA348809 AW959960 AW959962 A1565552 AW070702 AA973910 R85973 |
| | 429940 | 310884_1 | AW962128 AA355353 AA427363 |
| | 430968 | 326269_1 | AA884766 AW974271 AA592975 AA447312 |
| 25 | 432044 | 340773_1 | W25215 AA461079 AA461391 |
| | 432363 | 345469_1 | AW972830 AA527647 AA489820 AA570362 |
| | 435542 | 407744_1 | AW972727 AA524829 AW972733 |
| | 437437 | 43709_1 | AA534489 AW970240 AW970323 |
| 30 | 437945 | 44580_1 | AA687376 H74234 AW975503 |
| | 439518 | 47334_1 | AA226869 AA296516 AW959753 AA186390 A1359619 AA356195 AA148427 R22748 A1033624 BE548853 H95327 AW579751 BE561649 AA397533 |
| | 439566 | 47387_1 | BE617136 AA236444 T89946 AA247450 N55777 W38725 A1743846 A1808406 AA922229 A1051464 W04713 R11251 W19656 A1042319 AA489276 |
| | 439710 | 47550_1 | A1224533 H |
| 35 | 442476 | 543547_1 | T78519 H59898 U72516 |
| | 444168 | 593829_1 | W76326 AF086341 W72300 |
| | 449625 | 8113_1 | AF086387 W77884 W72711 |
| | 450166 | 82677_1 | AF086543 W96291 W96225 |
| 40 | 450375 | 83327_1 | AF069475 AF069477 AF069476 |
| | 450506 | 836_1 | AW379879 A1126285 H12014 |
| | 450625 | 84032_1 | NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 |
| | 451129 | 859870_1 | N48674 A1375997 R45432 D59344 A1203107 F07491 R35360 R25094 A1913631 A1498402 T61382 A1016320 N45526 T61415 AA331486 |
| | 451350 | 856945_1 | AA429504 R41904 AA279467 H09648 AA007236 |
| 45 | 452203 | 903_2 | AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 |
| 50 | 453085 | 94851_1 | AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 A1161014 AA099554 R69067 |
| | 453331 | 96214_1 | NM_004460 U09278 U76833 AW630055 AW471133 C02434 W45237 AW793518 BE070112 A1587479 A1624429 AW190535 A1446661 A1478772 |
| 55 | 453682 | 977454_1 | AW022667 AA528235 AA599775 AW613820 A1435793 AW594230 A1051768 A1200109 A1680296 AA436611 AW609728 W42634 A1682584 AA405569 |
| | 454860 | 1237732_1 | A1685653 AWO |
| | 455142 | 1254887_1 | AW970107 AA513951 AA010406 |
| 60 | 455481 | 1293182_1 | BE072881 BE072946 A1762181 |
| | 455646 | 1348557_1 | A1791447 A1791327 AW886809 |
| | 455899 | 1381547_1 | X57522 AW295947 A1346197 A1304693 L21205 L21206 L21207 L21208 L21204 NM_000593 F06770 F12630 X57521 R18264 T74462 AA346259 |
| | 456304 | 176820_1 | AW602508 AA904076 F08426 H23432 AA313737 AA393782 M78052 AA847441 AA487637 AA135770 AA353161 A1819778 AA054458 A1346733 |
| 65 | 457876 | 42814_2 | AW361447 A14 |
| 70 | 400533 | 6981826 | AW954243 AA829930 AA412478 AA828434 AA814538 A1927418 A1192435 W52897 AA443666 AA031913 A1683306 AA918481 A1183314 D83907 |
| 75 | 400850 | 1927150 | A1206832 AA876122 D83836 D83838 D82533 A1761290 A191125 A1143749 AW771909 A1241436 A1767267 W56507 AA847787 AA568692 T10502 |
| | 401454 | 9186923 | A1247870 |
| | 401841 | 7684597 | A1240665 T53681 N77468 H51833 AA147247 R75732 C18450 R73999 A1095755 T49904 H03868 AA411580 R33395 AA410586 T48869 D63292 |
| 80 | 402082 | 8117478 | R31981 H12498 H02568 AA035018 R75957 A1803329 R27528 R36203 A1809932 A1808765 R78948 AA411449 AA976929 A1378760 A1378620 T48870 |
| | 402105 | 8131588 | R7390 |
| | 402229 | 9965022 | T79703 T96307 AL079725 |
| | 402239 | 7690131 | AW835767 AW835537 BE160187 |
| | 402274 | 2935596 | AW861840 AW858329 AW858192 AW858189 AW858224 AW858351 |
| | 402523 | 9798518 | AW948317 AW948322 AW948329 AW948316 AW948298 AW948330 AW948325 AW948324 |
| | 402604 | 9909420 | BE064420 BE064435 BE064429 BE064414 BE064400 BE064517 |
| | | | BE155112 BE155154 BE155087 BE155247 BE155499 BE155367 BE155452 |
| | | | A1820973 A1734077 A1820984 AA225796 AA225060 AA225101 |
| | | | A1821940 N67106 A1744264 AA808846 AA643417 AA643416 Z70715 |

TABLE 16C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

| | | | | |
|----|--------|---------|-------|-------------------------|
| 5 | 402855 | 9662953 | Minus | 59763-59909 |
| | 403011 | 6693597 | Minus | 3468-3623 |
| | 403108 | 8980955 | Plus | 93253-93667 |
| | 403267 | 7887182 | Plus | 116078-121885 |
| | 403349 | 8569773 | Minus | 167815-168374 |
| | 403361 | 8570313 | Minus | 112496-112687 |
| | 403481 | 9965004 | Plus | 93496-93633 |
| | 403696 | 3135242 | Minus | 143467-143634 |
| 10 | 403780 | 8076989 | Plus | 93160-93409 |
| | 403849 | 7708855 | Plus | 95043-96519 |
| | 403961 | 7596976 | Minus | 110393-110803 |
| | 403969 | 8569909 | Plus | 31237-31375,32405-32506 |
| | 404209 | 5006246 | Minus | 11247-11514 |
| 15 | 404407 | 7329316 | Minus | 48154-48499 |
| | 404453 | 7657714 | Plus | 27768-29179 |
| | 404584 | 9857511 | Plus | 138651-139153 |
| | 404632 | 9796868 | Plus | 45096-45229 |
| | 405046 | 7596829 | Minus | 4373-4528 |
| 20 | 405141 | 8980911 | Plus | 99861-100054 |
| | 405303 | 2078453 | Minus | 130607-130802 |
| | 405348 | 2914717 | Minus | 43310-43462 |
| | 405558 | 1621110 | Plus | 4502-4644,5983-6083 |
| | 405605 | 5836195 | Minus | 117070-117270 |
| 25 | 406038 | 8389537 | Plus | 37764-37877 |
| | 406060 | 6899623 | Minus | 20339-20746 |
| | 406478 | 9857502 | Plus | 68314-68523,68853-68950 |

TABLE 17A: ABOUT 1040 GENES UP-REGULATED IN GLIOBLASTOMA MULTIFORMA COMPARED TO NORMAL ADULT TISSUES

Table 17A lists about 1040 genes up-regulated in glioblastoma multiforma (GBM) compared to normal normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" glioblastoma to "average" normal tissues was greater than or equal to 3.0. The "average" GBM level was set to the 85th percentile amongst various GBM tumors. The "average" normal tissue level was set to the 85th percentile amongst various non-malignant adult tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 Rt: Ratio of GLIOBLASTOMA MULTIFORMA compared to NORMAL ADULT TISSUES

| | | | | | |
|----|--------|-----------|-----------|--|------|
| 40 | Pkey | ExAccn | UnigenelD | Unigene Title | Rt |
| | 431917 | D16181 | Hs.2868 | peripheral myelin protein 2 | 57.9 |
| | 428321 | A1699994 | Hs.2868 | peripheral myelin protein 2 | 50.1 |
| | 427343 | A1880044 | Hs.176977 | protein kinase C binding protein 2 | 49.6 |
| 45 | 413472 | BE242870 | Hs.75379 | solute carrier family 1 (glial high affi | 43.9 |
| | 415817 | U88967 | Hs.78867 | protein tyrosine phosphatase, receptor-t | 42.9 |
| | 435147 | AL133731 | Hs.4774 | Homo sapiens mRNA; cDNA DKFZp761C1712 (f | 42.5 |
| | 430838 | N46664 | Hs.169395 | hypothetical protein FLJ12015 | 37.9 |
| | 418375 | NM_003081 | Hs.84389 | synaptosomal-associated protein, 25kD | 37.1 |
| 50 | 449494 | AW237014 | Hs.315369 | Homo sapiens cDNA: FLJ23075 fis, clone L | 37.0 |
| | 425088 | AA663372 | Hs.169395 | hypothetical protein FLJ12015 | 32.7 |
| | 425842 | A1587490 | Hs.159623 | NIK-2 (Drosophila) homolog B | 32.4 |
| | 419078 | M93119 | Hs.89584 | insulinoma-associated 1 | 32.1 |
| | 423849 | AL157425 | Hs.133315 | Homo sapiens mRNA; cDNA DKFZp761J1324 (f | 29.9 |
| 55 | 409389 | AB007979 | Hs.301281 | Homo sapiens mRNA, chromosome 1 specific | 28.8 |
| | 413333 | M74028 | Hs.75297 | fibroblast growth factor 1 (acidic) | 28.5 |
| | 417183 | R52089 | Hs.172717 | ESTs | 27.6 |
| | 426325 | D28114 | Hs.169309 | myelin-associated oligodendrocyte basic | 27.6 |
| | 412733 | AA984472 | Hs.74554 | KIAA0080 protein | 25.9 |
| 60 | 422656 | A1870435 | Hs.1569 | LIM homeobox protein 2 | 25.6 |
| | 436878 | BE465204 | Hs.47448 | ESTs | 24.9 |
| | 437204 | AL110216 | Hs.22826 | ESTs, Weakly similar to I55214 salivary | 24.3 |
| | 429007 | D80642 | | gb:HUM092E09B Human fetal brain (TFujiwa | 23.1 |
| | 429276 | AF056085 | Hs.198612 | G protein-coupled receptor 51 | 23.1 |
| 65 | 409395 | U46745 | Hs.336678 | dystrobrevin, alpha | 23.0 |
| | 435708 | A1362949 | Hs.75169 | ESTs | 22.5 |
| | 453392 | U23752 | Hs.32964 | SRY (sex determining region Y)-box 11 | 22.2 |
| | 431941 | AK000106 | Hs.272227 | Homo sapiens cDNA FLJ20099 fis, clone CO | 22.1 |
| | 418110 | R43523 | Hs.217754 | hypothetical protein FLJ22202 | 22.0 |
| 70 | 416829 | AB013805 | Hs.80220 | catenin (cadherin-associated protein), d | 21.7 |
| | 444513 | AL120214 | Hs.7117 | glutamate receptor, ionotropic, AMPA 1 | 20.9 |
| | 433551 | A1985544 | Hs.12450 | protocadherin 9 | 19.8 |
| | 452744 | A1267652 | Hs.246107 | Homo sapiens mRNA; cDNA DKFZp434E082 (fr | 19.1 |
| | 425057 | AA826434 | Hs.1619 | achaete-scute complex (Drosophila) homol | 19.0 |
| 75 | 429903 | AL134197 | Hs.93597 | cyclin-dependent kinase 5, regulatory su | 19.0 |
| | 447004 | AW296968 | Hs.157539 | ESTs | 18.6 |
| | 425048 | H05468 | Hs.164502 | ESTs | 18.2 |
| | 427897 | NM_017413 | Hs.303084 | apelin; peptide ligand for APJ receptor | 18.0 |
| 80 | 421264 | AL039123 | Hs.103042 | microtubule-associated protein 1B | 18.0 |
| | 453642 | A1370936 | Hs.34074 | dipeptidylpeptidase VI | 17.8 |
| | 424140 | Z48051 | Hs.141308 | myelin oligodendrocyte glycoprotein | 17.7 |
| | 444471 | AB020684 | Hs.11217 | KIAA0877 protein | 17.6 |
| | 441350 | AB020690 | Hs.7782 | paraneoplastic antigen MA2 | 17.2 |
| | 430691 | C14187 | Hs.103538 | ESTs | 16.7 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 433800 | AI034361 | Hs.135150 | lung type-I cell membrane-associated gly | 16.6 |
| | 424581 | M62062 | Hs.150917 | catenin (cadherin-associated protein), a | 16.6 |
| | 408562 | AI436323 | Hs.31141 | Homo sapiens mRNA for KIAA1568 protein, | 16.5 |
| | 423853 | AB011537 | Hs.133466 | slit (Drosophila) homolog 1 | 16.4 |
| 5 | 431019 | NM_005249 | Hs.2714 | forkhead box G1B | 16.4 |
| | 449539 | W80363 | Hs.58446 | ESTs | 16.4 |
| | 450133 | AW969769 | Hs.105201 | ESTs | 16.1 |
| | 425799 | T08133 | Hs.182906 | Homo sapiens mRNA for KIAA1872 protein, | 16.0 |
| 10 | 447359 | NM_012093 | Hs.18268 | adenylate kinase 5 | 15.4 |
| | 415910 | U20350 | Hs.78913 | chemokine (C-X3-C) receptor 1 | 15.3 |
| | 459516 | AI049662 | Hs.246858 | EST | 14.9 |
| | 456759 | BE259150 | Hs.127792 | delta (Drosophila)-like 3 | 14.7 |
| | 429466 | M85835 | Hs.12827 | ESTs | 14.7 |
| 15 | 439979 | AW600291 | Hs.6823 | hypothetical protein FLJ10430 | 14.7 |
| | 443785 | AW449952 | Hs.190125 | basic-helix-loop-helix-PAS protein | 14.6 |
| | 439415 | F05538 | Hs.4273 | ESTs | 14.5 |
| | 408604 | D51408 | Hs.21925 | ESTs | 14.5 |
| | 444378 | R41339 | Hs.47860 | neurotrophic tyrosine kinase, receptor, | 14.3 |
| | 428392 | H10233 | Hs.2265 | secretory granule, neuroendocrine protei | 14.0 |
| 20 | 418738 | AW388633 | Hs.6682 | solute carrier family 7, (cationic amino | 14.0 |
| | 409799 | D11928 | Hs.76845 | phosphoserine phosphatase-like | 13.9 |
| | 439239 | AI031540 | Hs.235331 | ESTs | 13.8 |
| | 428342 | AI739168 | | Homo sapiens cDNA FLJ13458 fis, clone PL | 13.7 |
| 25 | 448595 | AB014544 | Hs.21572 | KIAA0644 gene product | 13.6 |
| | 441285 | NM_002374 | Hs.167 | microtubule-associated protein 2 | 13.5 |
| | 428982 | NM_005097 | Hs.194704 | leucine-rich, glioma inactivated 1 | 13.4 |
| | 441440 | AI807981 | Hs.30495 | ESTs | 13.0 |
| | 412959 | D87458 | Hs.75090 | KIAA0282 protein | 12.8 |
| 30 | 413597 | AW302885 | Hs.117183 | ESTs | 12.8 |
| | 441016 | AW138653 | Hs.25845 | ESTs | 12.7 |
| | 418338 | NM_002522 | Hs.84154 | neuronal pentraxin I | 12.6 |
| | 423419 | R55336 | Hs.23539 | ESTs | 12.6 |
| | 445495 | BE622641 | Hs.38489 | ESTs, Weakly similar to I38022 hypotheti | 12.6 |
| 35 | 441497 | R51064 | Hs.23172 | ESTs | 12.4 |
| | 424893 | AW295112 | Hs.153648 | Homo sapiens cDNA FLJ13303 fis, clone OV | 12.2 |
| | 453941 | U39817 | Hs.36820 | Bloom syndrome | 12.2 |
| | 427701 | AA411101 | Hs.243886 | nuclear autoantigenic sperm protein (his | 12.2 |
| | 446782 | AI653048 | Hs.144006 | ESTs | 12.1 |
| 40 | 437268 | AI754847 | Hs.227571 | regulator of G-protein signalling 4 | 12.1 |
| | 411411 | AA345241 | Hs.55950 | ESTs, Weakly similar to KIAA1330 protein | 11.9 |
| | 448302 | AI480208 | Hs.182906 | Homo sapiens mRNA for KIAA1872 protein, | 11.9 |
| | 407034 | U84540 | | gb:Human dystrobrevin isoform DTN-3 (DTN | 11.9 |
| | 449625 | NM_014253 | | odz (odd Oz/ten-m, Drosophila) homolog 1 | 11.7 |
| 45 | 451099 | R52795 | Hs.25954 | interleukin 13 receptor, alpha 2 | 11.7 |
| | 424432 | AB037821 | Hs.146858 | protocadherin 10 | 11.6 |
| | 451996 | AW514021 | Hs.245510 | ESTs | 11.4 |
| | 423678 | AW963357 | Hs.7847 | ESTs | 11.4 |
| | 445041 | T64183 | Hs.282982 | solute carrier | 11.3 |
| 50 | 442613 | AI004002 | Hs.130522 | Kv channel-interacting protein 1 | 11.2 |
| | 419721 | NM_001650 | Hs.288650 | aquaporin 4 | 11.2 |
| | 446711 | AF169692 | Hs.12450 | protocadherin 9 | 11.1 |
| | 412986 | X81120 | Hs.75110 | cannabinoid receptor 1 (brain) | 11.0 |
| | 412140 | AA219691 | Hs.73625 | RAB6 interacting, kinesin-like (rabkines | 10.7 |
| 55 | 428728 | NM_016625 | Hs.191381 | hypothetical protein | 10.6 |
| | 415849 | R20529 | Hs.6806 | ESTs | 10.6 |
| | 447198 | D61523 | Hs.283435 | ESTs | 10.5 |
| | 420602 | AF060877 | Hs.99236 | regulator of G-protein signalling 20 | 10.3 |
| | 435793 | AB037734 | Hs.4993 | KIAA1313 protein | 10.3 |
| 60 | 409049 | AI423132 | Hs.146343 | ESTs | 10.2 |
| | 449511 | AI970394 | Hs.197075 | ESTs | 10.2 |
| | 402604 | | | Target Exon | 10.1 |
| | 434277 | X77748 | Hs.3786 | glutamate receptor, metabotropic 3 | 10.0 |
| | 440435 | AL042201 | Hs.21273 | transcription factor NYD-sp10 | 10.0 |
| 65 | 438080 | AA777381 | Hs.291530 | ESTs, Weakly similar to ALUC_HUMAN !!!! | 10.0 |
| | 419271 | N34901 | Hs.238532 | ESTs | 9.9 |
| | 426344 | H41821 | Hs.322469 | transcriptional activator of the c-fos p | 9.8 |
| | 449605 | AW138581 | Hs.198416 | ESTs | 9.8 |
| | 408081 | AW451597 | Hs.167409 | ESTs | 9.8 |
| 70 | 452526 | W38537 | Hs.280740 | hypothetical protein MGC3040 | 9.8 |
| | 411305 | BE241596 | Hs.69547 | myelin basic protein | 9.8 |
| | 443455 | AB001025 | Hs.9349 | ryanodine receptor 3 | 9.8 |
| | 427540 | R12014 | Hs.20976 | ESTs | 9.7 |
| | 424790 | AL119344 | Hs.13326 | ESTs, Weakly similar to 2004399A chromos | 9.7 |
| 75 | 416892 | L24498 | Hs.80409 | growth arrest and DNA-damage-inducible, | 9.6 |
| | 452461 | N78223 | Hs.108106 | transcription factor | 9.6 |
| | 449433 | AI672096 | Hs.9012 | ESTs, Weakly similar to S26650 DNA-bindi | 9.6 |
| | 454027 | R40192 | Hs.21527 | Human DNA sequence from clone GS1-115M3 | 9.5 |
| | 439199 | R40373 | Hs.26299 | ESTs | 9.5 |
| 80 | 433896 | AW294729 | Hs.274461 | ESTs | 9.3 |
| | 416072 | AL110370 | Hs.79000 | growth associated protein 43 | 9.3 |
| | 444119 | R41231 | Hs.184261 | ESTs, Weakly similar to T26686 hypotheti | 9.2 |
| | 435624 | AF218942 | Hs.24889 | formin 2 | 9.2 |
| | 412788 | AA120960 | Hs.198416 | ESTs | 9.2 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 409902 | AI337658 | Hs.156351 | ESTs | |
| | 427304 | AA761526 | Hs.163853 | ESTs | 9.2 |
| | 429918 | AW873886 | Hs.119383 | ESTs | 9.2 |
| 5 | 442910 | AI365130 | Hs.11307 | ESTs, Weakly similar to T19326 hypothe | 9.1 |
| | 425187 | AW014486 | Hs.22509 | ESTs | 9.1 |
| | 436954 | AA740151 | Hs.130425 | ESTs | 9.1 |
| | 442710 | AB015631 | Hs.23210 | ESTs | 9.1 |
| | 411078 | AI222020 | Hs.182364 | CocoaCrisp | 9.1 |
| 10 | 438209 | AL120659 | Hs.6111 | aryl-hydrocarbon receptor nuclear trans | 9.0 |
| | 437036 | AI571514 | Hs.133022 | ESTs | 9.0 |
| | 448672 | AI955511 | Hs.225106 | ESTs | 9.0 |
| | 451952 | AL120173 | Hs.301663 | ESTs | 9.0 |
| | 448743 | AB032962 | Hs.21896 | KIAA1136 protein | 8.9 |
| 15 | 412068 | S72043 | Hs.73133 | metallothionein 3 (growth inhibitory fac | 8.9 |
| | 439451 | AF086270 | Hs.278554 | heterochromatin-like protein 1 | 8.9 |
| | 419088 | AI538323 | Hs.52620 | integrin, beta 8 | 8.8 |
| | 445873 | AA250970 | Hs.251946 | poly(A)-binding protein, cytoplasmic 1-I | 8.8 |
| | 410102 | AW248508 | Hs.279727 | ESTs; homologue of PEM-3 (Ciona savignyi | 8.8 |
| 20 | 449571 | AW016812 | Hs.200266 | ESTs | 8.8 |
| | 425354 | U62027 | Hs.155935 | complement component 3a receptor 1 | 8.7 |
| | 452355 | N54926 | Hs.29202 | G protein-coupled receptor 34 | 8.7 |
| | 410276 | AI554545 | Hs.68301 | angiopoietin-2 | 8.7 |
| | 435501 | AW051819 | Hs.129908 | KIAA0591 protein | 8.7 |
| 25 | 407728 | AW071502 | Hs.175931 | ESTs | 8.6 |
| | 415293 | R49462 | Hs.106541 | ESTs | 8.6 |
| | 416857 | AA188775 | Hs.292453 | ESTs | 8.6 |
| | 425234 | AW152225 | Hs.165909 | ESTs, Weakly similar to I38022 hypothe | 8.6 |
| | 450375 | AA009647 | | a disintegrin and metalloproteinase doma | 8.5 |
| 30 | 413063 | AL035737 | Hs.75184 | chitinase 3-like 1 (cartilage glycoprote | 8.5 |
| | 438380 | T06430 | Hs.6194 | chondroitin sulfate proteoglycan BEHAB/b | 8.4 |
| | 421659 | NM_014459 | Hs.106511 | protocadherin 17 | 8.4 |
| | 418097 | R45137 | Hs.21868 | ESTs | 8.4 |
| | 429183 | AB014604 | Hs.197955 | KIAA0704 protein | 8.3 |
| 35 | 424945 | AI221919 | | hypothetical protein FLJ110582 | 8.2 |
| | 455601 | AI368680 | Hs.816 | SRY (sex determining region Y)-box 2 | 8.2 |
| | 453884 | AA355925 | Hs.36232 | KIAA0186 gene product | 8.2 |
| | 407881 | AW072003 | Hs.40968 | heparan sulfate (glucosamine) 3-O-sulfot | 8.2 |
| | 436887 | AW953157 | Hs.193235 | hypothetical protein DKFZp547D155 | 8.1 |
| 40 | 431721 | AB032996 | Hs.268044 | KIAA1170 protein | 8.1 |
| | 417160 | N76497 | Hs.1787 | proteolipid protein 1 (Pelizaeus-Merzbac | 8.1 |
| | 409041 | AB033025 | Hs.50081 | Hypothetical protein, XP_051860 (KIAA119 | 8.1 |
| | 424085 | NM_002914 | Hs.139226 | replication factor C (activator 1) 2 (40 | 8.1 |
| | 436039 | AW023323 | Hs.121070 | ESTs | 8.1 |
| 45 | 449444 | AW818436 | Hs.23590 | solute carrier family 16 (monocarboxylic | 8.0 |
| | 427463 | AA442224 | Hs.97900 | ESTs | 8.0 |
| | 440184 | AB002297 | Hs.7022 | dedicator of cyto-kinesis 3 | 8.0 |
| | 409731 | AA125985 | Hs.56145 | thymosin, beta, identified in neuroblast | 7.9 |
| | 451621 | AI879148 | Hs.26770 | fatty acid binding protein 7, brain | 7.8 |
| 50 | 419929 | U90268 | Hs.93810 | cerebral cavernous malformations 1 | 7.7 |
| | 419544 | AI909154 | | gb:QV-BT200-010499-007 BT200 Homo sapien | 7.7 |
| | 448555 | AI536697 | Hs.159863 | ESTs | 7.7 |
| | 414372 | AA143654 | | gb:z065a02.r1 Stratagene pancreas (93720 | 7.7 |
| | 438527 | AI969251 | Hs.115325 | RAB7, member RAS oncogene family-like 1 | 7.7 |
| 55 | 400293 | N51002 | Hs.306480 | Homo sapiens mRNA; cDNA DKFZp761E2112 (f | 7.7 |
| | 420362 | U79734 | Hs.97206 | huntinglin interacting protein 1 | 7.6 |
| | 430132 | AA204686 | Hs.234149 | hypothetical protein FLJ20647 | 7.5 |
| | 448543 | AW897741 | Hs.21380 | Homo sapiens mRNA; cDNA DKFZp586P1124 (f | 7.5 |
| | 436140 | W87355 | Hs.269587 | ESTs | 7.4 |
| 60 | 449340 | AW235786 | Hs.195359 | hypothetical protein MGC10954 | 7.4 |
| | 446372 | AB020644 | Hs.14945 | long fatty acyl-CoA synthetase 2 gene | 7.4 |
| | 454117 | BE410100 | Hs.40368 | adaptor-related protein complex 1, sigma | 7.4 |
| | 410434 | AF051152 | Hs.63668 | tol-like receptor 2 | 7.4 |
| | 454048 | H05626 | Hs.6921 | ESTs | 7.4 |
| 65 | 441523 | AW514263 | Hs.301771 | ESTs, Weakly similar to ALUF_HUMAN !!! | 7.4 |
| | 440074 | AA863045 | Hs.10669 | ESTs, Weakly similar to T00050 hypothe | 7.4 |
| | 438330 | AW450572 | Hs.257316 | ESTs | 7.4 |
| | 433556 | W56321 | Hs.111460 | calcium/calmodulin-dependent protein kin | 7.3 |
| | 434808 | AF155108 | Hs.256150 | Homo sapiens, Similar to RIKEN cDNA 2810 | 7.3 |
| 70 | 445900 | AF070526 | Hs.125036 | Homo sapiens clone 24787 mRNA sequence | 7.3 |
| | 402855 | | | NM_001839: Homo sapiens calponin 3, acid | 7.2 |
| | 422960 | AW890487 | Hs.63984 | cadherin 13, H-cadherin (heart) | 7.2 |
| | 439772 | AL365406 | Hs.10268 | Homo sapiens mRNA full length insert cDN | 7.2 |
| | 433447 | U29195 | Hs.3281 | neuronal pentraxin II | 7.2 |
| 75 | 412709 | AL022327 | Hs.74518 | KIAA0027 protein | 7.2 |
| | 445745 | AB007924 | Hs.13245 | KIAA0455 gene product | 7.2 |
| | 447101 | N72185 | Hs.44189 | ESTs | 7.2 |
| | 448935 | AL078596 | Hs.22591 | nuclear receptor subfamily 2, group E, m | 7.1 |
| | 409248 | AB033035 | Hs.51965 | KIAA1209 protein | 7.1 |
| 80 | 452785 | AL359942 | Hs.296434 | erythroid differentiation and denucleati | 7.1 |
| | 424998 | U58515 | Hs.154138 | chitinase 3-like 2 | 7.1 |
| | 436607 | AW661783 | Hs.211061 | ESTs | 7.1 |
| | 447197 | R36075 | | gb:yh88b01.s1 Soares placenta Mb2HP Homo | 7.1 |
| | 419249 | X14767 | Hs.89768 | gamma-aminobutyric acid (GABA) A recepto | 7.1 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 416111 | AA033813 | Hs.79018 | chromatin assembly factor 1, subunit A (| 7.1 |
| | 421633 | AF121860 | Hs.106260 | sorting nexin 10 | 7.0 |
| | 428976 | AL037824 | Hs.194695 | ras homolog gene family, member I | 7.0 |
| 5 | 444783 | AK001468 | Hs.62180 | anillin (Drosophila Scraps homolog), act | 7.0 |
| | 408096 | BE250162 | Hs.83765 | dihydrofolate reductase | 7.0 |
| | 426269 | H15302 | Hs.168950 | Homo sapiens mRNA; cDNA DKFZp566A1046 (I | 6.9 |
| | 439978 | BE139460 | Hs.124673 | Homo sapiens cDNA FLJ11477 fis, clone HE | 6.9 |
| | 439570 | T79925 | Hs.269165 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 6.9 |
| 10 | 422980 | N46569 | Hs.76722 | CCAAT/enhancer binding protein (C/EBP), | 6.9 |
| | 415279 | F04237 | Hs.1447 | glial fibrillary acidic protein | 6.9 |
| | 456965 | AW131888 | Hs.172792 | ESTs, Weakly similar to hypothetical pro | 6.9 |
| | 447773 | AI423930 | Hs.36790 | ESTs, Weakly similar to putative p150 (H | 6.9 |
| | 429927 | NM_001115 | Hs.2522 | adenylate cyclase 8 (brain) | 6.9 |
| | 447499 | AW262580 | Hs.147674 | protocadherin beta 16 | 6.8 |
| 15 | 414696 | AF002020 | Hs.76918 | Niemann-Pick disease, type C1 | 6.8 |
| | 441255 | R06350 | Hs.171635 | ESTs | 6.8 |
| | 429656 | X05608 | Hs.211584 | neurofilament, light polypeptide (68kD) | 6.8 |
| | 439566 | AF086387 | | gb:Homo sapiens full length insert cDNA | 6.8 |
| 20 | 435191 | R15912 | Hs.4817 | Homo sapiens clone 24461 mRNA sequence | 6.8 |
| | 420285 | AA258124 | Hs.293878 | ESTs, Moderately similar to ZN91_HUMAN Z | 6.8 |
| | 430968 | AW972830 | | gb:EST384925 MAGE resequences, MAGL Homo | 6.8 |
| | 458332 | AI000341 | Hs.220491 | ESTs | 6.8 |
| | 449048 | Z45051 | Hs.22920 | similar to S68401 (cattle) glucose induc | 6.7 |
| 25 | 413627 | BE182082 | Hs.246973 | ESTs | 6.7 |
| | 415079 | R43179 | Hs.22895 | hypothetical protein FLJ23548 | 6.7 |
| | 418677 | S83308 | Hs.87224 | SRY (sex determining region Y)-box 5 | 6.7 |
| | 432281 | AK001239 | Hs.274263 | hypothetical protein FLJ10377 | 6.7 |
| | 425741 | AF052152 | Hs.159412 | Homo sapiens clone 24628 mRNA sequence | 6.7 |
| 30 | 421141 | AW117261 | Hs.125914 | ESTs | 6.6 |
| | 408829 | NM_006042 | Hs.48384 | heparan sulfate (glucosamine) 3-O-sulfot | 6.6 |
| | 432154 | AI701523 | Hs.112577 | ESTs | 6.6 |
| | 425202 | AW962282 | Hs.152049 | ESTs, Weakly similar to I38022 hypothe | 6.6 |
| | 434164 | AW207019 | Hs.148135 | serine/threonine kinase 33 | 6.6 |
| 35 | 407182 | AA312551 | Hs.230157 | ESTs | 6.6 |
| | 445034 | AW293376 | Hs.143659 | ESTs | 6.6 |
| | 410909 | AW898161 | Hs.53112 | ESTs, Moderately similar to ALU8_HUMAN A | 6.6 |
| | 441102 | AA973905 | | intermediate filament protein syncollin | 6.6 |
| | 452834 | AI638627 | Hs.105685 | KIAA1688 protein | 6.6 |
| 40 | 429239 | AA448419 | Hs.45209 | ESTs | 6.6 |
| | 414175 | AI308876 | Hs.103849 | hypothetical protein DKFZp761D112 | 6.5 |
| | 449300 | AI656959 | Hs.346514 | ESTs | 6.5 |
| | 446727 | AB011095 | Hs.16032 | KIAA0523 protein | 6.5 |
| | 429250 | H56585 | Hs.198308 | tryptophan rich basic protein | 6.5 |
| 45 | 420560 | AW207748 | Hs.59115 | ESTs | 6.5 |
| | 448321 | NM_005883 | Hs.20912 | adenomatous polyposis coli like | 6.5 |
| | 441390 | AI692560 | Hs.131175 | ESTs | 6.5 |
| | 407168 | R45175 | Hs.117183 | ESTs | 6.4 |
| | 447414 | D82343 | Hs.74376 | neuroblastoma (nerve tissue) protein | 6.4 |
| 50 | 407235 | D20569 | Hs.169407 | SAC2 (suppressor of actin mutations 2, y | 6.4 |
| | 433597 | AA708205 | Hs.100343 | ESTs | 6.4 |
| | 414528 | AA148950 | Hs.188836 | ESTs | 6.4 |
| | 414214 | D49958 | Hs.75819 | glycoprotein M6A | 6.4 |
| | 446692 | Z44514 | | Homo sapiens mRNA for KIAA1763 protein, | 6.4 |
| 55 | 407896 | D76435 | Hs.41154 | Zic family member 1 (odd-paired Drosophi | 6.4 |
| | 440152 | AB002376 | Hs.7006 | KIAA0378 protein | 6.4 |
| | 453785 | AI368236 | Hs.283732 | ESTs, Moderately similar to ALU1_HUMAN A | 6.3 |
| | 412530 | AA766268 | Hs.266273 | hypothetical protein FLJ13346 | 6.3 |
| | 448902 | Z45998 | Hs.22543 | Homo sapiens mRNA; cDNA DKFZp76111912 (I | 6.3 |
| 60 | 452799 | AI948829 | Hs.213786 | ESTs | 6.3 |
| | 425523 | AB007948 | Hs.158244 | KIAA0479 protein | 6.3 |
| | 444396 | T65213 | Hs.4257 | ESTs | 6.3 |
| | 422094 | AF129535 | Hs.272027 | F-box only protein 5 | 6.3 |
| | 420649 | AI866964 | Hs.124704 | ESTs, Moderately similar to S65657 alpha | 6.3 |
| 65 | 424028 | AF055084 | Hs.153692 | Homo sapiens cDNA FLJ14354 fis, clone Y7 | 6.3 |
| | 447350 | AI375572 | Hs.172634 | ESTs | 6.2 |
| | 448148 | NM_016578 | Hs.20509 | HBV pX associated protein-8 | 6.2 |
| | 436936 | AL134451 | Hs.197478 | ESTs | 6.2 |
| | 448243 | AW369771 | Hs.52620 | integrin, beta 8 | 6.2 |
| 70 | 414727 | BE466904 | Hs.190162 | gb:h228f03.x1 NC1_CGAP_GC6 Homo sapiens | 6.2 |
| | 420608 | BE548277 | Hs.103104 | ESTs | 6.2 |
| | 422949 | AA319435 | | gb:EST21657 Adrenal gland tumor Homo sap | 6.2 |
| | 418506 | AA084248 | Hs.85339 | G protein-coupled receptor 39 | 6.1 |
| | 428242 | H55709 | Hs.2250 | leukemia inhibitory factor (cholinergic | 6.1 |
| 75 | 423361 | AW170055 | Hs.47628 | ESTs | 6.1 |
| | 417417 | F05745 | Hs.89512 | ATPase, Ca transporting, plasma membrane | 6.1 |
| | 447072 | D61594 | Hs.17279 | tyrosylprotein sulfotransferase 1 | 6.1 |
| | 415651 | AI207162 | Hs.3815 | slathmin-like-protein RB3 | 6.0 |
| | 418030 | BE207573 | Hs.83321 | neuromedin B | 6.0 |
| 80 | 429469 | M64590 | Hs.27 | glycine dehydrogenase (decarboxylating; | 6.0 |
| | 417873 | BE266659 | Hs.293659 | Homo sapiens, Similar to RIKEN cDNA A430 | 6.0 |
| | 429900 | AA460421 | Hs.30875 | ESTs | 6.0 |
| | 416439 | AA180363 | Hs.118769 | ESTs | 6.0 |
| | 439845 | AL355743 | Hs.56663 | Homo sapiens EST from clone 41214, full | 6.0 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 425905 | AB032959 | Hs.318584 | novel C3HC4 type Zinc finger (ring finger) | 6.0 |
| | 439518 | W76326 | | gb:zd60d04.r1 Soares_fetal_heart_NbHH19W | 6.0 |
| | 426919 | AL041228 | | ELAV (embryonic lethal, abnormal vision, | 6.0 |
| 5 | 440492 | R39127 | Hs.21433 | hypothetical protein DKFZp547J036 | 5.9 |
| | 432328 | A1572739 | Hs.195471 | 6-phosphofructo-2-kinase/fructose-2,6-bi | 5.9 |
| | 444190 | A1878918 | Hs.10526 | cysteine and glycine-rich protein 2 | 5.9 |
| | 425984 | AW836277 | Hs.165636 | hypothetical protein DKFZp761C07121 | 5.9 |
| | 425977 | R15138 | Hs.165570 | Homo sapiens clone 25052 mRNA sequence | 5.9 |
| 10 | 449318 | AW236021 | Hs.78531 | Homo sapiens, Similar to RIKEN cDNA 5730 | 5.9 |
| | 457465 | AW301344 | Hs.122908 | DNA replication factor | 5.9 |
| | 453362 | H14988 | Hs.107375 | ESTs | 5.9 |
| | 453924 | R49295 | Hs.24886 | ESTs | 5.9 |
| | 414825 | X06370 | Hs.77432 | epidermal growth factor receptor (avian | 5.8 |
| 15 | 433701 | AW445023 | Hs.15155 | ESTs | 5.8 |
| | 412777 | A1335773 | Hs.270123 | ESTs | 5.8 |
| | 419723 | AL120193 | Hs.339810 | longevity assurance (LAG1, S. cerevisiae | 5.8 |
| | 438054 | AA776626 | Hs.169309 | ESTs | 5.8 |
| | 416427 | BE244050 | Hs.79307 | Rac/Cdc42 guanine exchange factor (GEF) | 5.8 |
| 20 | 400292 | AA250737 | Hs.72472 | BMP-R1B | 5.8 |
| | 407748 | AL079409 | Hs.38176 | KIAA0606 protein; SCN Circadian Oscillat | 5.8 |
| | 453313 | BE005771 | Hs.153746 | hypothetical protein FLJ22490 | 5.8 |
| | 430188 | AL049242 | Hs.234794 | Homo sapiens mRNA; cDNA DKFZp564B083 (fr | 5.8 |
| | 411252 | AB018549 | Hs.69328 | MD-2 protein | 5.8 |
| 25 | 448986 | H42169 | Hs.347310 | hypothetical protein FLJ14627 | 5.7 |
| | 440052 | A1633744 | Hs.195648 | ESTs, Weakly similar to I38022 hypotheti | 5.7 |
| | 419704 | AA429104 | Hs.45057 | ESTs | 5.7 |
| | 420077 | AW512260 | Hs.87767 | ESTs | 5.7 |
| | 448966 | AW372914 | Hs.86149 | phosphoinositol 3-phosphate-binding prot | 5.7 |
| 30 | 436511 | AA721252 | Hs.291502 | ESTs | 5.7 |
| | 424560 | AA158727 | Hs.150555 | protein predicted by clone 23733 | 5.7 |
| | 423346 | A1267677 | Hs.127416 | synaptotagmin 1 | 5.7 |
| | 439249 | AF086060 | Hs.170053 | G-protein coupled receptor 88 | 5.7 |
| | 428588 | F12101 | Hs.185701 | Homo sapiens mRNA full length insert cDN | 5.7 |
| 35 | 450927 | A1807804 | Hs.134342 | TASP for testis-specific adriamycin sens | 5.7 |
| | 451752 | AB032997 | Hs.26966 | KIAA1171 protein | 5.7 |
| | 458814 | A498957 | Hs.170861 | ESTs, Weakly similar to Z195_HUMAN ZINC | 5.6 |
| | 416406 | D86961 | Hs.79299 | lipoma HMGIC fusion partner-like 2 | 5.6 |
| | 448275 | BE514434 | Hs.20830 | kinesin-like 2 | 5.6 |
| 40 | 413492 | D87470 | Hs.75400 | KIAA0280 protein | 5.6 |
| | 444600 | R41398 | Hs.6996 | ESTs | 5.6 |
| | 421988 | AW450481 | Hs.161333 | ESTs | 5.6 |
| | 443297 | A1049864 | Hs.133029 | ESTs | 5.6 |
| | 433244 | AB040943 | Hs.271285 | KIAA1510 protein | 5.6 |
| 45 | 458809 | AW972512 | Hs.20985 | sin3-associated polypeptide, 30kD | 5.5 |
| | 448499 | BE613280 | Hs.77550 | hypothetical protein MGC1780 | 5.5 |
| | 447458 | A1741082 | Hs.158961 | ESTs | 5.5 |
| | 436643 | AA757626 | Hs.10941 | ESTs, Weakly similar to IPP1_HUMAN PROTE | 5.5 |
| | 407886 | AW969688 | Hs.100826 | ESTs | 5.5 |
| 50 | 448944 | AB014605 | Hs.22599 | atrophin-1 interacting protein 1; activi | 5.5 |
| | 418630 | A1351311 | Hs.251946 | poly(A)-binding protein, cytoplasmic 1-I | 5.5 |
| | 415734 | NM_014747 | Hs.78748 | KIAA0237 gene product | 5.5 |
| | 410099 | AA081630 | | KIAA0036 gene product | 5.5 |
| | 453128 | AW026516 | Hs.31791 | acylphosphatase 2, muscle type | 5.5 |
| 55 | 444670 | H58373 | Hs.332938 | hypothetical protein MGC5370 | 5.5 |
| | 420345 | AW295230 | Hs.25231 | ESTs | 5.5 |
| | 420092 | AA814043 | Hs.88045 | ESTs | 5.5 |
| | 414821 | M63835 | Hs.77424 | Fc fragment of IgG, high affinity Ia, re | 5.5 |
| | 429876 | AB028977 | Hs.225974 | KIAA1054 protein | 5.4 |
| 60 | 419863 | AW952691 | Hs.93485 | Homo sapiens mRNA; cDNA DKFZp761D191 (fr | 5.4 |
| | 429149 | AW193360 | Hs.197962 | ESTs, Weakly similar to I38022 hypotheti | 5.4 |
| | 415486 | H12214 | Hs.13284 | ESTs, Weakly similar to 2109260A B cell | 5.4 |
| | 429643 | AA455889 | Hs.167279 | FYVE-finger-containing Rab5 effector pro | 5.4 |
| | 446657 | A1335191 | Hs.260702 | ESTs, Weakly similar to 2109260A B cell | 5.4 |
| 65 | 439662 | H97552 | Hs.269060 | ESTs | 5.4 |
| | 444165 | AL137443 | Hs.10441 | hypothetical protein FLJ11236 | 5.4 |
| | 439192 | AW970536 | Hs.105413 | ESTs | 5.4 |
| | 448769 | N66037 | Hs.38173 | ESTs | 5.3 |
| | 410555 | U92649 | Hs.64311 | a disintegrin and metalloproteinase doma | 5.3 |
| 70 | 424922 | BE386547 | Hs.217112 | hypothetical protein MGC10825 | 5.3 |
| | 423905 | AW579960 | Hs.135150 | lung type-I cell membrane-associated gly | 5.3 |
| | 429433 | AA452899 | Hs.213586 | ESTs, Weakly similar to KIAA1353 protein | 5.3 |
| | 427359 | AW020782 | Hs.79881 | Homo sapiens cDNA: FLJ23006 lis, clone L | 5.3 |
| | 422544 | AB018259 | Hs.118140 | KIAA0716 gene product | 5.3 |
| 75 | 420547 | AF155140 | Hs.98738 | gonadotropin-regulated testicular RNA he | 5.3 |
| | 424624 | AB032947 | Hs.151301 | Ca2+-dependent activator protein for secr | 5.2 |
| | 441797 | A1936933 | Hs.214635 | ESTs | 5.2 |
| | 428832 | AA578229 | Hs.324239 | ESTs, Moderately similar to ZN91_HUMAN Z | 5.2 |
| | 418079 | R40058 | Hs.6911 | ESTs | 5.2 |
| 80 | 445740 | T78281 | Hs.13226 | Homo sapiens clone 25181 mRNA sequence | 5.2 |
| | 416426 | AA180256 | Hs.210473 | Homo sapiens cDNA FLJ14872 lis, clone PL | 5.2 |
| | 436109 | AA922153 | Hs.132760 | hypothetical protein MGC15729 | 5.2 |
| | 433647 | AA603367 | Hs.222294 | ESTs | 5.2 |
| | 452786 | R61362 | Hs.106642 | ESTs, Weakly similar to T09052 hypotheti | 5.1 |

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|----|--------|-----------|-----------|--|-----|
| | 436443 | AW138211 | Hs.128746 | ESTs | 5.1 |
| | 408243 | Y00787 | Hs.624 | interleukin 8 | 5.1 |
| | 404819 | | | NM_002688:Homo sapiens peanut (Drosophi | 5.1 |
| 5 | 424914 | AA348410 | Hs.119065 | ESTs | 5.1 |
| | 453331 | AI240665 | | ESTs | 5.1 |
| | 444656 | AI277924 | Hs.145199 | ESTs | 5.1 |
| | 437387 | AI198874 | Hs.28847 | ADO26 protein | 5.1 |
| | 421027 | AA761198 | Hs.55254 | ESTs | 5.1 |
| 10 | 410631 | AA086469 | Hs.47171 | ESTs | 5.1 |
| | 454293 | H49739 | Hs.134013 | ESTs, Moderately similar to HK61_HUMAN H | 5.1 |
| | 416220 | N49776 | Hs.170994 | hypothetical protein MGC10946 | 5.1 |
| | 419498 | AL036591 | Hs.20887 | hypothetical protein FLJ10392 | 5.1 |
| | 421040 | AA715026 | Hs.135280 | ESTs | 5.1 |
| | 415170 | R44386 | Hs.164578 | ESTs | 5.1 |
| 15 | 412590 | AL134388 | Hs.135033 | ESTs, Weakly similar to I38022 hypothei | 5.1 |
| | 448985 | AA324885 | Hs.22777 | carbonic anhydrase XI | 5.0 |
| | 433929 | AI375499 | Hs.27379 | ESTs | 5.0 |
| | 409638 | AW450420 | Hs.21335 | ESTs | 5.0 |
| 20 | 437916 | BE566249 | Hs.20999 | hypothetical protein FLJ23142 | 5.0 |
| | 400533 | | | ENSP00000209376:PRED65 protein (Fragmen | 5.0 |
| | 430130 | AL137311 | Hs.234074 | Homo sapiens mRNA; cDNA DKFZp761G02121 (| 5.0 |
| | 437372 | AA323968 | Hs.283631 | hypothetical protein DKFZp547G183 | 5.0 |
| | 414737 | AI160386 | Hs.125087 | ESTs | 5.0 |
| 25 | 422864 | AA318323 | Hs.12827 | gb:EST20390 Retina II Homo sapiens cDNA | 5.0 |
| | 428878 | AA436884 | Hs.48926 | ESTs | 5.0 |
| | 428841 | AI418430 | Hs.104935 | ESTs | 5.0 |
| | 428110 | AI312485 | Hs.138294 | ESTs, Moderately similar to Z195_HUMAN Z | 5.0 |
| | 444170 | AW613879 | Hs.102408 | ESTs | 4.9 |
| 30 | 448765 | R15337 | Hs.21958 | Homo sapiens mRNA; cDNA DKFZp547D086 (fr | 4.9 |
| | 452106 | AI141031 | Hs.21342 | ESTs | 4.9 |
| | 417404 | NM_007350 | Hs.82101 | pleckstrin homology-like domain, family | 4.9 |
| | 414300 | AI304870 | Hs.188680 | ESTs | 4.9 |
| | 429399 | AA452244 | Hs.16727 | ESTs | 4.9 |
| 35 | 439726 | AW449893 | Hs.293707 | ESTs, Weakly similar to I38598 zinc fing | 4.9 |
| | 428873 | AI701609 | Hs.98908 | ESTs | 4.9 |
| | 451516 | AI800515 | Hs.12024 | ESTs | 4.9 |
| | 407792 | AI077715 | Hs.39384 | putative secreted ligand homologous to f | 4.9 |
| | 416836 | D54745 | Hs.80247 | cholecystokinin | 4.9 |
| 40 | 447247 | AW369351 | Hs.287955 | Homo sapiens cDNA FLJ13090 fis, clone NT | 4.9 |
| | 436805 | AA731533 | Hs.270751 | ESTs | 4.9 |
| | 423175 | W27595 | Hs.347310 | hypothetical protein FLJ14627 | 4.9 |
| | 415402 | AA164687 | Hs.177576 | mannosyl (alpha-1,3)-glycoprotein beta- | 4.9 |
| | 422263 | AA307639 | Hs.129908 | KIAA0591 protein | 4.8 |
| 45 | 443715 | AI583187 | Hs.9700 | cyclin E1 | 4.8 |
| | 413248 | T64858 | Hs.21433 | hypothetical protein DKFZp547J036 | 4.8 |
| | 434811 | AW971205 | Hs.114280 | ESTs | 4.8 |
| | 441287 | AW293132 | Hs.131373 | ESTs | 4.8 |
| | 428862 | NM_000346 | Hs.2316 | SRY (sex determining region Y)-box 9 (ca | 4.8 |
| 50 | 413834 | BE296896 | Hs.224179 | ESTs, Weakly similar to I38022 hypothesi | 4.8 |
| | 443740 | R56434 | Hs.21062 | ESTs | 4.8 |
| | 416871 | H98716 | | gb:yx13d08.s1 Soares melanocyte 2NbHM Ho | 4.8 |
| | 441916 | AA993571 | Hs.129075 | ESTs | 4.8 |
| | 413530 | AA130158 | Hs.19977 | ESTs, Moderately similar to ALU8_HUMAN A | 4.8 |
| 55 | 424240 | AB023185 | Hs.143535 | calcium/calmodulin-dependent protein kin | 4.8 |
| | 414998 | NM_002543 | Hs.77729 | oxidised low density lipoprotein (lectin | 4.8 |
| | 448425 | AI500359 | Hs.346112 | ESTs | 4.8 |
| | 423600 | AI633559 | Hs.310359 | ESTs | 4.8 |
| | 424687 | J05070 | Hs.151738 | matrix metalloproteinase 9 (gelatinase B | 4.8 |
| 60 | 423869 | BE409301 | Hs.134012 | C1q-related factor | 4.8 |
| | 425402 | AI215881 | Hs.24970 | ESTs, Weakly similar to B34323 GTP-bindi | 4.7 |
| | 422809 | AK001379 | Hs.121028 | hypothetical protein FLJ10549 | 4.7 |
| | 407808 | AA663559 | Hs.279789 | histone deacetylase 3 | 4.7 |
| | 428748 | AW593206 | Hs.98785 | Ksp37 protein | 4.7 |
| 65 | 434859 | BE255080 | Hs.299315 | collapsin response mediator protein-5; C | 4.7 |
| | 431820 | AW410408 | Hs.271167 | L-pipecolic acid oxidase | 4.7 |
| | 409100 | H98216 | Hs.42245 | ESTs, Moderately similar to I38022 hypot | 4.7 |
| | 420133 | AA426117 | Hs.155543 | ESTs | 4.7 |
| | 420297 | AI628272 | Hs.88323 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 4.7 |
| 70 | 443462 | AI064690 | Hs.171176 | ESTs | 4.7 |
| | 424481 | R19453 | Hs.1787 | proteolipid protein 1 (Pelizaeus-Merzbac | 4.7 |
| | 431454 | AW975980 | Hs.292918 | ESTs | 4.7 |
| | 432682 | AI376400 | Hs.159588 | ESTs | 4.7 |
| | 434933 | R91095 | Hs.4276 | KIAA1701 protein | 4.7 |
| 75 | 421247 | BE391727 | Hs.102910 | general transcription factor IIH, polype | 4.7 |
| | 435538 | AB011540 | Hs.4930 | low density lipoprotein receptor-related | 4.7 |
| | 441703 | AW390054 | Hs.192843 | leucine zipper protein FKSG14 | 4.7 |
| | 418661 | NM_001949 | Hs.1189 | E2F transcription factor 3 | 4.7 |
| 80 | 412265 | N59006 | Hs.26133 | ESTs | 4.7 |
| | 417675 | AI808607 | Hs.3781 | similar to murine leucine-rich repeat pr | 4.6 |
| | 422564 | AI148006 | Hs.222120 | ESTs | 4.6 |
| | 427250 | R35941 | Hs.25418 | ESTs | 4.6 |
| | 427695 | R88483 | Hs.172862 | ESTs | 4.6 |
| | 434269 | AK001991 | Hs.3781 | similar to murine leucine-rich repeat pr | 4.6 |

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|----|--------|-----------|-----------|--|-----|
| | 407603 | AW955705 | Hs.62604 | Homo sapiens, clone IMAGE:4299322, mRNA, | 4.6 |
| | 427687 | AW003867 | Hs.1570 | histamine receptor H1 | 4.6 |
| | 427194 | AA399018 | Hs.250835 | ESTs | 4.6 |
| 5 | 440286 | U29589 | Hs.7138 | cholinergic receptor, muscarinic 3 | 4.6 |
| | 427099 | AB032953 | Hs.173560 | odd Oz/ten-m homolog 2 (Drosophila, mous | 4.6 |
| | 458760 | AI498631 | Hs.111334 | feritin, light polypeptide | 4.6 |
| | 433675 | AW977653 | Hs.75319 | ribonucleotide reductase M2 polypeptide | 4.6 |
| | 429170 | NM_001394 | Hs.2359 | dual specificity phosphatase 4 | 4.6 |
| 10 | 427712 | AI368024 | Hs.283696 | ESTs | 4.6 |
| | 437834 | AA769294 | Hs.283854 | gb:nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens | 4.6 |
| | 408947 | AL080093 | Hs.49117 | Homo sapiens mRNA; cDNA DKFZp564N1662 (I | 4.6 |
| | 424458 | M29273 | Hs.1780 | myelin associated glycoprotein | 4.6 |
| | 450568 | AL050078 | Hs.25159 | Homo sapiens cDNA FLJ10784 fis, clone NT | 4.6 |
| 15 | 424635 | AA420687 | Hs.115455 | Homo sapiens cDNA FLJ14259 fis, clone PL | 4.6 |
| | 440491 | R35252 | Hs.130558 | ESTs, Weakly similar to 2109260A B cell | 4.6 |
| | 428409 | AW117207 | Hs.98523 | ESTs | 4.5 |
| | 423476 | AL035633 | | Human DNA sequence from clone RP5-1046G1 | 4.5 |
| | 421977 | W94197 | Hs.110165 | ribosomal protein L26 homolog | 4.5 |
| 20 | 440105 | AA694010 | Hs.6932 | Homo sapiens clone 23809 mRNA sequence | 4.5 |
| | 422411 | AW749443 | Hs.22511 | ESTs | 4.5 |
| | 443361 | AI792628 | Hs.133273 | ESTs | 4.5 |
| | 453857 | AL080235 | Hs.35861 | DKFZP586E1621 protein | 4.5 |
| | 408432 | AW195262 | | gb:zn67b05.x1 NCI_CGAP_CML1 Homo sapiens | 4.5 |
| 25 | 444127 | N63620 | Hs.13281 | ESTs | 4.5 |
| | 417435 | NM_005181 | Hs.82129 | carbonic anhydrase III, muscle specific | 4.5 |
| | 422661 | NM_014700 | Hs.119004 | KIAA0665 gene product | 4.5 |
| | 440684 | AI253123 | Hs.127356 | ESTs, Highly similar to S21424 nestin [H | 4.5 |
| | 407385 | AA610150 | Hs.272072 | ESTs, Weakly similar to I38022 hypothe | 4.5 |
| 30 | 425256 | BE297611 | Hs.155392 | collapsin response mediator protein 1 | 4.5 |
| | 441364 | AW450466 | Hs.126830 | ESTs, Weakly similar to YD38_YEAST HYPOT | 4.5 |
| | 430471 | AF064845 | Hs.241523 | hypothetical protein FLJ10142 | 4.5 |
| | 412043 | BE156622 | Hs.333371 | Homo sapiens clone TA40 untranslated mRN | 4.5 |
| | 426503 | AA380153 | | gb:EST93093 Skin tumor I Homo sapiens cD | 4.5 |
| 35 | 418771 | AA807881 | Hs.25329 | ESTs | 4.4 |
| | 414706 | AW340125 | Hs.76989 | KIAA0097 gene product | 4.4 |
| | 424800 | AL035588 | Hs.153203 | MyoD family inhibitor | 4.4 |
| | 441217 | AI922183 | Hs.213246 | ESTs | 4.4 |
| | 422421 | AA325138 | Hs.235873 | hypothetical protein FLJ22672 | 4.4 |
| 40 | 446619 | AU076643 | Hs.313 | secreted phosphoprotein 1 (osteopontin, | 4.4 |
| | 444153 | AK001610 | Hs.10414 | hypothetical protein FLJ10748 | 4.4 |
| | 435342 | AA687376 | | ESTs | 4.4 |
| | 443912 | R37257 | Hs.184780 | ESTs | 4.4 |
| | 414922 | D00723 | Hs.77631 | glycine cleavage system protein H (amino | 4.4 |
| 45 | 432527 | AW975028 | Hs.102754 | ESTs | 4.4 |
| | 410082 | AA081594 | Hs.158311 | Musashi (Drosophila) homolog 1 | 4.4 |
| | 446936 | H10207 | Hs.47314 | ESTs | 4.4 |
| | 425212 | AW962253 | Hs.171618 | ESTs | 4.4 |
| | 426925 | NM_001196 | Hs.315689 | Homo sapiens cDNA: FLJ22373 fis, clone H | 4.4 |
| 50 | 427221 | L15409 | Hs.174007 | von Hippel-Lindau syndrome | 4.4 |
| | 439274 | AF086092 | Hs.48372 | ESTs | 4.4 |
| | 412799 | AI267606 | | gb:aq91h03.x1 Stanley Frontal SB pool 1 | 4.4 |
| | 430676 | AF084866 | | gb:Homo sapiens envelope protein RIC-3 (| 4.4 |
| | 405348 | | | C7001664:gil12698061[dbj]BAB21849.1[AB | 4.4 |
| 55 | 419412 | AW161058 | Hs.90297 | synuclein, beta | 4.3 |
| | 447397 | BE247676 | Hs.18442 | E-1 enzyme | 4.3 |
| | 409125 | R17268 | Hs.343567 | axonal transport of synaptic vesicles | 4.3 |
| | 433323 | AA805132 | Hs.159142 | ESTs | 4.3 |
| | 450530 | NM_006668 | Hs.25121 | cytochrome P450, subfamily 46 (cholester | 4.3 |
| 60 | 428227 | AA321649 | Hs.2248 | small inducible cytokine subfamily B (Cy | 4.3 |
| | 408622 | AA056060 | Hs.202577 | Homo sapiens cDNA FLJ12166 fis, clone MA | 4.3 |
| | 433610 | AA806822 | Hs.112547 | ESTs | 4.3 |
| | 429281 | AA830856 | Hs.29808 | Homo sapiens cDNA: FLJ21122 fis, clone C | 4.3 |
| | 451320 | AW118072 | | diacylglycerol kinase, zeta (104kD) | 4.3 |
| 65 | 430979 | AI479755 | Hs.129010 | ESTs | 4.3 |
| | 452092 | BE245374 | Hs.27842 | hypothetical-protein FLJ11210 | 4.3 |
| | 438456 | AA913381 | Hs.20594 | ESTs | 4.3 |
| | 433236 | NM_004296 | Hs.3221 | regulator of G-protein signalling 6 | 4.3 |
| | 445133 | AW157646 | Hs.198689 | ESTs | 4.3 |
| 70 | 412125 | Y17114 | Hs.73393 | eyes absent (Drosophila) homolog 4 | 4.2 |
| | 432882 | NM_013257 | Hs.279696 | serum/glucocorticoid regulated kinase-li | 4.2 |
| | 407846 | AA426202 | Hs.40403 | Cbp/p300-interacting transactivator, wit | 4.2 |
| | 417918 | AA209205 | Hs.163754 | hypothetical protein FLJ12606 | 4.2 |
| | 424489 | T48851 | Hs.274470 | D-siglec precursor, | 4.2 |
| 75 | 453682 | T79703 | | ghyd71e08.r1 Soares fetal liver spleen | 4.2 |
| | 445568 | H00918 | Hs.268744 | KIAA1796 protein | 4.2 |
| | 448526 | AB028946 | Hs.21361 | KIAA1023 protein | 4.2 |
| | 426457 | AW894667 | Hs.169965 | chimerin (chimaerin) 1 | 4.2 |
| | 415796 | R87548 | Hs.78854 | ATPase, Na? transporting, beta 2 polypep | 4.2 |
| 80 | 438875 | AA827640 | Hs.189059 | ESTs | 4.2 |
| | 428001 | H97428 | Hs.219907 | ESTs, Moderately similar to Transforming | 4.2 |
| | 410361 | BE391804 | Hs.62661 | guanylate binding protein 1, interferon- | 4.2 |
| | 445921 | AW015211 | Hs.146181 | ESTs | 4.2 |
| | 412190 | R16180 | Hs.274461 | ESTs | 4.2 |

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|----|--------|-----------|-----------|--|-----|
| | 445666 | R59960 | Hs.282386 | ESTs | 4.2 |
| | 439538 | AA837323 | Hs.56407 | ESTs | 4.2 |
| | 437814 | AI088192 | Hs.135474 | ESTs, Weakly similar to DDX9_HUMAN ATP-D | 4.2 |
| 5 | 410264 | AK001853 | Hs.61508 | Homo sapiens cDNA FLJ10991 fis, clone PL | 4.2 |
| | 409091 | AW970386 | Hs.269423 | ESTs | 4.2 |
| | 459527 | AW977556 | Hs.291735 | ESTs, Weakly similar to I78885 serine/th | 4.2 |
| | 426271 | AF026547 | Hs.169047 | chondroitin sulfate proteoglycan 3 (neur | 4.2 |
| | 432731 | R31178 | Hs.287820 | fibronectin 1 | 4.2 |
| | 423135 | N67655 | Hs.26411 | ESTs | 4.2 |
| 10 | 446131 | NM_000929 | Hs.290 | phospholipase A2, group V | 4.2 |
| | 424736 | AF230877 | Hs.152701 | microtubule-interacting protein that ass | 4.2 |
| | 408298 | AI745325 | Hs.271923 | Homo sapiens cDNA: FLJ22785 fis, clone K | 4.2 |
| | 452234 | AW084176 | Hs.223296 | ESTs, Weakly similar to I38022 hypotheti | 4.2 |
| | 451468 | AW503398 | Hs.293663 | ESTs, Moderately similar to I38022 hypot | 4.2 |
| 15 | 429421 | AL031658 | | Human DNA sequence from clone RP1-310013 | 4.2 |
| | 422374 | AW732869 | Hs.1519 | protein kinase, cAMP-dependent, regulato | 4.1 |
| | 402145 | | | Target Exon | 4.1 |
| | 440483 | AI200836 | Hs.150386 | ESTs | 4.1 |
| 20 | 425018 | BE245277 | Hs.154196 | E4F transcription factor 1 | 4.1 |
| | 448048 | BE281291 | Hs.170408 | ESTs, Moderately similar to A47582 B-cel | 4.1 |
| | 445868 | BE169357 | Hs.207428 | ESTs | 4.1 |
| | 431725 | X65724 | Hs.2839 | Norrie disease (pseudoglioma) | 4.1 |
| | 435575 | AF213457 | Hs.44234 | triggering receptor expressed on myeloid | 4.1 |
| 25 | 424726 | AK001007 | Hs.138760 | Homo sapiens cDNA FLJ10145 fis, clone HE | 4.1 |
| | 450325 | AI935962 | Hs.26289 | ESTs | 4.1 |
| | 450639 | AI703186 | Hs.277174 | ESTs | 4.1 |
| | 445102 | AW204610 | Hs.22270 | ESTs | 4.1 |
| | 416547 | H62914 | Hs.268946 | ESTs, Weakly similar to PC4259 ferritin | 4.1 |
| 30 | 430387 | AW372884 | Hs.240770 | nuclear cap binding protein subunit 2, 2 | 4.1 |
| | 408296 | AL117452 | Hs.44155 | DKFZP586G1517 protein | 4.1 |
| | 439519 | AA837118 | Hs.118366 | ESTs | 4.1 |
| | 442326 | H92962 | Hs.124813 | hypothetical protein MGC14817 | 4.1 |
| | 404150 | | | Target Exon | 4.1 |
| 35 | 420805 | L10333 | Hs.99947 | reticulin 1 | 4.1 |
| | 429125 | AA446854 | Hs.271004 | ESTs, Weakly similar to I38022 hypotheti | 4.1 |
| | 427302 | AA400540 | Hs.135282 | Homo sapiens cDNA FLJ11554 fis, clone HE | 4.1 |
| | 444534 | AW271626 | Hs.42294 | ESTs | 4.1 |
| | 437414 | AW894071 | Hs.48448 | hypothetical protein DKFZp547C176 | 4.1 |
| 40 | 418512 | AW498974 | | diacylglycerol kinase, zeta (104kD) | 4.1 |
| | 414217 | AI309298 | Hs.279898 | Homo sapiens cDNA: FLJ23165 fis, clone L | 4.1 |
| | 449328 | AI962493 | Hs.345303 | ESTs | 4.1 |
| | 432683 | AW995441 | Hs.10475 | ESTs | 4.1 |
| | 435312 | AJ243396 | Hs.4865 | voltage-gated sodium channel beta-3 subu | 4.1 |
| 45 | 429163 | AA884766 | | gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s | 4.1 |
| | 453096 | AW294631 | Hs.11325 | ESTs | 4.1 |
| | 414683 | S78296 | Hs.76888 | hypothetical protein MGC12702 | 4.0 |
| | 433523 | H29882 | | ESTs | 4.0 |
| | 422170 | AI791949 | Hs.112432 | anti-Mullerian hormone | 4.0 |
| 50 | 424120 | T80579 | Hs.290270 | ESTs | 4.0 |
| | 448548 | R13209 | Hs.21413 | solute carrier family 12, (potassium-chl | 4.0 |
| | 433009 | AA761668 | | gb:nz24c08.s1 NCI_CGAP_GC81 Homo sapiens | 4.0 |
| | 434834 | AF156774 | Hs.324020 | 1-acylglycerol-3-phosphate O-acyltransfe | 4.0 |
| | 439099 | AB037800 | Hs.6462 | protein kinase C and casein kinase subst | 4.0 |
| 55 | 444001 | AI095087 | Hs.152299 | ESTs, Moderately similar to S65657 alpha | 4.0 |
| | 413554 | AA319146 | Hs.75426 | secretogranin II (chromogranin C) | 4.0 |
| | 423279 | AW959861 | Hs.290943 | ESTs | 4.0 |
| | 457211 | AW972565 | Hs.32399 | ESTs, Weakly similar to S51797 vasodilat | 4.0 |
| | 450581 | AF081513 | Hs.25195 | TGF-beta 4 | 4.0 |
| 60 | 435854 | AJ278120 | Hs.4996 | putative ankyrin-repeat containing prote | 4.0 |
| | 433615 | AA732982 | Hs.269607 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 4.0 |
| | 424001 | W67883 | Hs.137476 | paternally expressed 10 | 4.0 |
| | 432058 | AW665996 | Hs.130729 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 4.0 |
| | 423713 | AW754182 | | gb:RC2-CT0321-131199-011-c01 CT0321 Homo | 4.0 |
| 65 | 419629 | AB020695 | Hs.91662 | KIAA0888 protein | 4.0 |
| | 439108 | AW163034 | Hs.6467 | synaptogyrin 3 | 4.0 |
| | 440866 | AI703103 | Hs.271360 | hypothetical protein MGC16275 | 4.0 |
| | 422887 | AI751848 | Hs.49215 | ESTs | 4.0 |
| | 405331 | | | NM_024560:Homo sapiens hypothetical prot | 4.0 |
| 70 | 457005 | AJ007421 | Hs.172597 | sal (Drosophila)-like 3 | 4.0 |
| | 437948 | AA772920 | Hs.303527 | ESTs | 4.0 |
| | 440471 | AA886146 | Hs.307944 | ESTs | 4.0 |
| | 432149 | AW614326 | Hs.133483 | ESTs, Weakly similar to T34549 probable | 4.0 |
| | 449655 | AJ021987 | Hs.59970 | ESTs | 4.0 |
| 75 | 448299 | AA497044 | Hs.20887 | hypothetical protein FLJ10392 | 4.0 |
| | 435743 | T66861 | Hs.12962 | ESTs | 4.0 |
| | 412659 | AW753865 | Hs.74376 | olfactomedin related ER localized protei | 4.0 |
| | 430694 | AA810624 | Hs.30936 | ESTs, Weakly similar to H2BH_HUMAN H8STO | 3.9 |
| | 437807 | AI017875 | Hs.136829 | ESTs | 3.9 |
| 80 | 440085 | BE270761 | Hs.23158 | ESTs | 3.9 |
| | 449722 | BE280074 | Hs.23960 | cyclin B1 | 3.9 |
| | 445523 | Z30118 | Hs.293788 | ESTs, Moderately similar to unnamed prot | 3.9 |
| | 420948 | AB016898 | Hs.100469 | myeloid/lymphoid or mixed-lineage leukem | 3.9 |
| | 407198 | H91679 | | gb:yv04a07.s1 Soares fetal liver spleen | 3.9 |

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|----|--------|-----------|-----------|--|-----|
| | 447519 | U46258 | Hs.339665 | ESTs | |
| | 429038 | AL023513 | Hs.194766 | seizure related gene 6 (mouse)-like | 3.9 |
| | 414761 | AU077228 | Hs.77256 | enhancer of zeste (Drosophila) homolog 2 | 3.9 |
| 5 | 404584 | | | Target Exon | 3.9 |
| | 449670 | F07693 | Hs.85603 | Homo sapiens mRNA; cDNA DKFZp434K2172 (f | 3.9 |
| | 414117 | W88559 | Hs.1787 | proteolipid protein 1 (Pelizaeus-Merzbac | 3.9 |
| | 433290 | R20977 | Hs.302185 | Homo sapiens clone 23618 mRNA sequence | 3.9 |
| | 441707 | R42637 | Hs.21963 | hypothetical protein DKFZp761B0514 | 3.9 |
| 10 | 431789 | H19500 | Hs.269222 | mitogen-activated protein kinase 4 | 3.9 |
| | 434149 | Z43829 | Hs.244624 | hypothetical protein MGC5469 | 3.9 |
| | 446896 | T15767 | Hs.22452 | Homo sapiens mRNA for KIAA1737 protein, | 3.9 |
| | 411555 | AF113537 | Hs.70669 | HMP19 protein | 3.9 |
| | 426646 | AA382787 | Hs.122713 | ESTs | 3.9 |
| 15 | 450297 | AW901347 | Hs.38592 | hypothetical protein FLJ23342 | 3.9 |
| | 429228 | AI553633 | Hs.326447 | ESTs | 3.9 |
| | 451433 | AA021140 | Hs.269265 | ESTs, Weakly similar to A46010 X-linked | 3.9 |
| | 447937 | AL109716 | Hs.20034 | Homo sapiens mRNA full length insert cDN | 3.9 |
| | 436734 | AI937612 | Hs.273758 | hypothetical protein FLJ23112 | 3.9 |
| 20 | 417576 | AA339449 | Hs.82285 | phosphorylserine transfer formyltransfer | 3.9 |
| | 417632 | R20855 | Hs.5422 | glycoprotein M6B | 3.9 |
| | 414245 | BE148072 | Hs.75850 | WAS protein family, member 1 | 3.9 |
| | 418203 | X54942 | Hs.83758 | CDC28 protein kinase 2 | 3.9 |
| | 453438 | AI469935 | Hs.22792 | ESTs | 3.9 |
| 25 | 408449 | NM_004408 | Hs.166161 | dynamitin 1 | 3.9 |
| | 411048 | AK001742 | Hs.67991 | hypothetical protein DKFZp434G0522 | 3.8 |
| | 405819 | | | NM_002578:Homo sapiens p21 (CDKN1A)-acti | 3.8 |
| | 445255 | NM_014841 | Hs.12477 | synaptosomal-associated protein, 91 kDa | 3.8 |
| | 432715 | AA247152 | Hs.200483 | ESTs, Weakly similar to KIAA1074 protein | 3.8 |
| 30 | 457292 | AI921270 | Hs.281462 | hypothetical protein FLJ14251 | 3.8 |
| | 432593 | AW301003 | Hs.51483 | ESTs, Weakly similar to hypothetical pro | 3.8 |
| | 413589 | AW452631 | Hs.313803 | ESTs, Highly similar to AF157833 1 noncl | 3.8 |
| | 426847 | S78723 | Hs.298623 | 5-hydroxytryptamine (serotonin) receptor | 3.8 |
| | 410768 | AF038185 | Hs.66187 | Homo sapiens clone 23700 mRNA sequence | 3.8 |
| 35 | 417791 | AW965339 | Hs.111471 | ESTs | 3.8 |
| | 454120 | AB032990 | Hs.40719 | hypothetical protein KIAA1164 | 3.8 |
| | 425154 | NM_001851 | Hs.154850 | collagen, type IX, alpha 1 | 3.8 |
| | 449145 | AI632122 | Hs.198408 | ESTs | 3.8 |
| 40 | 446997 | AA383439 | Hs.16758 | Spir-1 protein | 3.8 |
| | 407304 | AA565832 | Hs.271649 | gdnj32b03.s1 NCL_CGAP_AA1 Homo sapiens | 3.8 |
| | 437269 | AA334384 | Hs.149420 | ESTs | 3.8 |
| | 443539 | AI076182 | Hs.134074 | ESTs, Moderately similar to ALU6_HUMAN A | 3.8 |
| | 426855 | AL117427 | Hs.172778 | Homo sapiens mRNA; cDNA DKFZp566P013 (fr | 3.8 |
| | 418821 | AA436002 | Hs.183161 | ESTs | 3.8 |
| 45 | 408875 | NM_015434 | Hs.48604 | DKFZP434B168 protein | 3.8 |
| | 422175 | N79885 | Hs.6382 | ESTs, Highly similar to T00391 hypothesi | 3.8 |
| | 432488 | AA551010 | Hs.216640 | ESTs | 3.8 |
| | 450582 | AI339732 | | G-rich RNA sequence binding factor 1 | 3.8 |
| 50 | 426380 | AI291267 | Hs.149990 | ESTs | 3.8 |
| | 451407 | AA131376 | Hs.343809 | fibroblast growth factor 12B | 3.8 |
| | 451778 | AI826131 | Hs.62954 | ESTs, Weakly similar to zinc finger prot | 3.8 |
| | 425652 | AB021742 | Hs.322431 | neurogenic differentiation 2 | 3.8 |
| | 412820 | BE001236 | | gb:CM3-BN0075-240200-101-d11 BN0075 Homo | 3.8 |
| | 412193 | AI684467 | Hs.144057 | ESTs | 3.8 |
| 55 | 431117 | AF003522 | Hs.250500 | delta (Drosophila)-like 1 | 3.8 |
| | 433042 | AW193534 | Hs.281895 | Homo sapiens cDNA FLJ11660 fis, clone HE | 3.8 |
| | 437756 | AA767537 | Hs.197096 | ESTs | 3.8 |
| | 451367 | AA923729 | Hs.26322 | cell cycle related kinase | 3.8 |
| 60 | 425390 | AI092634 | Hs.156114 | protein tyrosine phosphatase, non-recept | 3.8 |
| | 445292 | AV653264 | Hs.13982 | Homo sapiens cDNA FLJ14666 fis, clone NT | 3.8 |
| | 425843 | BE313280 | Hs.159627 | death associated protein 3 | 3.8 |
| | 443301 | AI733614 | Hs.220587 | ESTs, Moderately similar to ALU5_HUMAN A | 3.8 |
| | 440210 | AW674562 | Hs.125296 | ESTs | 3.7 |
| 65 | 430287 | AW182459 | Hs.125759 | ESTs, Weakly similar to LEU5_HUMAN LEUKE | 3.7 |
| | 437252 | AI433833 | Hs.164159 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.7 |
| | 409327 | L41162 | Hs.53563 | collagen, type IX, alpha 3 | 3.7 |
| | 429084 | AJ001443 | Hs.195614 | splicing factor 3b, subunit 3, 130kD | 3.7 |
| | 457183 | H91882 | Hs.118569 | Dvl-binding protein IDAX (inhibition of | 3.7 |
| 70 | 403696 | | | C4001100: gij5852342[gb]AADS4015.1) (AF0 | 3.7 |
| | 408670 | AF160967 | Hs.46784 | potassium large conductance calcium-act | 3.7 |
| | 416677 | T83470 | Hs.334840 | ESTs, Moderately similar to I78885 serin | 3.7 |
| | 422253 | W81526 | Hs.118329 | ESTs, Moderately similar to GAD_HUMAN GA | 3.7 |
| | 450154 | R15891 | Hs.281587 | Human (clone CTG-A4) mRNA sequence | 3.7 |
| | 408453 | AI369838 | Hs.45127 | chondroitin sulfate proteoglycan 5 (neur | 3.7 |
| 75 | 440553 | AA689416 | Hs.344043 | Homo sapiens cDNA FLJ14459 fis, clone HE | 3.7 |
| | 428536 | AI143139 | Hs.2288 | visinin-like 1 | 3.7 |
| | 426413 | AA377823 | | gb:EST90805 Synovial sarcoma Homo sapien | 3.7 |
| | 409172 | Z99399 | Hs.122593 | ESTs | 3.7 |
| 80 | 441627 | AA947552 | Hs.58086 | branched chain aminotransferase 1, cytos | 3.7 |
| | 418216 | AA662240 | Hs.283099 | AF15q14 protein | 3.7 |
| | 408790 | AW580227 | Hs.47860 | neurotrophic tyrosine kinase, receptor, | 3.7 |
| | 437449 | AL390153 | Hs.208339 | Homo sapiens mRNA; cDNA DKFZp762G113 (fr | 3.7 |
| | 436035 | AA703679 | Hs.106999 | ESTs, Weakly similar to SYT5_HUMAN SYNAP | 3.7 |
| | 451697 | AW449774 | Hs.296380 | POM (POM121 rat homolog) and ZP3 fusion | 3.7 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 436961 | AW375974 | Hs.156704 | ESTs | 3.7 |
| | 409953 | AA332277 | Hs.57691 | cadherin 18, type 2 | 3.7 |
| | 435832 | AA425688 | Hs.41641 | Bruno (Drosophila) -like 4, RNA binding | 3.7 |
| 5 | 424343 | AW956360 | Hs.4748 | adenylate cyclase activating polypeptide | 3.6 |
| | 437470 | AL390147 | Hs.134742 | hypothetical protein DKFZp547D065 | 3.6 |
| | 440168 | AA868507 | Hs.126141 | ESTs | 3.6 |
| | 427624 | AA406245 | Hs.24895 | ESTs | 3.6 |
| | 418293 | AI224483 | Hs.16063 | hypothetical protein FLJ21877 | 3.6 |
| 10 | 445888 | AF070564 | Hs.13415 | Homo sapiens clone 24571 mRNA sequence | 3.6 |
| | 458912 | AI911066 | | ESTs | 3.6 |
| | 419390 | AI701162 | Hs.90207 | hypothetical protein MGC11138 | 3.6 |
| | 449256 | AA059050 | Hs.59847 | ESTs | 3.6 |
| | 425010 | T16837 | Hs.4241 | ESTs | 3.6 |
| 15 | 412754 | AW160375 | Hs.74565 | amyloid beta (A4) precursor-like protein | 3.6 |
| | 400777 | | | NM_007325*:Homo sapiens glutamate recept | 3.6 |
| | 438831 | BE263273 | Hs.6439 | synapsin II | 3.6 |
| | 419235 | AW470411 | Hs.288433 | neurotrimin | 3.6 |
| | 424947 | R77952 | | ESTs, Weakly similar to alternatively sp | 3.6 |
| 20 | 407624 | AW157431 | Hs.248941 | ESTs | 3.6 |
| | 440351 | AF030933 | Hs.7179 | RAD1 (S. pombe) homolog | 3.6 |
| | 440404 | AI015881 | Hs.324527 | mitochondrial ribosomal protein S5 | 3.6 |
| | 439267 | AA287747 | Hs.173012 | ESTs, Weakly similar to A46010 X-linked | 3.6 |
| | 424340 | AA339036 | Hs.7033 | ESTs | 3.6 |
| 25 | 423178 | AI033140 | Hs.124983 | Homo sapiens mRNA; cDNA DKFZp564C142 (fr | 3.6 |
| | 418064 | BE387287 | Hs.83384 | S100 calcium-binding protein, beta (neur | 3.6 |
| | 428483 | AI908539 | Hs.184592 | KIAA0344 gene product | 3.6 |
| | 453875 | AW001783 | Hs.232711 | ESTs | 3.6 |
| | 430183 | BE010038 | | gb:PM3-BN0176-100400-001-g04 BN0176 Homo | 3.6 |
| 30 | 431552 | AI815863 | Hs.259873 | axonal transport of synaptic vesicles | 3.6 |
| | 424278 | AK000723 | Hs.144517 | hypothetical protein FLJ20716 | 3.6 |
| | 434131 | AI858275 | Hs.143659 | ESTs | 3.6 |
| | 435923 | BE301930 | Hs.5010 | Homo sapiens clone 24672 mRNA sequence | 3.6 |
| | 415709 | AA649850 | Hs.278558 | ESTs | 3.6 |
| 35 | 437640 | AA764893 | Hs.272155 | ESTs, Weakly similar to I38022 hypothe | 3.6 |
| | 419586 | AI088485 | Hs.144759 | ESTs, Weakly similar to I38022 hypothe | 3.6 |
| | 414040 | N58513 | Hs.32171 | ESTs | 3.6 |
| | 427315 | AA179949 | Hs.175563 | Homo sapiens mRNA; cDNA DKFZp564N0763 (f | 3.6 |
| | 410711 | AB002316 | Hs.65746 | KIAA0318 protein | 3.6 |
| 40 | 445953 | AI612775 | Hs.145710 | ESTs | 3.6 |
| | 444794 | AI419991 | Hs.145225 | ESTs | 3.6 |
| | 411968 | AI207410 | Hs.69280 | Homo sapiens, clone IMAGE:3636299, mRNA, | 3.6 |
| | 428180 | AI129767 | Hs.182874 | guanine nucleotide binding protein (G pr | 3.6 |
| | 415283 | R40504 | Hs.21245 | ESTs | 3.6 |
| 45 | 433160 | AW207002 | Hs.134342 | TASP for testis-specific adriamycin sens | 3.5 |
| | 410386 | W26187 | Hs.3327 | Homo sapiens cDNA: FLJ22219 fis, clone H | 3.5 |
| | 430818 | AI311928 | Hs.348156 | gb:q089h04.x1 NCI_CGAP_Kd5 Homo sapiens | 3.5 |
| | 433932 | AW954599 | Hs.169330 | neuronal protein | 3.5 |
| | 420578 | AA813546 | Hs.99034 | GTP-binding protein Rho7 | 3.5 |
| 50 | 456723 | Z43902 | Hs.4748 | adenylate cyclase activating polypeptide | 3.5 |
| | 416340 | N31772 | Hs.79226 | fasciculation and elongation protein zet | 3.5 |
| | 451455 | AI937227 | Hs.8821 | hepcidin antimicrobial peptide | 3.5 |
| | 412719 | AW016610 | Hs.816 | ESTs | 3.5 |
| | 435910 | AI084152 | Hs.21782 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 3.5 |
| 55 | 439340 | AB032436 | Hs.6535 | brain-specific Na-dependent inorganic ph | 3.5 |
| | 458072 | AI890347 | Hs.271923 | Homo sapiens cDNA: FLJ22785 fis, clone K | 3.5 |
| | 439710 | AF086543 | | gb:Homo sapiens full length insert cDNA | 3.5 |
| | 453896 | AW293483 | Hs.255205 | KIAA1853 protein | 3.5 |
| | 407253 | AA411175 | Hs.141939 | ESTs, Moderately similar to S65657 alpha | 3.5 |
| 60 | 449969 | AW295142 | Hs.180187 | Homo sapiens cDNA FLJ14337 fis, clone PL | 3.5 |
| | 439231 | AW581935 | Hs.141480 | Homo sapiens mRNA; cDNA DKFZp434N079 (fr | 3.5 |
| | 424332 | AA338919 | Hs.101615 | ESTs | 3.5 |
| | 456497 | AW967956 | Hs.123648 | ESTs, Weakly similar to AF108460 1 ubinu | 3.5 |
| | 442264 | AI278777 | Hs.263455 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.5 |
| 65 | 404295 | | | Target Exon | 3.5 |
| | 427209 | H06509 | Hs.92423 | KIAA1566 protein | 3.5 |
| | 439627 | BE621702 | Hs.29076 | hypothetical protein FLJ21841 | 3.5 |
| | 427513 | AI476318 | Hs.192480 | ESTs | 3.5 |
| | 458435 | AI418718 | Hs.144121 | ESTs, Weakly similar to T46916 hypothe | 3.5 |
| 70 | 435545 | AA687415 | Hs.28107 | ESTs | 3.5 |
| | 413199 | M62843 | Hs.75236 | ELAV (embryonic lethal, abnormal vision, | 3.5 |
| | 441607 | NM_005010 | Hs.7912 | neuronal cell adhesion molecule | 3.5 |
| | 452449 | AW068658 | Hs.20943 | ESTs | 3.5 |
| | 443257 | AI334040 | Hs.11614 | HSPC065 protein | 3.5 |
| 75 | 423641 | AL137256 | Hs.130489 | ATPase, aminophospholipid transporter-li | 3.5 |
| | 427581 | NM_014788 | Hs.179703 | KIAA0129 gene product | 3.5 |
| | 424090 | X99699 | Hs.139262 | XIAP associated factor-1 | 3.5 |
| | 422906 | U80773 | Hs.121580 | Human EST clone 42944 mariner transposon | 3.5 |
| | 429698 | AI685086 | Hs.26339 | ESTs, Weakly similar to S21348 probable | 3.5 |
| 80 | 439920 | H05430 | Hs.288433 | neurotrimin | 3.5 |
| | 436899 | AA764852 | Hs.291567 | ESTs | 3.5 |
| | 414178 | AW957372 | Hs.46791 | ESTs, Weakly similar to I38022 hypothe | 3.5 |
| | 418365 | AW014345 | Hs.161690 | ESTs | 3.4 |
| | 414598 | AI094221 | Hs.135150 | lung type-I cell membrane-associated gly | 3.4 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 452571 | W31518 | Hs.34665 | ESTs | |
| | 443633 | AL031290 | Hs.9654 | similar to pregnancy-associated plasma p | 3.4 |
| | 408955 | BE315170 | Hs.8087 | Target CAT | 3.4 |
| 5 | 443206 | AB011420 | Hs.9075 | serine/threonine kinase 17a (apoptosis-i | 3.4 |
| | 419617 | AL008563 | Hs.91622 | neuronal pentraxin receptor | 3.4 |
| | 454171 | AW854832 | | gb:OV2-CT0261-201099-011-005 CT0261 Homo | 3.4 |
| | 426529 | AF090100 | Hs.170241 | Homo sapiens clone IMAGE 23915 | 3.4 |
| | 440652 | AI216751 | Hs.143977 | ESTs | 3.4 |
| 10 | 450813 | AI739625 | Hs.203376 | ESTs | 3.4 |
| | 429323 | NM_001649 | Hs.2391 | apical protein, Xenopus laevis-like | 3.4 |
| | 439774 | AL360257 | Hs.213493 | Homo sapiens mRNA full length insert cDN | 3.4 |
| | 409892 | AW956113 | Hs.7149 | gb:EST368183 MAGE resequences, MAGD Homo | 3.4 |
| | 439963 | AW247529 | Hs.6793 | platelet-activating factor acetylhydrola | 3.4 |
| 15 | 416658 | U03272 | Hs.79432 | fibrillin 2 (congenital contractural ara | 3.4 |
| | 453740 | AL120295 | Hs.311809 | ESTs, Moderately similar to PC4259 ferri | 3.4 |
| | 435256 | AF193766 | Hs.13872 | cytokine-like protein C17 | 3.4 |
| | 453305 | R39224 | Hs.267997 | EHM2 gene | 3.4 |
| | 425287 | R88249 | Hs.155524 | peanut (Drosophila)-like 2 | 3.4 |
| 20 | 417663 | R07483 | Hs.180461 | ESTs | 3.4 |
| | 448533 | AL119710 | Hs.21365 | nucleosome assembly protein 1-like 3 | 3.4 |
| | 441834 | AL138034 | Hs.7979 | KIAA0736 gene product | 3.4 |
| | 457876 | AI821940 | | ESTs, Moderately similar to ALU8_HUMAN A | 3.4 |
| | 407842 | BE410100 | Hs.40368 | adaptor-related protein complex 1, sigma | 3.4 |
| 25 | 422676 | D28481 | Hs.1570 | histamine receptor H1 | 3.4 |
| | 408926 | AF217525 | Hs.49002 | Down syndrome cell adhesion molecule | 3.4 |
| | 430762 | AI343652 | Hs.105667 | ESTs | 3.4 |
| | 430890 | X54232 | Hs.2699 | glypican 1 | 3.4 |
| | 445078 | AI869975 | Hs.4775 | junctophilin 3 | 3.4 |
| 30 | 423257 | AW161039 | Hs.125878 | synapsin III | 3.4 |
| | 417402 | BE503227 | Hs.134759 | ESTs | 3.4 |
| | 410011 | AB020641 | Hs.57856 | PFTAIR protein kinase 1 | 3.4 |
| | 404541 | | | NM_030795:Homo sapiens statthmin-like 4 (| 3.4 |
| 35 | 436291 | BE568452 | Hs.344037 | protein regulator of cytokinesis 1 | 3.4 |
| | 443672 | AA323362 | Hs.9667 | butyrobetaine (gamma), 2-oxoglutarate di | 3.4 |
| | 432140 | AK000404 | Hs.272688 | hypothetical protein FLJ20397 | 3.4 |
| | 451061 | AW291487 | Hs.213659 | ESTs, Weakly similar to KIAA1357 protein | 3.4 |
| | 425782 | U66468 | Hs.159525 | cell growth regulatory with EF-hand doma | 3.4 |
| 40 | 420692 | AW976345 | | gb:EST388454 MAGE resequences, MAGN Homo | 3.4 |
| | 410507 | AA355288 | Hs.76064 | transitional epithelia response protein | 3.4 |
| | 412436 | AA665089 | | gb:nu76d01.s1 NCL_CGAP_Alv1 Homo sapiens | 3.4 |
| | 448112 | AW245919 | Hs.34969 | hypothetical protein DKFZp566N034 | 3.4 |
| | 429269 | AA449013 | Hs.99203 | ESTs | 3.4 |
| | 408037 | AW271720 | Hs.42233 | hypothetical protein FLJ10300 | 3.4 |
| 45 | 418858 | AW961605 | Hs.21145 | hypothetical protein RG083M05.2 | 3.3 |
| | 420050 | AL118615 | Hs.94653 | neurochondrin | 3.3 |
| | 436277 | R88520 | Hs.120917 | ESTs | 3.3 |
| | 430412 | AW341754 | Hs.189305 | ESTs | 3.3 |
| | 408554 | AA836381 | Hs.315111 | nuclear receptor co-repressor/HDAC3 comp | 3.3 |
| 50 | 432663 | AI984317 | Hs.122589 | ESTs | 3.3 |
| | 449919 | AI674685 | Hs.200141 | ESTs | 3.3 |
| | 438509 | R45367 | Hs.101191 | ESTs | 3.3 |
| | 429037 | X81895 | Hs.194765 | H.sapiens GENX-5624 mRNA, 3' UTR | 3.3 |
| 55 | 445537 | AJ245671 | Hs.12844 | EGF-like-domain, multiple 6 | 3.3 |
| | 425537 | AB007913 | Hs.158291 | KIAA0444 protein | 3.3 |
| | 408369 | R38438 | Hs.182575 | solute carrier family 15 (H??? transport | 3.3 |
| | 449686 | AW072813 | Hs.270868 | ESTs, Moderately similar to ALU4_HUMAN A | 3.3 |
| | 417333 | AL157545 | Hs.173179 | bromodomain and PHD finger containing, 3 | 3.3 |
| | 410592 | R94088 | Hs.43569 | ESTs | 3.3 |
| 60 | 439444 | AI277652 | Hs.54578 | ESTs, Weakly similar to I38022 hypothesi | 3.3 |
| | 435375 | AI733610 | Hs.187832 | ESTs | 3.3 |
| | 409746 | NM_004794 | Hs.56294 | RAB33A, member RAS oncogene family | 3.3 |
| | 425588 | F07396 | Hs.46627 | ESTs | 3.3 |
| | 412155 | R38167 | Hs.12449 | Homo sapiens transmembrane protein HTMP1 | 3.3 |
| 65 | 425242 | D13635 | Hs.155287 | KIAA0010 gene product | 3.3 |
| | 417280 | AW173116 | Hs.250103 | ESTs | 3.3 |
| | 423748 | AI149048 | Hs.30211 | hypothetical protein FLJ22313 | 3.3 |
| | 452856 | AF034799 | Hs.30881 | protein tyrosine phosphatase, receptor I | 3.3 |
| | 419103 | Z40229 | Hs.96423 | hypothetical protein FLJ23033 | 3.3 |
| 70 | 435718 | R06569 | Hs.269534 | ESTs | 3.3 |
| | 449249 | T52285 | Hs.193115 | Homo sapiens mRNA for KIAA1764 protein, | 3.3 |
| | 423770 | AW976766 | Hs.132776 | Homo sapiens cDNA FLJ10077 fls, clone HE | 3.3 |
| | 409557 | BE182896 | Hs.211193 | ESTs | 3.3 |
| | 439285 | AL133916 | | hypothetical protein FLJ20093 | 3.3 |
| 75 | 421183 | AL135740 | Hs.102447 | TSC-22-like | 3.3 |
| | 433894 | AI907682 | Hs.243293 | ESTs | 3.3 |
| | 445225 | AI216555 | Hs.202398 | ESTs | 3.3 |
| | 411379 | AI816344 | Hs.12554 | ESTs, Weakly similar to NPL4_HUMAN NUCLE | 3.3 |
| | 436207 | AA334774 | Hs.12845 | hypothetical protein MGC13159 | 3.3 |
| 80 | 436870 | AW204219 | Hs.155560 | catenin | 3.3 |
| | 441791 | AW372449 | Hs.61271 | hypothetical protein FLJ21159 | 3.3 |
| | 408547 | AA574291 | Hs.57837 | ESTs | 3.3 |
| | 420982 | AW576160 | Hs.100729 | KIAA0692 protein | 3.3 |
| | 451625 | R56793 | Hs.106576 | alanine-glyoxylate aminotransferase 2-li | 3.3 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 418932 | L34059 | Hs.89484 | cadherin 4, type 1, R-cadherin (retinal) | 3.3 |
| | 453496 | AA442103 | Hs.33084 | solute carrier family 2 (facilitated glu | 3.3 |
| | 423169 | BED47009 | Hs.21837 | ESTs, Weakly similar to KIAA0927 protein | 3.3 |
| | 418049 | AA211467 | Hs.190488 | Homo sapiens, Similar to nuclear localiz | 3.3 |
| 5 | 441243 | AI767056 | Hs.193002 | ESTs | 3.3 |
| | 444427 | H25094 | Hs.293663 | ESTs, Moderately similar to I38022 hypot | 3.3 |
| | 449115 | AW959952 | Hs.37528 | ESTs, Weakly similar to AF090944 1 PRO06 | 3.3 |
| | 446416 | AV658299 | Hs.163959 | ESTs | 3.3 |
| | 437762 | T78028 | Hs.154679 | synaptotagmin I | 3.3 |
| 10 | 450336 | AA046814 | Hs.288928 | Homo sapiens cDNA: FLJ23296 fis, clone H | 3.3 |
| | 433842 | AI652156 | Hs.26346 | ESTs | 3.3 |
| | 444124 | R43097 | Hs.6818 | ESTs | 3.3 |
| | 423858 | AL137326 | Hs.133483 | Homo sapiens mRNA; cDNA DKFZp434B0650 (f | 3.3 |
| | 454792 | AW820794 | Hs.252406 | hypothetical protein FLJ12296 similar to | 3.3 |
| 15 | 412775 | AA709046 | Hs.27552 | Homo sapiens mRNA; cDNA DKFZp586N2424 (f | 3.3 |
| | 429609 | AF002246 | Hs.210863 | cell adhesion molecule with homology to | 3.2 |
| | 413951 | AW051200 | Hs.75640 | natriuretic peptide precursor A | 3.2 |
| | 433325 | AW206986 | Hs.143905 | ESTs | 3.2 |
| | 449092 | U91641 | Hs.22985 | alpha2,8-sialyltransferase | 3.2 |
| 20 | 422390 | AW450893 | Hs.121830 | ESTs, Weakly similar to T42682 hypotheti | 3.2 |
| | 424899 | AL119387 | Hs.119062 | ESTs | 3.2 |
| | 454253 | AV660717 | Hs.47144 | DKFZP586N0819 protein | 3.2 |
| | 410126 | BE169274 | | KIAA0036 gene product | 3.2 |
| | 456508 | AA502764 | Hs.123469 | ESTs, Weakly similar to AF208855 1 BM-01 | 3.2 |
| 25 | 405303 | | | Target Exon | 3.2 |
| | 420871 | AA702972 | Hs.66300 | ESTs | 3.2 |
| | 442432 | BE093589 | Hs.38178 | hypothetical protein FLJ23468 | 3.2 |
| | 425769 | U72513 | Hs.159486 | Human RPL13-2 pseudogene mRNA, complete | 3.2 |
| | 442320 | AI287817 | Hs.129636 | ESTs | 3.2 |
| 30 | 407378 | AA299264 | Hs.57776 | ESTs, Moderately similar to I38022 hypot | 3.2 |
| | 439764 | T26535 | Hs.22744 | hypothetical protein MGC13105 | 3.2 |
| | 410425 | BE278367 | Hs.63510 | KIAA0141 gene product | 3.2 |
| | 422156 | N34524 | | gb:yy56d10.s1 Soares_multiple_sclerosis_ | 3.2 |
| | 451489 | NM_005503 | Hs.26468 | amyloid beta (A4) precursor protein-bind | 3.2 |
| 35 | 457358 | AI479755 | Hs.129010 | ESTs | 3.2 |
| | 407721 | Y12735 | Hs.38018 | dual-specificity tyrosine-(Y)-phosphoryl | 3.2 |
| | 452372 | AI885742 | Hs.228474 | ESTs | 3.2 |
| | 459660 | M79082 | | ESTs | 3.2 |
| | 437085 | AA743935 | Hs.202329 | ESTs | 3.2 |
| 40 | 419852 | AW503756 | Hs.286184 | hypothetical protein dJ551D2.5 | 3.2 |
| | 440080 | AW051597 | Hs.143707 | ESTs | 3.2 |
| | 449714 | AB033015 | Hs.23941 | KIAA1189 protein | 3.2 |
| | 450407 | NM_000810 | Hs.24969 | gamma-aminobutyric acid (GABA) A recepto | 3.2 |
| | 423165 | AI937547 | Hs.124915 | hypothetical protein MGC2601 | 3.2 |
| 45 | 449961 | AW265634 | Hs.133100 | ESTs | 3.2 |
| | 454036 | AA374756 | Hs.93560 | Homo sapiens mRNA for KIAA1771 protein, | 3.2 |
| | 419865 | NM_007020 | Hs.93502 | U1-snRNP binding protein homolog (70kD) | 3.2 |
| | 423420 | AI571364 | Hs.128382 | Homo sapiens mRNA; cDNA DKFZp76111224 (f | 3.2 |
| | 420352 | BE258835 | | gb:601117374F1 NIH_MGC_16 Homo sapiens c | 3.2 |
| 50 | 424641 | AB001106 | Hs.151413 | glia maturation factor, beta | 3.2 |
| | 453544 | AA831785 | Hs.171914 | Homo sapiens cDNA FLJ14209 fis, clone NT | 3.2 |
| | 447877 | AI435184 | Hs.164252 | ESTs | 3.2 |
| | 419683 | AA248897 | Hs.48784 | ESTs | 3.2 |
| | 451026 | AA013218 | Hs.157492 | cer-d4 (mouse) homolog | 3.2 |
| 55 | 422709 | AA315331 | Hs.153485 | ESTs | 3.2 |
| | 432809 | AA565509 | Hs.131703 | ESTs | 3.2 |
| | 446593 | W79572 | Hs.13277 | hypothetical protein FLJ22054 | 3.2 |
| | 457728 | AW974811 | | gb:EST386916 MAGE resequences, MAGN Homo | 3.2 |
| | 403790 | | | NM_001334*:Homo sapiens cathepsin O (CTS | 3.2 |
| 60 | 445413 | AA151342 | Hs.12677 | CGI-147 protein | 3.2 |
| | 438703 | AI803373 | Hs.31599 | ESTs | 3.1 |
| | 434577 | R37316 | Hs.179769 | Homo sapiens cDNA: FLJ22487 fis, clone H | 3.1 |
| | 422772 | AL119585 | Hs.120228 | KIAA0749 protein | 3.1 |
| 65 | 433434 | AA588429 | | gb:nc22b03.s1 NCI_CGAP_Pr22 Homo sapiens | 3.1 |
| | 427961 | AW293165 | Hs.143134 | ESTs | 3.1 |
| | 414430 | AI346201 | Hs.76118 | ubiquitin carboxyl-terminal esterase L1 | 3.1 |
| | 420552 | AK000492 | Hs.98806 | hypothetical protein | 3.1 |
| | 456209 | W60633 | Hs.297792 | ESTs | 3.1 |
| | 418819 | AA228776 | Hs.191721 | ESTs | 3.1 |
| 70 | 438944 | AA302517 | Hs.92732 | KIAA1444 protein | 3.1 |
| | 439086 | AF085947 | | gb:Homo sapiens full length insert cDNA | 3.1 |
| | 451734 | NM_006176 | Hs.26944 | neurogranin (protein kinase C substrate, | 3.1 |
| | 415257 | F03016 | Hs.27513 | ESTs | 3.1 |
| | 442789 | AW904361 | Hs.131191 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 3.1 |
| 75 | 432675 | AI791855 | Hs.105884 | ESTs | 3.1 |
| | 426600 | NM_003378 | Hs.171014 | VGF nerve growth factor inducible | 3.1 |
| | 435092 | AL137310 | Hs.4749 | Homo sapiens mRNA; cDNA DKFZp761E13121 (| 3.1 |
| | 439039 | AI656707 | Hs.48713 | ESTs | 3.1 |
| | 450358 | AB010098 | Hs.24907 | coronin, actin-binding protein, 2B | 3.1 |
| 80 | 400850 | | | Target Exon | 3.1 |
| | 417636 | R08916 | Hs.191212 | ESTs | 3.1 |
| | 425790 | AW136286 | Hs.288446 | ESTs | 3.1 |
| | 415314 | N88802 | Hs.5422 | glycoprotein M6B | 3.1 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 436456 | AW292677 | Hs.248122 | G protein-coupled receptor 24 | |
| | 408601 | U47928 | Hs.86122 | protein A | 3.1 |
| | 420886 | AA805453 | | ESTs, Weakly similar to T29012 hypotheti | 3.1 |
| 5 | 437162 | AW005505 | Hs.5464 | thyroid hormone receptor coactivating pr | 3.1 |
| | 445704 | AA493742 | Hs.167700 | ESTs, Moderately similar to I38022 hypot | 3.1 |
| | 440700 | AW952281 | Hs.296184 | guanine nucleotide binding protein (G pr | 3.1 |
| | 414747 | U30872 | Hs.77204 | centromere protein F (350/400kD, mitosi | 3.1 |
| | 431553 | X78075 | Hs.2799 | cartilage linking protein 1 | 3.1 |
| | 405605 | | | C2001342:gil127814[sp]P26434/JNAH4_RAT SO | 3.1 |
| 10 | 431467 | N71831 | Hs.256398 | Homo sapiens mRNA; cDNA DKFZp434E0528 (f | 3.1 |
| | 457561 | AA331517 | Hs.286055 | chimerin (chimaerin) 2 | 3.1 |
| | 412507 | L36645 | Hs.73964 | EphA4 | 3.1 |
| | 413448 | AL134467 | Hs.25307 | Homo sapiens clone 24812 mRNA sequence | 3.1 |
| 15 | 444168 | AW379879 | | gb:RC1-HT0256-081199-011-401 HT0256 Homo | 3.1 |
| | 400090 | | | Eos Control | 3.1 |
| | 433642 | BE466341 | Hs.189746 | ESTs, Weakly similar to I38022 hypotheti | 3.1 |
| | 422938 | NM_001809 | Hs.1594 | centromere protein A (17kD) | 3.1 |
| | 426318 | AA375125 | Hs.147112 | Homo sapiens cDNA: FLJ22322 fis, clone H | 3.1 |
| 20 | 428896 | AW291932 | Hs.98936 | ESTs | 3.1 |
| | 449277 | AA001064 | Hs.43670 | ESTs | 3.1 |
| | 426509 | M31166 | Hs.2050 | pentactin-related gene, rapidly induced b | 3.1 |
| | 412216 | AW901517 | | gb:RC5-NN1013-310300-021-C03 NN1013 Homo | 3.1 |
| | 428845 | AL157579 | Hs.153610 | KIAA0751 gene product | 3.1 |
| 25 | 431512 | BE270734 | Hs.2795 | lactate dehydrogenase A | 3.1 |
| | 418113 | AI272141 | Hs.83484 | SRY (sex determining region Y)-box 4 | 3.1 |
| | 450661 | AW952160 | Hs.83849 | ESTs | 3.0 |
| | 448448 | NM_014954 | Hs.21239 | KIAA0985 protein | 3.0 |
| | 422631 | BE218919 | Hs.118793 | hypothetical protein FLJ10688 | 3.0 |
| 30 | 419687 | AI638859 | Hs.227699 | ESTs, Weakly similar to T203_HUMAN TRANS | 3.0 |
| | 450963 | AI864668 | Hs.48832 | ESTs | 3.0 |
| | 435060 | AI422719 | Hs.120873 | ESTs, Weakly similar to fork head like p | 3.0 |
| | 440274 | R24595 | Hs.7122 | scrapie responsive protein 1 | 3.0 |
| | 437438 | AL359620 | Hs.14217 | hypothetical protein DKFZp762P2111 | 3.0 |
| 35 | 435401 | R44477 | Hs.10056 | hypothetical protein FLJ14621 | 3.0 |
| | 416737 | AF154335 | Hs.79691 | UIM domain protein | 3.0 |
| | 445314 | AI689948 | Hs.65489 | Homo sapiens cDNA: FLJ21517 fis, clone C | 3.0 |
| | 425870 | R13406 | Hs.56782 | ESTs | 3.0 |
| | 425294 | AF033827 | Hs.155553 | HNK-1 sulfotransferase | 3.0 |
| 40 | 416404 | AA180138 | Hs.107924 | ESTs | 3.0 |
| | 413995 | BE048146 | Hs.75671 | syntactin 1A (brain) | 3.0 |
| | 422798 | R92347 | Hs.34574 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.0 |
| | 426384 | AI472078 | Hs.303662 | hypothetical protein FLJ13189 (FLJ13189) | 3.0 |
| | 430147 | R60704 | Hs.234434 | hair/enhancer-of-split related with YRP | 3.0 |
| 45 | 425264 | AA353953 | Hs.20369 | ESTs, Weakly similar to gonadotropin ind | 3.0 |
| | 406917 | X65964 | | gb:H.sapiens nestin gene. | 3.0 |
| | 425262 | D87119 | Hs.155418 | GS3955 protein | 3.0 |
| | 401558 | | | ENSP00000220478*:SECRETGRANIN III. | 3.0 |
| | 439345 | AW444759 | Hs.146171 | ESTs | 3.0 |
| 50 | 414865 | AA157155 | Hs.274414 | hypothetical protein FLJ14457 | 3.0 |
| | 453976 | BE463830 | Hs.163714 | ESTs | 3.0 |
| | 404283 | | | ENSP00000244751*:Copine-like protein KIA | 3.0 |
| | 432890 | NM_014442 | Hs.279751 | sialic acid binding Ig-like lectin 8 | 3.0 |
| | 451491 | AI972094 | Hs.286221 | Homo sapiens cDNA FLJ13741 fis, clone PL | 3.0 |
| 55 | 442573 | H93366 | Hs.7567 | branched chain aminotransferase 1, cytos | 3.0 |
| | 428361 | NM_015905 | Hs.183858 | transcriptional intermediary factor 1 | 3.0 |
| | 443753 | AW367578 | Hs.134749 | ESTs | 3.0 |
| | 417868 | AI078534 | Hs.122592 | ESTs | 3.0 |
| | 443898 | AW804296 | Hs.9950 | Sec61 gamma | 3.0 |
| 60 | 438869 | AF075009 | | gb:Homo sapiens full length insert cDNA | 3.0 |
| | 453900 | AW003582 | Hs.226414 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 3.0 |
| | 447714 | AW296313 | Hs.255537 | ESTs | 3.0 |
| | 426581 | AB040956 | Hs.135890 | KIAA1523 protein | 3.0 |
| | 421126 | M74587 | Hs.102122 | insulin-like growth factor binding prote | 3.0 |
| 65 | 410762 | AF226053 | Hs.66170 | HSKM-B protein | 3.0 |
| | 431462 | AW583672 | Hs.256311 | granin-like neuroendocrine peptide precu | 3.0 |
| | 452221 | C21322 | Hs.288057 | hypothetical protein FLJ2242 | 3.0 |
| | 412326 | R07566 | Hs.73817 | small inducible cytokine A3 (homologous | 3.0 |
| | 428600 | AW863261 | Hs.242413 | hypothetical protein DKFZp434K1421 | 3.0 |
| 70 | 426501 | AW043782 | Hs.293616 | ESTs | 3.0 |
| | 405558 | | | Target Exon | 3.0 |
| | 421483 | NM_003388 | Hs.104717 | hypothetical protein MGC11333 | 3.0 |
| | 448681 | AL109781 | Hs.21754 | Homo sapiens mRNA full length insert cDN | 3.0 |
| | 452108 | AW135982 | Hs.203013 | hypothetical protein FLJ12748 | 3.0 |
| 75 | 429569 | AA454993 | Hs.138343 | ESTs, Weakly similar to I78885 serine/th | 3.0 |
| | 450728 | AW162923 | Hs.25363 | presenilin 2 (Alzheimer disease 4) | 3.0 |
| | 429371 | NM_001703 | Hs.200586 | brain-specific angiogenesis inhibitor 2 | 3.0 |
| | 437435 | AA249439 | Hs.27027 | hypothetical protein DKFZp762H1311 | 3.0 |
| | 432188 | AI362952 | Hs.2928 | solute carrier family 7 (cationic amino | 3.0 |
| 80 | 404632 | | | NM_022490:Homo sapiens hypothetical prot | 3.0 |
| | 452619 | AW298597 | Hs.61884 | Homo sapiens, clone IMAGE:4298026, mRNA, | 3.0 |
| | 421458 | NM_003654 | Hs.104576 | carbohydrate (keratan sulfate Gal-6) sul | 3.0 |
| | 419038 | AW134924 | Hs.190325 | ESTs | 3.0 |
| | 453563 | AW508906 | Hs.181163 | hypothetical protein MGC5629 | 3.0 |

405239 U89281 oxidative 3 alpha hydroxysteroid dehydro

3.0

TABLE 17B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

| Pkey | CAT Number | Accession |
|--------|------------|--|
| 408432 | 1058667_1 | AW195262 R27868 AW811262 |
| 410099 | 117647_1 | AA081630 T08671 A1174254 D83874 AW959843 AA364503 AA693467 AW993370 BE327037 AA167714 N79906 AW901977 AW901980 W52882 T07735 AA484549 W60090 D52685 T23811 BE327043 AW901768 BE551237 AA917004 AA716027 A1439658 AA283724 A1805992 A1457096 AA084618 BE467736 A1092635 A1887863 A1697593 AA436618 A1167419 A1418634 T31586 AA436630 AA706191 A1041169 A1422304 T03534 AA211402 A1204899 A1366472 AW827081 AA788593 T32736 A1767935 AA167791 AA747914 AA663870 A1865504 |
| 410126 | 117761_1 | BE169274 AW993230 AA210998 H24222 AA081774 BE000935 BE000834 AA334880 |
| 412216 | 1283670_1 | AW901517 AW901523 AW901521 AW901547 |
| 412436 | 129439_1 | AA665089 AA135130 AA484059 AA102419 AW877765 |
| 412799 | 132817_1 | A1267606 AA121045 AA126521 |
| 412820 | 1330039_1 | BE001236 BE001177 BE001180 BE001234 |
| 414372 | 143909_1 | AA143654 AW753140 AA213770 AW970865 AA569075 AA492132 |
| 415871 | 1626761_1 | H98716 N90792 N24283 |
| 418512 | 176394_1 | AW498974 T09332 R58460 AA350990 T33786 T30936 AA350905 T08592 T09274 AA224297 D54678 T08951 R15346 AW953188 AA350074 AW890649 |
| 419544 | 185760_2 | A1909154 AA526337 AA244193 A1909153 |
| 420352 | 192979_1 | BE258835 AW968316 AA258918 AW843305 R14744 A1580388 BE071923 R35280 |
| 420692 | 195649_1 | AW976345 AA279423 AA761070 |
| 420886 | 197344_1 | AA805453 AA281379 |
| 422156 | 212379_1 | N34524 AA305071 AW954803 AA502335 A1433430 A1203597 AW026670 AW265323 AW850787 AA317554 AW993643 AW835572 AW385512 A1334966 W32951 H62656 H53902 R88904 AW835732 |
| 422949 | 223184_1 | AA319435 N56456 AA319377 AW961532 T48452 AA894424 |
| 423476 | 22861_1 | AL035633 F11794 F11783 H18042 T66089 H29379 R19493 AW134660 A1299437 AL133995 AA057405 N78357 AA917450 A1002692 T09262 T65008 H29290 A1200874 AA894415 A1732887 A1791768 A1733447 AA988785 N62128 T09261 AW956936 |
| 423713 | 231290_1 | AW754182 AW754198 AA329983 |
| 424945 | 245223_1 | A1221919 Z19967 AA348780 AW964077 AW166028 BE540193 N94800 AA452368 N99604 A1341345 AW298800 AA724961 AA931158 A1741227 A1806660 A1982626 D81263 D53937 D52496 AA974487 AW043854 N50483 Z39997 A1492961 A1361526 F04002 AA452141 T23551 A1472655 A193667 A1341984 N92658 T32870 R52664 N50428 AW089291 A1934175 A1423737 D60665 |
| 424947 | 245247_1 | R77952 AA348809 AW959960 AW959962 A1565552 AW070702 AA973910 R85973 |
| 426413 | 266650_1 | AA377823 AW954494 A1022688 |
| 426503 | 268283_1 | AA380153 AA380233 AW963529 |
| 426919 | 273507_1 | AL041228 D82004 D61361 A1203314 A1990307 AW900295 A1018308 AW087473 AW183530 AA393346 H50055 AA935601 |
| 428342 | 290035_2 | A1739168 AA426249 A1199636 AW505198 AW977291 AA824583 AA883419 AA724079 A1015524 A1377728 AW293682 A1928140 AA731438 A1092404 A1085630 AA731340 |
| 429007 | 298301_1 | D80642 AA443145 AL119015 AW904500 |
| 429163 | 300543_1 | AA884766 AW974271 AA592975 AA447312 |
| 429421 | 30431_1 | AL031658 A1693758 AL040619 AW977914 AA811957 A1352198 AW104364 AA648367 AA897604 AW341668 A1201382 AL040620 |
| 430183 | 31412_2 | BE010038 AA676833 A1311783 T86895 W68032 BE064393 BE064394 BE157228 BE183282 A1936370 AA552514 T67280 AA039909 |
| 430676 | 32168_1 | AF084866 AF084870 AF084864 AF084867 AF084869 AF084865 AF084868 AW818206 AW812038 BE144813 BE144812 AW812041 AW812040 AW812067 BE061583 BE061604 T05808 A1352469 AA580921 BE141783 BE141782 BE061601 AW814393 AW885029 |
| 430968 | 326269_1 | AW972830 AA527647 AA489820 AA570362 |
| 433009 | 357371_1 | AA761668 AA573621 R92814 R09670 |
| 433434 | 366095_1 | AA588429 A1972567 AW504832 A1299694 |
| 433523 | 368873_1 | H29882 AW665533 AW149901 A1572917 AA598500 A1686466 A1336390 AW864390 AW864320 |
| 435542 | 407744_1 | AA687376 H74234 AW975503 |
| 438869 | 46651_1 | AF075009 R63109 R63068 |
| 439086 | 46852_1 | AF085947 H70981 H78989 |
| 439285 | 47065_1 | AL133916 N79113 AF086101 N76721 AW950828 AA364013 AW955684 A1346341 A1867454 N54784 A1655270 A1421279 AW014882 AA775552 N62351 N59253 AA626243 A1341407 BE175639 AA456968 A1358918 AA457077 |
| 439518 | 47334_1 | W76326 AF086341 W72300 |
| 439566 | 47387_1 | AF086387 W77884 W72711 |
| 439710 | 47550_1 | AF086543 W96291 W96225 |
| 441102 | 509604_1 | AA973905 A1293888 AA917019 H63235 T90771 |
| 444168 | 593829_1 | AW379879 A1126285 H12014 |
| 446692 | 689623_1 | Z44514 A1352097 A1803984 AW235923 AW196558 A1954637 A1336983 |
| 447197 | 711623_1 | R36075 A1366546 R36167 |
| 449625 | 8113_1 | NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 A1375997 R45432 D59344 A1203107 F07491 R35360 R25094 A1913631 A1498402 T61382 A1016320 N45526 T61415 AA331486 |
| 450375 | 83327_1 | AA009647 AA131254 AA374293 AW954405 H04410 AW606284 AA151166 BE157467 BE157601 H04384 W46291 AW663674 H04021 H01532 AA190993 H03231 H59605 H01642 AA852876 AA113758 AA626915 AA746952 A1161014 AA099554 R69067 |
| 450582 | 83933_1 | A1339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878 |
| 451320 | 86576_1 | AW118072 A1631982 T15734 AA224195 A1701458 W20198 F26326 AA890570 N90552 AW071907 A1671352 A1375892 T03517 R88265 A1124088 AA224388 A1084316 A1354686 T33652 A1140719 A1720211 T03490 A1372637 T15415 AW205836 AA630384 T03515 T33230 AA017131 AA443303 T33623 A1222556 T33511 T33785 A1419606 D55612 |
| 453331 | 96214_1 | A1240665 T53681 N77468 H51833 AA147247 R75732 C18450 R73999 A1095755 T49904 H03868 AA411580 R33395 AA410586 T48869 D63292 R31981 H12498 H02668 AA035018 R75957 A1803329 R27528 R36203 A1809932 A1808765 R78948 AA411449 AA976929 A1378760 A1378620 T48870 R73906 R75632 H03612 AA909684 N50695 H02580 H12839 N58781 AA742532 A1360919 H03502 BE208298 R68588 A1350463 R31935 AW069127 AA411621 R25671 R36105 H12451 H03869 H51263 AA035486 R25109 R25110 AA147933 |
| 453682 | 977454_1 | T79703 T96307 AL079725 |
| 454171 | 1049240_1 | AW854832 AW854798 AW854857 AW854816 AW854834 AW854817 |
| 457728 | 393853_1 | AW974811 AA651634 AA650072 |
| 457876 | 42814_2 | A1821940 N67106 A1744264 AA808846 AA643417 AA643416 Z70715 |
| 458912 | 823104_1 | A1911066 A1933734 A1680888 A1003599 |

TABLE 17C:

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

NI_position: Indicates nucleotide positions of predicted exons.

| Pkey | Ref | Strand | NI_position |
|--------|---------|--------|---|
| 400533 | 6981826 | Minus | 277132-277595 |
| 400777 | 8131663 | Plus | 70745-71121 |
| 400850 | 1927150 | Minus | 4506-4691 |
| 401558 | 7139678 | Plus | 103510-104090 |
| 402145 | 8018280 | Plus | 113086-114800 |
| 402604 | 9909420 | Plus | 20393-20767 |
| 402855 | 9662953 | Minus | 59763-59909 |
| 403696 | 3135242 | Minus | 143467-143634 |
| 403790 | 8084957 | Minus | 87826-87947,89835-90002 |
| 404150 | 7534008 | Plus | 165811-165943 |
| 404283 | 2276311 | Minus | 99460-99564 |
| 404295 | 9856663 | Minus | 75747-75947 |
| 404541 | 8318559 | Plus | 103456-103664 |
| 404584 | 9857511 | Plus | 138651-139153 |
| 404632 | 9796668 | Plus | 45096-45229 |
| 404819 | 4678240 | Plus | 16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578 |
| 405239 | 7249119 | Plus | 144345-144464,144690-144836,151750-151883,152407-152484 |
| 405303 | 2078453 | Minus | 130607-130802 |
| 405331 | 3236226 | Minus | 32502-32690 |
| 405348 | 2914717 | Minus | 43310-43462 |
| 405558 | 1621110 | Plus | 4502-4644,5983-6083 |
| 405605 | 5836195 | Minus | 117070-117270 |
| 405819 | 4007557 | Plus | 2830-2967 |

TABLE 18A: ABOUT 446 CNS-ENRICHED GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA MULTIFORMA COMPARED TO NORMAL ADULT CNS

Table 18A lists about 446 CNS-enriched genes significantly down-regulated in glioblastoma multiforma (GBM) compared to normal adult CNS tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal CNS to "average" GBM was greater than or equal to 2. The "average" normal CNS level was set to the 85th percentile amongst various normal CNS tissues. The "average" GBM level was set to the 85th percentile amongst various tumor samples. To enrich for CNS specific genes, the ratio of "average" CNS to "average" non-CNS normal adult tissues was calculated to be greater than or equal to 3. The "average" CNS level was set to the 85th percentile amongst various CNS tissues. The "average" normal non-CNS adult tissue level was set to the 95th percentile amongst various non-CNS normal tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratios were evaluated.

| | | | | | |
|----|---|---|-----------|--|-----------|
| 40 | the denominator before the ratios were evaluated. | | | | |
| | Pkey: | Unique Eos probeset identifier number | | | |
| | ExAccn: | Exemplar Accession number, Genbank accession number | | | |
| | UnigeneID: | Unigene number | | | |
| | Unigene Title: | Unigene gene title | | | |
| 45 | R1: | Ratio of CNS to GLIOBLASTOMA MULTIFORMA | | | |
| | R2: | Ratio of CNS to NON-CNS NORMAL ADULT TISSUES | | | |
| | Pkey | ExAccn | UnigeneID | Unigene Title | R1 R2 |
| | 425489 | M58594 | Hs.1905 | prolactin | 38.8 10.5 |
| 50 | 410330 | AW023630 | Hs.159425 | ESTs | 23.4 23.4 |
| | 430538 | AB032435 | Hs.242821 | differentiation-associated Na-dependent | 22.6 22.6 |
| | 417275 | X63578 | Hs.295449 | parvalbumin | 22.6 6.0 |
| | 453590 | AF150278 | Hs.33578 | KIAA0820 protein | 22.3 22.3 |
| | 428505 | AL035461 | Hs.2281 | chromogranin B (secretogranin 1) | 21.8 21.8 |
| 55 | 453220 | AB033089 | Hs.32452 | Homo sapiens mRNA for KIAA1263 protein, | 19.9 19.9 |
| | 411498 | NM_014210 | Hs.70499 | ecotropic viral integration site 2A | 19.4 19.4 |
| | 408040 | AI266496 | Hs.22905 | ESTs, Weakly similar to RHG6_HUMAN RHO-G | 19.4 19.4 |
| | 435145 | AI277259 | Hs.116631 | ESTs | 18.5 3.8 |
| | 407039 | X00368 | | gb:Human prolactin gene 5' region. | 18.1 18.1 |
| 60 | 409263 | AA069573 | Hs.50319 | ESTs | 16.8 16.8 |
| | 449078 | AK001256 | Hs.22975 | KIAA1576 protein | 16.1 16.1 |
| | 426968 | U07616 | Hs.173034 | amphiphysin (Stiff-Mann syndrome with br | 15.3 15.3 |
| | 432298 | AL118812 | Hs.274293 | Homo sapiens mRNA; cDNA DKFZp761G1111 (f | 15.1 15.1 |
| | 424645 | NM_014682 | Hs.151449 | KIAA0535 gene product | 15.1 15.1 |
| 65 | 450590 | AI701507 | Hs.273740 | ESTs | 14.9 3.8 |
| | 417175 | R44558 | Hs.94002 | ESTs | 14.6 8.9 |
| | 423449 | AI497900 | Hs.33067 | ESTs | 14.5 14.5 |
| | 441869 | NM_003947 | Hs.8004 | huntingtin-associated protein interactin | 14.4 14.9 |
| | 405560 | AW887701 | | hypothetical protein FLJ20628 | 14.0 8.0 |
| 70 | 440209 | H05049 | Hs.247837 | neurexin 3 | 13.9 18.7 |
| | 439238 | N47305 | Hs.302161 | ESTs | 13.9 5.3 |
| | 452022 | AW072330 | Hs.293875 | ESTs | 13.8 13.8 |
| | 459080 | AW192083 | Hs.290855 | ESTs | 13.5 13.5 |
| | 425649 | U30930 | Hs.158540 | UDP glycosyltransferase 8 (UDP-galactose | 13.4 38.6 |
| 75 | 413324 | V00571 | Hs.75294 | corticotropin releasing hormone | 13.2 13.2 |
| | 443992 | AW022228 | Hs.322922 | ESTs | 13.1 13.1 |
| | 410635 | D58863 | Hs.334372 | chorionic somatomammotropin hormone 1 (p | 12.9 6.6 |
| | 420156 | AW449258 | Hs.6187 | ESTs | 12.5 12.5 |
| | 416490 | AF090116 | Hs.79348 | regulator of G-protein signalling 7 | 12.5 12.5 |
| | 450757 | BE081050 | Hs.31570 | ESTs, Weakly similar to KIAA1324 protein | 12.2 3.2 |
| 80 | 410037 | AB020725 | Hs.58009 | KIAA0918 protein | 12.2 12.2 |
| | 433940 | H05129 | | cyclic AMP-regulated phosphoprotein, 21 | 12.0 12.0 |
| | 434367 | AB020700 | Hs.3830 | KIAA0893 protein | 11.6 5.6 |
| | 410657 | AF063228 | Hs.65248 | dynein, cytoplasmic, intermediate polype | 11.5 11.5 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|------|
| | 431988 | AC002302 | Hs.77202 | protein kinase C, beta 1 | 11.2 | 10.5 |
| | 451783 | R42554 | Hs.210862 | T-box, brain, 1 | 11.2 | 11.2 |
| | 453165 | S74727 | Hs.32042 | aspartoacylase (aminoacylase 2, Canavan | 10.7 | 10.7 |
| | 452238 | F01811 | Hs.345757 | ESTs | 10.6 | 3.8 |
| 5 | 417167 | AW206437 | Hs.4290 | ESTs | 10.4 | 10.4 |
| | 420033 | D59502 | Hs.292590 | ESTs | 10.4 | 10.4 |
| | 427224 | AL135554 | Hs.101937 | sine oculis homeobox (Drosophila) homolo | 10.4 | 3.9 |
| | 424153 | AA451737 | Hs.141496 | MAGE-4like 2 | 10.3 | 5.1 |
| 10 | 413293 | AL047483 | Hs.302498 | GTP-binding protein homologous to Saccha | 10.0 | 10.0 |
| | 400438 | AF185611 | Hs.115352 | Target | 9.9 | 5.1 |
| | 447750 | AI422234 | Hs.143434 | contactin 1 | 9.8 | 9.8 |
| | 419347 | C15944 | Hs.90005 | superiorcervical ganglia, neural specifi | 9.8 | 22.2 |
| | 418207 | C14685 | Hs.34772 | ESTs | 9.8 | 9.8 |
| | 413409 | AI638418 | Hs.1440 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypep | 9.4 | 9.4 |
| 15 | 447746 | AW015920 | Hs.161359 | ESTs | 9.2 | 9.9 |
| | 406311 | | | NM_021979: Homo sapiens heat shock 70kD | 9.1 | 11.5 |
| | 444330 | AI597655 | Hs.49265 | ESTs | 9.1 | 9.1 |
| | 426365 | AA376667 | Hs.10283 | RNA binding motif protein 6B | 9.0 | 4.1 |
| 20 | 427322 | AK002017 | Hs.176227 | hypothetical protein FLJ111155 | 8.9 | 8.9 |
| | 439450 | R51613 | Hs.125304 | ESTs | 8.7 | 8.3 |
| | 429096 | AB011106 | Hs.196012 | KIAA0534 protein | 8.6 | 8.6 |
| | 428652 | AA584272 | Hs.336224 | transmembrane protein with EGF-like and | 8.6 | 8.6 |
| | 408814 | N62499 | Hs.176227 | hypothetical protein FLJ111155 | 8.6 | 8.6 |
| 25 | 410309 | BE043077 | Hs.278153 | ESTs | 8.5 | 8.5 |
| | 408950 | AA707814 | Hs.14945 | long fatty acyl-CoA synthetase 2 gene | 8.5 | 8.5 |
| | 426814 | AF036943 | Hs.172619 | myelin transcription factor 1-like | 8.5 | 14.2 |
| | 416851 | AW963951 | Hs.85618 | ESTs | 8.5 | 8.5 |
| | 430004 | U27768 | Hs.227571 | regulator of G-protein signalling 4 | 8.4 | 15.7 |
| 30 | 412155 | R38167 | Hs.12449 | Homo sapiens transmembrane protein HTMP1 | 8.4 | 27.9 |
| | 427061 | AB032971 | Hs.173392 | KIAA1145 protein | 8.4 | 8.4 |
| | 412049 | N53437 | Hs.18268 | adenylate kinase 5 | 8.3 | 10.7 |
| | 452752 | AW044058 | Hs.33578 | KIAA0820 protein | 8.2 | 13.4 |
| | 414699 | AI815523 | Hs.76930 | synuclein, alpha (non A4 component of am | 8.2 | 4.5 |
| 35 | 422756 | AA441787 | Hs.119689 | glycoprotein hormones, alpha polypeptide | 8.1 | 5.8 |
| | 435648 | H24347 | Hs.27524 | ESTs | 8.1 | 8.1 |
| | 429470 | AI878901 | Hs.203862 | guanine nucleotide binding protein (G pr | 8.0 | 8.0 |
| | 416133 | NM_001683 | Hs.89512 | ATPase, Ca transporting, plasma membrane | 8.0 | 8.0 |
| | 438208 | AL041224 | Hs.65379 | ESTs | 7.9 | 5.8 |
| | 436427 | AI344378 | Hs.143399 | ESTs | 7.8 | 7.8 |
| 40 | 441005 | Z41305 | Hs.303172 | Homo sapiens mRNA; cDNA DKFZp547G133 (fr | 7.7 | 7.7 |
| | 442023 | AI187878 | Hs.144549 | ESTs | 7.7 | 5.6 |
| | 444458 | BE041526 | Hs.31745 | hypothetical protein DKFZp547F072 | 7.7 | 7.7 |
| | 429033 | NM_007374 | Hs.194756 | sine oculis homeobox (Drosophila) homolo | 7.6 | 5.5 |
| 45 | 450642 | R39773 | Hs.7130 | copine IV | 7.6 | 5.6 |
| | 446544 | AI631932 | Hs.7047 | ESTs, Weakly similar to Unknown (H.sapie | 7.5 | 12.4 |
| | 438283 | AI458931 | Hs.37282 | ESTs | 7.5 | 7.5 |
| | 437073 | AI885608 | Hs.94122 | ESTs | 7.5 | 7.5 |
| | 408577 | H50572 | Hs.19515 | ESTs, Highly similar to NRG3_HUMAN PRO-N | 7.4 | 7.4 |
| 50 | 424264 | D80400 | Hs.239388 | Human DNA sequence from clone RP1-304B14 | 7.3 | 7.3 |
| | 441264 | AA927170 | Hs.23290 | ESTs | 7.3 | 7.3 |
| | 450474 | AW872844 | Hs.117494 | ESTs | 7.2 | 7.2 |
| | 425352 | NM_000939 | Hs.1897 | proopiomelanocortin (adrenocorticotropin | 7.2 | 6.1 |
| | 450715 | AI266484 | Hs.31570 | ESTs, Weakly similar to KIAA1324 protein | 7.2 | 7.2 |
| 55 | 450181 | H05254 | Hs.201198 | ESTs | 7.2 | 7.2 |
| | 415076 | NM_000857 | Hs.77890 | guanylate cyclase 1, soluble, beta 3 | 7.1 | 4.8 |
| | 419318 | AW969742 | Hs.291005 | ESTs | 7.1 | 3.1 |
| | 423003 | AL120077 | Hs.122967 | kelch (Drosophila)-like 2 (Mayven) | 7.0 | 7.0 |
| | 434460 | AA478486 | Hs.3852 | KIAA0368 protein | 7.0 | 4.8 |
| 60 | 433921 | AA618174 | | gb:nq14f01.s1 NCL_CGAP_Thy1 Homo sapiens | 7.0 | 7.0 |
| | 418940 | H17739 | Hs.288513 | Human DNA sequence from clone RPS-899C14 | 7.0 | 7.0 |
| | 410765 | AI694972 | Hs.66180 | nucleosome assembly protein 1-like 2 | 7.0 | 8.0 |
| | 457012 | R41480 | Hs.302754 | ESTs | 6.9 | 6.9 |
| | 416018 | AW138239 | Hs.78977 | proprotein convertase subtilisin/kexin 1 | 6.9 | 14.0 |
| 65 | 445898 | AF070623 | Hs.13423 | Homo sapiens clone 24468 mRNA sequence | 6.9 | 6.9 |
| | 415669 | NM_005025 | Hs.78589 | serine (or cysteine) proteinase inhibito | 6.9 | 10.2 |
| | 433558 | AA833757 | Hs.201769 | ESTs, Weakly similar to T24435 hypotheti | 6.9 | 6.9 |
| | 409031 | AA376836 | Hs.288856 | ESTs | 6.8 | 6.8 |
| | 409339 | AB020686 | Hs.54037 | ectonucleotide pyrophosphatase/phosphodi | 6.8 | 3.6 |
| 70 | 436568 | H12049 | Hs.91564 | ESTs | 6.8 | 6.8 |
| | 442593 | R39804 | Hs.31961 | ESTs | 6.7 | 6.7 |
| | 437948 | AA772920 | Hs.303527 | ESTs | 6.7 | 24.8 |
| | 412266 | N59006 | Hs.26133 | ESTs | 6.6 | 30.9 |
| | 422980 | N46569 | Hs.76722 | CCAAT/enhancer binding protein (C/EBP), | 6.6 | 45.2 |
| 75 | 442026 | AI243749 | Hs.8074 | brain-specific angiogenesis inhibitor 3 | 6.5 | 6.5 |
| | 429946 | R49390 | Hs.254129 | KIAA1678 | 6.4 | 4.5 |
| | 445279 | R41900 | Hs.22245 | ESTs | 6.4 | 6.4 |
| | 428414 | AL049980 | Hs.184216 | DKFZP564C152 protein | 6.4 | 6.4 |
| | 407868 | NM_000950 | Hs.40637 | proline-rich Glu (G-carboxyglutamic acid | 6.4 | 3.3 |
| 80 | 434104 | AF116691 | Hs.116459 | hypothetical protein PRO2198 | 6.4 | 4.0 |
| | 443244 | AI457235 | Hs.166479 | ESTs | 6.3 | 3.0 |
| | 442042 | AI990506 | Hs.8077 | Homo sapiens mRNA; cDNA DKFZp547E184 (fr | 6.2 | 6.2 |
| | 444783 | AK001468 | Hs.62180 | anillin (Drosophila Scraps homolog), act | 6.2 | 43.2 |
| | 428536 | AI143139 | Hs.2288 | visinin-like 1 | 6.0 | 22.1 |

| | | | | | | |
|----|--------|-----------|-----------|--|-----|------|
| 5 | 415114 | D60468 | Hs.94181 | ESTs | 6.0 | 6.0 |
| | 448958 | AB020651 | Hs.22653 | KIAA0844 protein | 5.9 | 5.9 |
| | 431467 | N71831 | Hs.256398 | Homo sapiens mRNA; cDNA DKFZp434E0528 (f | 5.9 | 6.0 |
| | 447138 | AI439112 | Hs.93828 | ESTs, Weakly similar to 2109260A B cell | 5.8 | 5.8 |
| | 414545 | AA149287 | Hs.76605 | ESTs | 5.8 | 3.6 |
| | 418202 | N48521 | Hs.26549 | KIAA1708 protein | 5.8 | 5.8 |
| | 410389 | AW954049 | Hs.8177 | ESTs, Weakly similar to PIHUB6 salivary | 5.7 | 9.6 |
| | 444124 | R43097 | Hs.6818 | ESTs | 5.7 | 9.3 |
| 10 | 408065 | AW954272 | | gb:EST366342 MAGE resequences, MAGC Homo | 5.6 | 5.6 |
| | 448533 | AL119710 | Hs.21365 | nucleosome assembly protein 1-like 3 | 5.6 | 9.6 |
| | 425523 | AB007948 | Hs.158244 | KIAA0479 protein | 5.6 | 35.0 |
| | 459697 | AA408062 | Hs.98002 | ESTs | 5.6 | 5.4 |
| | 408428 | NM_014787 | Hs.44896 | DnaJ (Hsp40) homolog, subfamily B, membe | 5.6 | 5.6 |
| 15 | 420111 | AA255652 | | gb:z21h11.1 NCI_CGAP_GCB1 Homo sapiens | 5.5 | 3.2 |
| | 450149 | AW969781 | Hs.132863 | Zic family member 2 (odd-paired Drosophi | 5.4 | 5.4 |
| | 424918 | R13982 | Hs.169309 | myelin-associated oligodendrocyte basic | 5.3 | 5.3 |
| | 438202 | AW169287 | Hs.22588 | ESTs | 5.3 | 5.3 |
| | 448605 | AL109678 | Hs.21597 | Homo sapiens mRNA full length insert cDN | 5.3 | 5.3 |
| 20 | 425580 | L11144 | Hs.1907 | gatanin | 5.3 | 3.5 |
| | 418866 | T65754 | | gb:yc11c07.s1 Stratagene lung (937210) H | 5.3 | 3.8 |
| | 430091 | AB032958 | Hs.233023 | KIAA1132 protein | 5.3 | 4.9 |
| | 448786 | BE048842 | Hs.179075 | Homo sapiens cDNA FLJ11881 fis, clone HE | 5.2 | 5.2 |
| | 427283 | AL119796 | Hs.174185 | ectonucleotide pyrophosphatase/phosphodi | 5.2 | 3.0 |
| 25 | 415666 | H72693 | | gb:yu03c11.1 Soares fetal liver spleen | 5.2 | 5.2 |
| | 410240 | AL157424 | Hs.61289 | synaptojanin 2 | 5.2 | 4.6 |
| | 428784 | Y12851 | Hs.193470 | purinergic receptor P2X, ligand-gated io | 5.2 | 7.7 |
| | 446692 | Z44514 | | Homo sapiens mRNA for KIAA1763 protein, | 5.2 | 33.0 |
| | 428508 | BE252383 | Hs.184668 | SBB131 protein | 5.2 | 4.1 |
| 30 | 446353 | AJ290919 | Hs.153661 | ESTs | 5.1 | 5.1 |
| | 423135 | N67655 | Hs.26411 | ESTs | 5.1 | 8.2 |
| | 437331 | AL353933 | Hs.21710 | hypothetical protein DKFZp761G0313 | 5.1 | 5.1 |
| | 413988 | M81883 | Hs.324784 | glutamate decarboxylase 1 (brain, 67kD) | 5.1 | 5.1 |
| | 429859 | NM_007050 | Hs.225952 | protein tyrosine phosphatase, receptor (| 5.1 | 5.1 |
| 35 | 411379 | AJ816344 | Hs.12554 | ESTs, Weakly similar to NPL4_HUMAN NUCLE | 5.0 | 11.2 |
| | 408068 | AW148652 | Hs.167398 | ESTs | 5.0 | 5.0 |
| | 415734 | NM_014747 | Hs.78748 | KIAA0237 gene product | 5.0 | 27.4 |
| | 439607 | BE540565 | Hs.159460 | ESTs | 5.0 | 5.6 |
| | 425984 | AW836277 | Hs.165636 | hypothetical protein DKFZp761C07121 | 4.9 | 29.3 |
| 40 | 414631 | AW970130 | Hs.65405 | ESTs | 4.9 | 4.9 |
| | 437117 | AL049256 | Hs.122593 | ESTs | 4.9 | 3.8 |
| | 418527 | AA450386 | Hs.7149 | Homo sapiens cDNA: FLJ21950 fis, clone H | 4.9 | 4.9 |
| | 425073 | W39609 | Hs.22003 | solute carrier family 6 (neurotransmitte | 4.9 | 4.9 |
| | 455364 | H72176 | Hs.4273 | hypothetical protein FLJ13159 | 4.9 | 4.9 |
| 45 | 443150 | AI034467 | Hs.34650 | ESTs | 4.9 | 7.6 |
| | 422411 | AW749443 | Hs.22511 | ESTs | 4.9 | 12.0 |
| | 414931 | AK000342 | Hs.77646 | Homo sapiens mRNA; cDNA DKFZp761M0223 (f | 4.9 | 3.4 |
| | 430456 | AA314998 | Hs.241503 | hypothetical protein | 4.8 | 4.7 |
| 50 | 428186 | AW504300 | Hs.295605 | mannosidase, alpha, class 2A, member 2 | 4.8 | 3.9 |
| | 433516 | AA595802 | Hs.33410 | ESTs, Weakly similar to T17279 hypotheti | 4.8 | 4.8 |
| | 427287 | NM_014903 | Hs.174188 | KIAA0938 protein | 4.8 | 4.8 |
| | 416101 | R24854 | Hs.268806 | ESTs | 4.8 | 3.3 |
| | 447252 | R90916 | Hs.12449 | Homo sapiens transmembrane protein HTMP1 | 4.8 | 3.2 |
| 55 | 458268 | AA428403 | Hs.106131 | ESTs | 4.7 | 3.9 |
| | 440105 | AA694010 | Hs.6932 | Homo sapiens clone 23809 mRNA sequence | 4.7 | 8.2 |
| | 445102 | AW204610 | Hs.22270 | ESTs | 4.7 | 19.2 |
| | 419643 | F06066 | Hs.91791 | chromosome 11 open reading frame 25 | 4.7 | 4.7 |
| | 414949 | C15314 | Hs.323349 | ESTs | 4.7 | 3.8 |
| 60 | 453534 | NM_014796 | Hs.33187 | KIAA0748 gene product | 4.7 | 4.7 |
| | 445729 | H21066 | Hs.13223 | Homo sapiens mRNA full length insert cDN | 4.7 | 4.0 |
| | 451032 | W03692 | Hs.323079 | Homo sapiens mRNA; cDNA DKFZp564P116 (fr | 4.7 | 4.9 |
| | 434792 | AA649253 | Hs.132458 | ESTs | 4.7 | 3.8 |
| | 447104 | R19085 | Hs.210706 | Homo sapiens cDNA FLJ13182 fis, clone NT | 4.7 | 3.0 |
| 65 | 430537 | X62692 | Hs.2593 | phosphodiesterase 6B, cGMP-specific, rod | 4.6 | 4.6 |
| | 453431 | AF094754 | Hs.32973 | glycine receptor, beta | 4.6 | 4.6 |
| | 453302 | NM_000838 | Hs.32945 | glutamate receptor, metabotropic 1 | 4.6 | 4.6 |
| | 429876 | AB028977 | Hs.225974 | KIAA1054 protein | 4.6 | 16.8 |
| | 451516 | AI800515 | Hs.12024 | ESTs | 4.6 | 6.3 |
| | 433670 | AA604405 | | gb:nc087h09.s1 NCI_CGAP_AA1 Homo sapiens | 4.6 | 3.9 |
| 70 | 437380 | AL359577 | Hs.112198 | Homo sapiens mRNA; cDNA DKFZp547M073 (fr | 4.5 | 3.8 |
| | 410366 | AI267589 | Hs.302689 | hypothetical protein | 4.5 | 10.4 |
| | 419191 | U17195 | Hs.89666 | A kinase (PRKA) anchor protein 6 | 4.5 | 4.5 |
| | 429290 | AF203032 | Hs.198760 | neurofilament, heavy polypeptide (200kD) | 4.5 | 3.3 |
| | 424932 | R14070 | Hs.315369 | Homo sapiens cDNA: FLJ23075 fis, clone L | 4.5 | 10.2 |
| 75 | 432736 | AA788898 | Hs.179902 | transporter-like protein | 4.4 | 4.0 |
| | 421952 | AA300900 | Hs.98849 | ESTs, Moderately similar to AF161511 1 H | 4.4 | 3.2 |
| | 428963 | AW382682 | Hs.258208 | Homo sapiens, clone MGC:15606, mRNA, com | 4.3 | 3.3 |
| | 435040 | AI932350 | Hs.152825 | ESTs | 4.3 | 4.7 |
| | 451301 | AI769514 | Hs.209890 | EST | 4.3 | 4.3 |
| 80 | 452381 | H23329 | Hs.290880 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 4.3 | 4.3 |
| | 410305 | AF030409 | Hs.62185 | solute carrier family 9 (sodium/hydrogen | 4.3 | 7.8 |
| | 433109 | N58907 | Hs.162430 | EST | 4.3 | 3.9 |
| | 431342 | AW971018 | Hs.21659 | ESTs | 4.3 | 8.0 |
| | 447163 | AW292770 | Hs.5542 | DnaJ (Hsp40) homolog, subfamily C, membe | 4.3 | 3.4 |

| | | | | | | |
|----|--------|-----------|-----------|--|-----|------|
| | 422414 | AW875237 | Hs.13701 | ESTs | 4.2 | 5.3 |
| | 439274 | AF086092 | Hs.48372 | ESTs | 4.2 | 18.3 |
| | 423589 | AA328082 | Hs.209569 | ESTs | 4.2 | 4.2 |
| | 429956 | AI374651 | Hs.22542 | ESTs | 4.2 | 3.2 |
| 5 | 427317 | AB028955 | Hs.175780 | KIAA1032 protein | 4.2 | 5.3 |
| | 426847 | S78723 | Hs.298623 | 5-hydroxytryptamine (serotonin) receptor | 4.1 | 7.9 |
| | 408206 | AF041853 | Hs.43670 | kinesin family member 3A | 4.1 | 4.1 |
| | 433803 | AI823593 | Hs.27688 | ESTs | 4.1 | 4.1 |
| 10 | 413024 | AF036268 | Hs.75149 | SH3-domain GRB2-like 2 | 4.1 | 4.0 |
| | 448117 | H49129 | Hs.172982 | ESTs | 4.1 | 4.1 |
| | 450600 | BE079478 | Hs.24880 | ESTs | 4.1 | 3.9 |
| | 429550 | AW293055 | Hs.113357 | ESTs | 4.1 | 6.4 |
| | 448681 | AL109781 | Hs.21754 | Homo sapiens mRNA full length insert cDN | 4.0 | 7.2 |
| | 458694 | F12832 | Hs.3610 | ESTs | 4.0 | 4.0 |
| 15 | 452197 | AW023595 | Hs.232048 | ESTs | 4.0 | 4.0 |
| | 423728 | AW891294 | Hs.132136 | solute carrier family 4, sodium bicarbon | 4.0 | 7.9 |
| | 429656 | X05608 | Hs.211584 | neurofilament, light polypeptide (68kD) | 4.0 | 13.1 |
| | 448583 | NM_015239 | Hs.21542 | KIAA1035 protein | 4.0 | 4.0 |
| 20 | 419863 | AW952691 | Hs.93485 | Homo sapiens mRNA; cDNA DKFZp761D191 (fr | 3.9 | 21.4 |
| | 442412 | R77677 | Hs.346644 | ESTs | 3.9 | 3.9 |
| | 424001 | W67883 | Hs.137476 | paternally expressed 10 | 3.9 | 5.4 |
| | 440293 | AI004193 | Hs.22123 | ESTs | 3.9 | 3.9 |
| | 422890 | Z43784 | | ankyrin 3, node of Ranvier (ankyrin G) | 3.9 | 3.6 |
| | 426054 | U12431 | Hs.166109 | ELAV (embryonic lethal, abnormal vision, | 3.9 | 3.9 |
| 25 | 412949 | AI471639 | Hs.71913 | ESTs | 3.8 | 3.7 |
| | 427457 | AW779105 | Hs.164682 | ESTs | 3.8 | 11.1 |
| | 416530 | U62801 | Hs.79361 | kallikrein 6 (neurosin, zyme) | 3.8 | 4.4 |
| | 442676 | AI733585 | Hs.130897 | ESTs | 3.8 | 3.8 |
| | 434998 | AW975157 | Hs.26037 | ESTs | 3.7 | 3.7 |
| 30 | 424945 | AI221919 | | hypothetical protein FLJ10582 | 3.7 | 30.5 |
| | 415257 | F03016 | Hs.27513 | ESTs | 3.7 | 8.6 |
| | 407886 | AW969688 | Hs.100826 | ESTs | 3.7 | 20.2 |
| | 400844 | | | NM_003105*:Homo sapiens sortilin-related | 3.7 | 3.1 |
| | 456765 | AI497900 | Hs.33067 | ESTs | 3.7 | 3.7 |
| 35 | 430287 | AW182459 | Hs.125759 | ESTs, Weakly similar to LEU5_HUMAN LEUKE | 3.6 | 7.6 |
| | 452667 | T87219 | Hs.13219 | ESTs | 3.6 | 3.6 |
| | 436773 | AW078629 | | PC4 and SFRS1 interacting protein 1 | 3.6 | 3.6 |
| | 424120 | T80579 | Hs.290270 | ESTs | 3.6 | 14.7 |
| | 446574 | AI310135 | Hs.335933 | ESTs | 3.6 | 3.5 |
| 40 | 432453 | AI885537 | Hs.27172 | ESTs, Moderately similar to PC4259 feni | 3.6 | 3.9 |
| | 408119 | W26213 | Hs.101672 | ESTs, Weakly similar to T00331 hypotheti | 3.6 | 3.6 |
| | 449093 | AB035356 | Hs.22998 | neurexin 1 | 3.6 | 3.6 |
| | 439239 | AI031540 | Hs.235331 | ESTs | 3.6 | 49.5 |
| 45 | 451625 | R56793 | Hs.106576 | alanine-glyoxylate aminotransferase 2-li | 3.6 | 4.1 |
| | 435059 | Z45270 | Hs.235873 | hypothetical protein FLJ22672 | 3.6 | 4.8 |
| | 423346 | AI267677 | Hs.127416 | synaptotagmin 1 | 3.6 | 20.1 |
| | 442738 | AW002370 | Hs.131055 | ESTs, Weakly similar to NPM_HUMAN NUCLEO | 3.5 | 3.5 |
| | 442106 | AW205881 | Hs.326728 | ESTs | 3.5 | 3.2 |
| | 449117 | AW449310 | Hs.210262 | ESTs, Weakly similar to HSS2_HUMAN HEPAR | 3.5 | 3.5 |
| 50 | 405819 | | | NM_002578:Homo sapiens p21 (CDKN1A)-acti | 3.5 | 13.5 |
| | 452311 | AW304029 | Hs.252744 | ESTs | 3.5 | 3.5 |
| | 448902 | Z45998 | Hs.22543 | Homo sapiens mRNA; cDNA DKFZp761I1912 (f | 3.5 | 21.8 |
| | 410224 | M55513 | Hs.150208 | potassium voltage-gated channel, shaker- | 3.4 | 3.4 |
| | 400098 | | | Eos Control | 3.4 | 3.4 |
| 55 | 428001 | H97428 | Hs.219907 | ESTs, Moderately similar to Transforming | 3.4 | 5.9 |
| | 437268 | AI754847 | Hs.227571 | regulator of G-protein signaling 4 | 3.4 | 14.0 |
| | 443682 | AI383061 | Hs.47248 | ESTs, Highly similar to similar to Cdc14 | 3.4 | 3.3 |
| | 417417 | F05745 | Hs.89512 | ATPase, Ca transporting, plasma membrane | 3.3 | 17.1 |
| 60 | 419629 | AB020695 | Hs.91662 | KIAA0888 protein | 3.3 | 13.4 |
| | 419852 | AW503756 | Hs.286184 | hypothetical protein dJ55102.5 | 3.3 | 4.1 |
| | 417063 | N50515 | Hs.45061 | ESTs | 3.3 | 3.3 |
| | 435071 | D60683 | Hs.35495 | ESTs | 3.3 | 3.3 |
| | 446377 | AW014022 | Hs.170953 | ESTs | 3.3 | 3.3 |
| | 412453 | R20205 | Hs.75236 | ESTs | 3.3 | 3.3 |
| 65 | 450561 | R49674 | Hs.25909 | ESTs | 3.3 | 3.3 |
| | 423829 | R44107 | Hs.240905 | ESTs | 3.3 | 4.4 |
| | 415527 | F11624 | | gb:HSC2ZD101 normalized infant brain cDN | 3.3 | 3.3 |
| | 427386 | AW836261 | Hs.6727 | ESTs | 3.3 | 3.3 |
| 70 | 425121 | AI797511 | Hs.154679 | synaptotagmin I | 3.2 | 3.9 |
| | 452856 | AF034799 | Hs.30881 | protein tyrosine phosphatase, receptor t | 3.2 | 10.7 |
| | 442879 | AF032922 | Hs.8813 | syntaxin binding protein 3 | 3.2 | 3.2 |
| | 417284 | N62889 | Hs.107242 | Homo sapiens cDNA FLJ12965 fis, clone NT | 3.2 | 3.2 |
| | 416805 | F13271 | Hs.79981 | Human clone 23560 mRNA sequence | 3.2 | 6.7 |
| 75 | 429477 | AI275514 | Hs.6658 | ESTs | 3.2 | 3.2 |
| | 453169 | AB037815 | Hs.32156 | KIAA1394 protein | 3.2 | 5.7 |
| | 408039 | AA131424 | Hs.336636 | ESTs | 3.2 | 3.2 |
| | 426269 | H15302 | Hs.168950 | Homo sapiens mRNA; cDNA DKFZp566A1046 (f | 3.2 | 22.1 |
| | 409746 | NM_004794 | Hs.56294 | RAB33A, member RAS oncogene family | 3.2 | 10.6 |
| | 416874 | H98752 | Hs.42558 | ESTs | 3.2 | 6.0 |
| 80 | 453919 | AW959912 | Hs.7076 | KIAA1705 protein | 3.2 | 3.2 |
| | 444861 | R46789 | Hs.76118 | ubiquitin carboxyl-terminal esterase L1 | 3.2 | 3.2 |
| | 433315 | R96754 | Hs.239706 | GRB2-associated binding protein 1 | 3.2 | 3.1 |
| | 419103 | Z40229 | Hs.96423 | hypothetical protein FLJ23033 | 3.2 | 8.4 |

| | | | | | | |
|----|--------|-----------|-----------|--|-----|------|
| | 424140 | Z48051 | Hs.141308 | myelin oligodendrocyte glycoprotein | | |
| | 421790 | AW896201 | Hs.22654 | sodium channel, voltage-gated, type I, a | 3.2 | 56.0 |
| | 432809 | AA565509 | Hs.131703 | ESTs | 3.2 | 4.1 |
| | 445225 | AI216555 | Hs.202398 | ESTs | 3.1 | 9.9 |
| 5 | 424087 | N69333 | Hs.143434 | contactin 1 | 3.1 | 5.5 |
| | 437924 | AI935344 | Hs.164118 | ESTs, Weakly similar to SL51_HUMAN SODIU | 3.1 | 3.1 |
| | 419683 | AA248897 | Hs.48784 | ESTs | 3.1 | 3.2 |
| | 420173 | AA256151 | Hs.22999 | ESTs | 3.1 | 5.9 |
| 10 | 411666 | AF106564 | Hs.71346 | neurofilament 3 (150kD medium) | 3.1 | 4.1 |
| | 416220 | N49776 | Hs.170994 | hypothetical protein MGC10946 | 3.1 | 6.6 |
| | 425138 | H08849 | Hs.167464 | glutamate receptor, ionotropic, N-methyl | 3.1 | 4.5 |
| | 422234 | AF119818 | Hs.113287 | discs, large (Drosophila) homolog-associ | 3.1 | 4.2 |
| | 445194 | AI215667 | Hs.175044 | ESTs | 3.1 | 3.1 |
| 15 | 438054 | AA776626 | Hs.169309 | ESTs | 3.1 | 3.1 |
| | 432149 | AW614326 | Hs.133483 | ESTs, Weakly similar to T34549 probable | 3.1 | 10.2 |
| | 445725 | AK000956 | Hs.13209 | hypothetical protein FLJ10094 | 3.1 | 12.2 |
| | 414245 | BE148072 | Hs.75850 | WAS protein family, member 1 | 3.0 | 3.0 |
| | 447673 | AI823987 | Hs.182285 | ESTs | 3.0 | 11.7 |
| 20 | 428392 | H10233 | Hs.2265 | secretory granule, neuroendocrine protei | 3.0 | 3.0 |
| | 418410 | AA811441 | Hs.107393 | chromosome 3 open reading frame 4 | 3.0 | 42.3 |
| | 429024 | AI652297 | Hs.119302 | complement-c1q tumor necrosis factor-rel | 3.0 | 3.9 |
| | 426919 | AL041228 | | ELAV (embryonic lethal, abnormal vision, | 3.0 | 3.7 |
| | 424724 | T06532 | Hs.287709 | Homo sapiens cDNA: FLJ22674 fs, clone H | 3.0 | 9.0 |
| 25 | 410011 | AB020641 | Hs.57856 | PFTAIRE protein kinase 1 | 3.0 | 3.0 |
| | 408947 | AL080093 | Hs.49117 | Homo sapiens mRNA: cDNA DKFZp564N1662 (f | 3.0 | 10.0 |
| | 426325 | D28114 | Hs.169309 | myelin-associated oligodendrocyte basic | 3.0 | 13.5 |
| | 429006 | AA443143 | Hs.50929 | hypothetical protein FLJ13842 | 2.9 | 81.1 |
| | 410711 | AB002316 | Hs.65746 | KIAA0318 protein | 2.9 | 6.6 |
| 30 | 415486 | H12214 | Hs.13284 | ESTs, Weakly similar to 2109260A B cell | 2.9 | 6.1 |
| | 424474 | AA308883 | Hs.148680 | calcyon; D1 dopamine receptor-interactin | 2.9 | 15.7 |
| | 448299 | AA497044 | Hs.20887 | hypothetical protein FLJ10392 | 2.9 | 3.6 |
| | 419518 | U79289 | Hs.90798 | Human clone 23695 mRNA sequence | 2.9 | 11.5 |
| | 426529 | AF090100 | Hs.170241 | Homo sapiens clone IMAGE 23915 | 2.9 | 3.6 |
| 35 | 430347 | NM_002039 | Hs.239706 | GRB2-associated binding protein 1 | 2.9 | 5.1 |
| | 429401 | AW296102 | Hs.99272 | ESTs, Weakly similar to S32567 A4 protei | 2.9 | 3.2 |
| | 450154 | R15891 | Hs.281587 | Human (clone CTG-A4) mRNA sequence | 2.9 | 6.1 |
| | 434277 | X77748 | Hs.3786 | glutamate receptor, metabotropic 3 | 2.9 | 5.9 |
| 40 | 424790 | AL119344 | Hs.13326 | ESTs, Weakly similar to 2004399A chromos | 2.8 | 28.5 |
| | 416836 | D54745 | Hs.80247 | cholecystokinin | 2.8 | 23.1 |
| | 449277 | AA001064 | Hs.43670 | ESTs | 2.8 | 6.8 |
| | 451952 | AL120173 | Hs.301663 | ESTs | 2.8 | 8.5 |
| | 408554 | AA836381 | Hs.315111 | nuclear receptor co-repressor/HDAC3 comp | 2.7 | 19.2 |
| 45 | 413408 | R51793 | Hs.1440 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypep | 2.7 | 3.7 |
| | 410343 | AA084273 | Hs.76561 | ESTs, Weakly similar to S47072 finger pr | 2.7 | 3.0 |
| | 420489 | AA815089 | Hs.193513 | ESTs | 2.7 | 3.2 |
| | 447359 | NM_012093 | Hs.18268 | adenylate kinase 5 | 2.7 | 4.1 |
| | 423731 | T08814 | | gb:EST06706 Infant Brain, Bento Soares H | 2.7 | 17.2 |
| 50 | 409953 | AA332277 | Hs.57691 | cadherin 18, type 2 | 2.7 | 4.0 |
| | 424481 | R19453 | Hs.1787 | proteolipid protein 1 (Pelizaeus-Merzbac | 2.7 | 5.5 |
| | 449714 | AB033015 | Hs.23941 | KIAA1189 protein | 2.7 | 11.5 |
| | 424922 | BE386547 | Hs.217112 | hypothetical protein MGC10825 | 2.7 | 7.5 |
| | 432447 | X92681 | Hs.2998 | contactin 2 (axonal) | 2.7 | 3.7 |
| | 420071 | AB028985 | Hs.94806 | ATP-binding cassette, sub-family A (ABC1 | 2.7 | 4.1 |
| 55 | 438068 | AI927209 | Hs.306210 | Homo sapiens cDNA: FLJ23133 fs, clone L | 2.7 | 5.1 |
| | 418512 | AW498974 | | diacylglycerol kinase, zeta (104kD) | 2.6 | 5.1 |
| | 447761 | AF061573 | Hs.19492 | protocadherin 8 | 2.6 | 7.9 |
| | 448743 | AB032962 | Hs.21896 | KIAA1136 protein | 2.6 | 6.3 |
| | 408547 | AA574291 | Hs.57837 | ESTs | 2.6 | 23.2 |
| 60 | 426380 | AI291267 | Hs.149990 | ESTs | 2.6 | 4.0 |
| | 420898 | AB002379 | Hs.100113 | KIAA0381 protein | 2.6 | 6.9 |
| | 440357 | AA379353 | Hs.20950 | phosphotyrosine phosphohistidine inorganic | 2.6 | 3.7 |
| | 424572 | M19650 | | 2',3'-cyclic nucleotide 3' phosphodiester | 2.6 | 3.7 |
| 65 | 418338 | NM_002522 | Hs.84154 | neuronal pentraxin I | 2.6 | 5.9 |
| | 427658 | H61387 | Hs.30868 | nogo receptor | 2.5 | 6.1 |
| | 410359 | R38624 | Hs.106313 | ESTs | 2.5 | 3.0 |
| | 449717 | AB040935 | Hs.23954 | cerebral cell adhesion molecule | 2.5 | 6.3 |
| | 424458 | M29273 | Hs.1780 | myelin associated glycoprotein | 2.5 | 4.5 |
| 70 | 450133 | AW969769 | Hs.105201 | ESTs | 2.5 | 10.1 |
| | 428976 | AL037824 | Hs.194695 | ras homolog gene family, member I | 2.5 | 40.5 |
| | 454293 | H49739 | Hs.134013 | ESTs, Moderately similar to HK61_HUMAN H | 2.5 | 17.4 |
| | 408447 | AK002089 | Hs.45080 | Homo sapiens cDNA FLJ11227 fs, clone PL | 2.5 | 9.5 |
| | 414583 | S78296 | Hs.76888 | hypothetical protein MGC12702 | 2.5 | 3.9 |
| | 422927 | AW247388 | Hs.301423 | calcium binding protein 1 (calbrain) | 2.5 | 7.1 |
| 75 | 449568 | AL157479 | Hs.23740 | KIAA1598 protein | 2.5 | 3.0 |
| | 454053 | AW023006 | Hs.27172 | ESTs, Moderately similar to PC4259 ferri | 2.5 | 3.6 |
| | 428495 | NM_013279 | Hs.184640 | hypothetical protein MGC10781 | 2.5 | 3.6 |
| | 431096 | AA324358 | Hs.249227 | Homo sapiens DNA, cosmid clones TN62 and | 2.5 | 3.2 |
| | 452371 | R40990 | Hs.21658 | ESTs | 2.4 | 3.6 |
| 80 | 424997 | AL138167 | Hs.96920 | ESTs | 2.4 | 3.3 |
| | 450310 | N62341 | Hs.94116 | ESTs | 2.4 | 6.2 |
| | 452898 | AA814497 | Hs.78792 | ESTs | 2.4 | 3.6 |
| | 436734 | AI937612 | Hs.273758 | hypothetical protein FLJ23112 | 2.4 | 3.9 |
| | 421931 | NM_000814 | Hs.1440 | gamma-aminobutyric acid (GABA) A recepto | 2.4 | 4.7 |
| | | | | | 2.4 | 3.1 |

| | | | | | | |
|----|--------|-----------|-----------|--|-----|------|
| 5 | 439428 | AA835825 | Hs.190490 | ESTs | 2.4 | 3.0 |
| | 445255 | NM_014841 | Hs.12477 | synaptosomal-associated protein, 91 kDa | 2.4 | 8.1 |
| | 436420 | AA443966 | Hs.31595 | ESTs | 2.4 | 3.7 |
| | 408822 | AW500715 | Hs.57079 | Homo sapiens cDNA FLJ13267 fis, clone OV | 2.4 | 3.0 |
| | 451407 | AA131376 | Hs.343809 | fibroblast growth factor 12B | 2.4 | 7.2 |
| | 419757 | AA773820 | Hs.63970 | ESTs | 2.4 | 3.3 |
| | 446100 | AW967109 | Hs.13804 | hypothetical protein dJ462023.2 | 2.4 | 3.6 |
| | 439199 | R40373 | Hs.26299 | ESTs | 2.3 | 9.5 |
| 10 | 427627 | R87582 | Hs.179915 | guanine nucleotide binding protein (G pr | 2.3 | 5.6 |
| | 454048 | H05626 | Hs.6921 | ESTs | 2.3 | 9.9 |
| | 412675 | AA460716 | Hs.9788 | hypothetical protein MGC10924 similar to | 2.3 | 3.3 |
| | 434811 | AW971205 | Hs.114280 | ESTs | 2.3 | 6.7 |
| | 431677 | AK000496 | Hs.306989 | hypothetical protein FLJ20489 | 2.3 | 3.1 |
| 15 | 451386 | AB029006 | Hs.26334 | spastic paraplegia 4 (autosomal dominant | 2.3 | 3.1 |
| | 447028 | AI973128 | Hs.167257 | brain link protein-1 | 2.3 | 5.6 |
| | 451050 | AW937420 | Hs.69662 | ESTs | 2.3 | 4.4 |
| | 437397 | AA349847 | Hs.4221 | hypothetical protein DKFZp761H039 | 2.3 | 4.8 |
| | 408838 | AI669535 | Hs.40369 | ESTs | 2.3 | 3.0 |
| 20 | 408777 | U71204 | Hs.47826 | Ric (Drosophila)-like, expressed in neur | 2.3 | 3.8 |
| | 453924 | R49295 | Hs.24886 | ESTs | 2.3 | 13.4 |
| | 422709 | AA315331 | Hs.153485 | ESTs | 2.3 | 4.4 |
| | 438911 | AF085841 | Hs.301920 | ESTs | 2.3 | 3.3 |
| 25 | 439108 | AW163034 | Hs.6467 | synaptogyrin 3 | 2.2 | 6.9 |
| | 420297 | AI628272 | Hs.88323 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.2 | 4.1 |
| | 404819 | | | NM_002688*:Homo sapiens peanut (Drosophi | 2.2 | 5.8 |
| | 422544 | AB018259 | Hs.118140 | KIAA0716 gene product | 2.2 | 11.8 |
| | 433597 | AA708205 | Hs.100343 | ESTs | 2.2 | 11.0 |
| | 440152 | AB002376 | Hs.7006 | KIAA0378 protein | 2.2 | 14.2 |
| 30 | 418375 | NM_003081 | Hs.84389 | synaptosomal-associated protein, 25kD | 2.2 | 82.9 |
| | 409892 | AW956113 | Hs.7149 | gb:EST368183 MAGE resequences, MAGD Homo | 2.2 | 4.2 |
| | 425287 | R88249 | Hs.155524 | peanut (Drosophila)-like 2 | 2.2 | 6.0 |
| | 433657 | AI244368 | Hs.8124 | PH domain containing protein in retina 1 | 2.2 | 5.0 |
| | 438703 | AI803373 | Hs.31599 | ESTs | 2.2 | 6.2 |
| 35 | 428845 | AL157579 | Hs.153610 | KIAA0751 gene product | 2.2 | 6.7 |
| | 417865 | AW086059 | Hs.6529 | ESTs, Weakly similar to I78885 serine/th | 2.2 | 3.5 |
| | 425897 | AA935315 | Hs.48965 | Homo sapiens cDNA: FLJ21693 fis, clone C | 2.2 | 3.2 |
| | 419271 | N34901 | Hs.238532 | ESTs | 2.2 | 7.5 |
| | 448548 | R13209 | Hs.21413 | solute carrier family 12, (potassium-chl | 2.2 | 7.3 |
| 40 | 439415 | F05538 | Hs.4273 | ESTs | 2.2 | 31.3 |
| | 415170 | R44386 | Hs.164578 | ESTs | 2.2 | 10.9 |
| | 423641 | AL137256 | Hs.130489 | ATPase, aminophospholipid transporter-li | 2.1 | 6.2 |
| | 443728 | AI083876 | Hs.148383 | ESTs | 2.1 | 4.1 |
| | 452108 | AW135982 | Hs.203013 | hypothetical protein FLJ12748 | 2.1 | 5.7 |
| 45 | 429037 | X81895 | Hs.194765 | H.sapiens GENX-5624 mRNA, 3' UTR | 2.1 | 7.1 |
| | 418900 | BE207357 | Hs.3454 | KIAA1821 protein | 2.1 | 4.3 |
| | 421268 | AI126821 | Hs.30514 | ESTs | 2.1 | 4.2 |
| | 446372 | AB020644 | Hs.14945 | long fatty acyl-CoA synthetase 2 gene | 2.1 | 15.6 |
| | 425741 | AF052152 | Hs.159412 | Homo sapiens clone 24628 mRNA sequence | 2.1 | 6.5 |
| 50 | 450214 | BE439763 | Hs.227571 | regulator of G-protein signalling 4 | 2.1 | 3.3 |
| | 452738 | AL133800 | Hs.7086 | hypothetical protein MGC12435 | 2.1 | 3.5 |
| | 447877 | AI435184 | Hs.164252 | ESTs | 2.1 | 5.1 |
| | 422421 | AA325138 | Hs.235873 | hypothetical protein FLJ22672 | 2.1 | 8.3 |
| 55 | 432882 | NM_013257 | Hs.279696 | serum/glucocorticoid regulated kinase-li | 2.1 | 4.2 |
| | 410631 | AA086469 | Hs.47171 | ESTs | 2.1 | 5.8 |
| | 407808 | AA663559 | Hs.279789 | histone deacetylase 3 | 2.1 | 5.7 |
| | 424379 | Z42034 | Hs.93597 | cyclin-dependent kinase 5, regulatory su | 2.1 | 3.2 |
| | 448410 | AK000227 | Hs.21126 | hypothetical protein FLJ20220 | 2.1 | 3.0 |
| | 433932 | AW954599 | Hs.169330 | neuronal protein | 2.1 | 6.9 |
| 60 | 425130 | AA448208 | Hs.99163 | ESTs | 2.1 | 3.1 |
| | 402027 | | | Target Exon | 2.0 | 3.5 |
| | 435191 | R15912 | Hs.4817 | Homo sapiens clone 24461 mRNA sequence | 2.0 | 7.5 |
| | 420547 | AF155140 | Hs.98738 | gonadotropin-regulated testicular RNA he | 2.0 | 10.7 |
| | 404541 | | | NM_030795:Homo sapiens stathmin-like 4 (| 2.0 | 6.0 |
| 65 | 420050 | AL118615 | Hs.94653 | neurochondrin | 2.0 | 6.5 |
| | 417868 | AI078534 | Hs.122592 | ESTs | 2.0 | 5.6 |
| | 416602 | NM_006159 | Hs.79389 | nel (chicken)-like 2 | 2.0 | 3.2 |
| | 436315 | BE390513 | Hs.27935 | hypothetical protein MGC4837 | 2.0 | 4.2 |
| | 439340 | AB032436 | Hs.6535 | brain-specific Na-dependent inorganic ph | 2.0 | 6.3 |
| 70 | 429900 | AA460421 | Hs.30875 | ESTs | 2.0 | 4.2 |
| | 437762 | T78028 | Hs.154679 | synaptotagmin 1 | 2.0 | 4.6 |
| | 425172 | AA447729 | Hs.12714 | ESTs | 2.0 | 3.1 |
| | 419587 | S62907 | Hs.91343 | gamma-aminobutyric acid (GABA) A recepto | 2.0 | 3.1 |
| | 451734 | NM_006176 | Hs.26944 | neurogranin (protein kinase C substrate, | 2.0 | 4.9 |
| 75 | 423603 | AB007880 | Hs.129883 | Homo sapiens KIAA0420 mRNA, complete cds | 2.0 | 4.3 |
| | 438277 | AL022326 | Hs.6139 | synaptogyrin 1 | 2.0 | 3.4 |
| | 423767 | H18283 | Hs.132753 | F-box only protein 2 | 2.0 | 3.2 |
| | 434933 | R91095 | Hs.4276 | KIAA1701 protein | 2.0 | 6.1 |
| 80 | 426575 | M74826 | Hs.170808 | glutamate decarboxylase 2 (pancreatic is | 2.0 | 4.6 |

TABLE 189:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

| Pkey | CAT Number | Accession |
|--------|------------|--|
| 408065 | 103646_1 | AW954272 AI003154 AA059300 AA046911 |
| 415527 | 1539393_1 | F11624 Z43212 H08936 R56332 H09256 R52303 R13075 |
| 415666 | 1543492_1 | H72693 R08673 H72694 F20990 R08580 |
| 418512 | 176394_1 | AW498974 T09332 R58460 AA350990 T33786 T30936 AA350905 T08592 T09274 AA224297 D54678 T08951 R15346 AW953188 AA350074 |
| 418866 | 179788_1 | AW890649 |
| 420111 | 190755_1 | T65754 AA229857 AA229658 |
| 422890 | 222707_1 | AA255652 AA280911 AW967920 AA262684 |
| 423731 | 231466_1 | Z43784 R13382 AWS72911 AA449369 H17037 R19603 AI632565 AW004030 BE502530 Z25032 AA805324 AA449241 AI651825 AI264863 AW196918 |
| 424572 | 24097_1 | AA948267 AI953735 AI263703 AA319159 AW964436 AI903440 AW594171 AI867447 AW204071 AW956110 C15616 D81142 H17038 AW162343 |
| 424945 | 245223_1 | T87230 AI3 |
| 426919 | 273507_1 | T08814 H19198 AL120536 AA330218 AW961552 N47159 |
| 433670 | 372721_1 | M19650 R18810 R18721 AW896146 AW889520 AA192362 AA176814 F12085 BE255264 BE251393 T65248 AA380585 AA380465 BE408684 |
| 433921 | 377350_1 | AA459037 AW498869 AA776107 BE274289 D45269 M61958 AA378818 AW663180 AW672958 H08611 M78164 BE393721 AA348660 R36303 |
| 433940 | 37787_1 | AW498662 AA019090 AA001 |
| 436773 | 426857_1 | AI221919 Z19967 AA348780 AW964077 AW166028 BE540193 N94800 AA452368 N99604 AI341345 AW298800 AA724961 AA931158 AI741227 |
| 446692 | 689623_1 | AI806660 AI982626 D81263 D53937 D52496 AA974487 AW043854 N50483 Z39997 AI492961 AI361526 F04002 AA452141 T23551 AI472655 |
| | | AI193667 AI341 |
| | | AL041228 D82004 D61361 AI203314 AI990307 AW900295 AI018308 AW087473 AW183530 AA393346 H50055 AA93601 |
| | | AA604405 BE062234 AW748386 |
| | | AA618174 AI114549 R36464 R36465 |
| | | H05129 N63433 AI651350 AA984734 AI368716 N40915 AI989705 F09042 T03905 R88588 AF112220 |
| | | AW078629 AI857375 N64357 AA731069 |
| | | Z44514 AI352097 AI803984 AW235923 AW196558 AI954637 AI336983 |

TABLE 18C:

| Pkey: | Ref: | Strand: | NT_position: |
|--------|---------|---------|---|
| | | | Unique number corresponding to an Eos probeset |
| | | | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA |
| | | | sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. |
| | | | Indicates DNA strand from which exons were predicted. |
| | | | Indicates nucleotide positions of predicted exons. |
| 400844 | 9188605 | Plus | 24746-24872,25035-25204 |
| 402027 | 7622350 | Plus | 51645-51888,52917-53005 |
| 404541 | 8318559 | Plus | 103456-103664 |
| 404819 | 4678240 | Plus | 16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578 |
| 405560 | 183148 | Plus | 5495-5655,6077-6241,6495-6692 |
| 405819 | 4007557 | Plus | 2830-2967 |
| 406311 | 9211559 | Minus | 137114-139033 |

TABLE 19A: ABOUT 356 CNS-ENRICHED GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS

| | | | | | |
|----|---|---|--|--|--|
| 45 | Table 19A lists about 356 CNS-enriched genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal CNS to "average" glioblastoma was greater than or equal to 2. The "average" normal CNS level was set to the 85 th percentile amongst various normal CNS tissues. The "average" glioblastoma level was set to the 85 th percentile amongst various tumor samples. To enrich for CNS specific genes, the ratio of "average" CNS to "average" non-CNS normal adult tissues was calculated to be greater than or equal to 3. The "average" CNS level was set to the 85 th percentile amongst various CNS tissues. The "average" non-CNS normal adult tissue level was set to the 95 th percentile amongst various non-CNS normal tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10 th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratios were evaluated. | | | | |
| 50 | Pkey: | Unique Eos probeset identifier number | | | |
| | ExAccn: | Exemplar Accession number, Genbank accession number | | | |
| | UnigenelD: | Unigenel number | | | |
| | Unigene Title: | Unigene gene title | | | |
| 55 | R1: | Ratio of CNS to Glioblastoma | | | |
| | R2: | Ratio of CNS to NON-CNS NORMAL ADULT TISSUES | | | |

| Pkey | ExAccn | UnigenelD | Unigene Title | R1 | R2 |
|--------|-----------|-----------|--|------|------|
| 425489 | M58594 | Hs.1905 | protactin | 24.8 | 10.5 |
| 410330 | AW023630 | Hs.159425 | ESTs | 23.4 | 23.4 |
| 430538 | AB032435 | Hs.242821 | differentiation-associated Na-dependent | 22.6 | 22.6 |
| 417275 | X63578 | Hs.295449 | parvalbumin | 22.4 | 6.0 |
| 428505 | AL035461 | Hs.2281 | chromogranin B (secretogranin 1) | 21.8 | 21.8 |
| 408040 | AI266496 | Hs.22905 | ESTs, Weakly similar to RHG_HUMAN RHO-G | 19.4 | 19.4 |
| 435145 | AI277259 | Hs.116631 | ESTs | 18.5 | 3.8 |
| 407039 | X00368 | | gb:Human protactin gene 5' region. | 18.1 | 18.1 |
| 409263 | AA069573 | Hs.50319 | ESTs | 16.8 | 16.8 |
| 432298 | AL118812 | Hs.274293 | Homo sapiens mRNA: cDNA DKFZp761G1111 (I | 15.1 | 15.1 |
| 424645 | NM_014682 | Hs.151449 | KIAA0535 gene product | 15.1 | 15.1 |
| 416018 | AW138239 | Hs.78977 | proprotein convertase subtilisin/kexin 1 | 14.0 | 14.0 |
| 405560 | AW887701 | | hypothetical protein FLJ20628 | 13.9 | 8.0 |
| 452022 | AW072330 | Hs.293875 | ESTs | 13.8 | 13.8 |
| 413324 | V00571 | Hs.75294 | corticotropin releasing hormone | 13.2 | 13.2 |
| 411498 | NM_014210 | Hs.70499 | ecotropic viral integration site 2A | 12.9 | 19.4 |
| 423449 | AI497900 | Hs.33067 | ESTs | 12.4 | 14.5 |
| 433940 | H05129 | | cyclic AMP-regulated phosphoprotein, 21 | 12.0 | 12.0 |
| 410657 | AF063228 | Hs.65248 | dynein, cytoplasmic, intermediate polype | 11.5 | 11.5 |
| 449078 | AK001256 | Hs.22975 | KIAA1576 protein | 11.0 | 16.1 |
| 410635 | D58863 | Hs.334372 | chorionic somatomammotropin hormone 1 (p | 11.0 | 6.6 |
| 453165 | S74727 | Hs.32042 | aspartoacylase (aminoacylase 2, Canavan | 10.7 | 10.7 |
| 417167 | AW206437 | Hs.4290 | ESTs | 10.4 | 10.4 |
| 420033 | D59502 | Hs.292590 | ESTs | 10.4 | 10.4 |
| 413293 | AL047483 | Hs.302498 | GTP-binding protein homologous to Saccha | 10.0 | 10.0 |

| | | | | | | |
|----|--------|-----------|-----------|---|-----|------|
| | 418207 | C14685 | Hs.34772 | ESTs | 9.8 | 9.8 |
| | 417175 | R44558 | Hs.94002 | ESTs | 9.6 | 8.9 |
| | 444330 | AI597655 | Hs.49265 | ESTs | 9.1 | 9.1 |
| 5 | 427322 | AK002017 | Hs.176227 | hypothetical protein FLJ111155 | 8.9 | 8.9 |
| | 429096 | AB011106 | Hs.196012 | KIAA0534 protein | 8.6 | 8.6 |
| | 428652 | AA584272 | Hs.336224 | transmembrane protein with EGF-like and | 8.6 | 8.6 |
| | 419347 | C15944 | Hs.90005 | superiorcervical ganglia, neural specific | 8.6 | 22.2 |
| | 410309 | BE043077 | Hs.278153 | ESTs | 8.5 | 8.5 |
| 10 | 416851 | AW963951 | Hs.85618 | ESTs | 8.5 | 8.5 |
| | 427061 | AB032971 | Hs.173392 | KIAA1145 protein | 8.4 | 8.4 |
| | 400438 | AF185611 | Hs.115352 | Target | 8.3 | 5.1 |
| | 402029 | H05049 | Hs.247837 | neurexin 3 | 8.2 | 18.7 |
| | 422756 | AA441787 | Hs.119689 | glycoprotein hormones, alpha polypeptide | 8.1 | 5.8 |
| 15 | 435648 | H24347 | Hs.27524 | ESTs | 8.1 | 8.1 |
| | 429470 | AI878901 | Hs.203862 | guanine nucleotide binding protein (G pr | 8.0 | 8.0 |
| | 416133 | NM_001683 | Hs.89512 | ATPase, Ca transporting, plasma membrane | 8.0 | 8.0 |
| | 408814 | N62499 | Hs.176227 | hypothetical protein FLJ111155 | 7.9 | 8.6 |
| | 430004 | U27768 | Hs.227571 | regulator of G-protein signalling 4 | 7.9 | 15.7 |
| 20 | 436427 | AI344378 | Hs.143399 | ESTs | 7.8 | 7.8 |
| | 434367 | AB020700 | Hs.3830 | KIAA0893 protein | 7.8 | 5.6 |
| | 429876 | AB028977 | Hs.225974 | KIAA1054 protein | 7.8 | 16.8 |
| | 441005 | Z41305 | Hs.303172 | Homo sapiens mRNA; cDNA DKFZp547G133 (fr | 7.7 | 7.7 |
| | 442023 | AI187878 | Hs.144549 | ESTs | 7.7 | 5.6 |
| 25 | 429033 | NM_007374 | Hs.194756 | sine oculis homeobox (Drosophila) homolo | 7.6 | 5.5 |
| | 450642 | R39773 | Hs.7130 | copine IV | 7.6 | 5.6 |
| | 437073 | AI885608 | Hs.94122 | ESTs | 7.5 | 7.5 |
| | 441264 | AA927170 | Hs.23290 | ESTs | 7.3 | 7.3 |
| | 424153 | AA451737 | Hs.141496 | MAGE-6ka 2 | 7.3 | 5.1 |
| 30 | 450474 | AW872844 | Hs.117494 | ESTs | 7.2 | 7.2 |
| | 450715 | AI266484 | Hs.31570 | ESTs, Weakly similar to KIAA1324 protein | 7.2 | 7.2 |
| | 415076 | NM_000857 | Hs.77890 | guanylate cyclase 1, soluble, beta 3 | 7.1 | 4.8 |
| | 423003 | AL120077 | Hs.122967 | kelch (Drosophila)-like 2 (Mayven) | 7.0 | 7.0 |
| | 433921 | AA618174 | | gb:nc14f01.s1 NCI_CGAP_Thy1 Homo sapiens | 7.0 | 7.0 |
| 35 | 425352 | NM_000939 | Hs.1897 | proopiomelanocortin (adrenocorticotropin | 6.9 | 6.1 |
| | 457012 | R41480 | Hs.302754 | ESTs | 6.9 | 6.9 |
| | 445898 | AF070623 | Hs.13423 | Homo sapiens clone 24468 mRNA sequence | 6.9 | 6.9 |
| | 433558 | AA833757 | Hs.201769 | ESTs, Weakly similar to T24435 hypotheti | 6.9 | 6.9 |
| | 409031 | AA376836 | Hs.288856 | ESTs | 6.8 | 6.8 |
| 40 | 453590 | AF150278 | Hs.33578 | KIAA0820 protein | 6.6 | 22.3 |
| | 450181 | H05254 | Hs.201198 | ESTs | 6.6 | 7.2 |
| | 425580 | L11144 | Hs.1907 | galanin | 6.5 | 3.5 |
| | 445279 | R41900 | Hs.22245 | ESTs | 6.4 | 6.4 |
| | 428414 | AL049980 | Hs.184216 | DKFZP564C152 protein | 6.4 | 6.4 |
| 45 | 434104 | AF116691 | Hs.116459 | hypothetical protein PRO2198 | 6.4 | 4.0 |
| | 443244 | AI457235 | Hs.166479 | ESTs | 6.3 | 3.0 |
| | 447750 | AI422234 | Hs.143434 | contactin 1 | 6.2 | 9.8 |
| | 415114 | D60468 | Hs.94181 | ESTs | 6.0 | 6.0 |
| | 450600 | BE079478 | Hs.24880 | ESTs | 5.9 | 3.9 |
| 50 | 444458 | BE041526 | Hs.31746 | hypothetical protein DKFZp547F072 | 5.9 | 7.7 |
| | 448958 | AB020651 | Hs.22653 | KIAA0844 protein | 5.9 | 5.9 |
| | 447138 | AI439112 | Hs.93828 | ESTs, Weakly similar to 2109260A B cell | 5.8 | 5.8 |
| | 414545 | AA149287 | Hs.76605 | ESTs | 5.8 | 3.6 |
| | 410389 | AW954049 | Hs.8177 | ESTs, Weakly similar to PIHUB6 salivary | 5.6 | 9.6 |
| 55 | 450590 | AI701507 | Hs.273740 | ESTs | 5.6 | 3.8 |
| | 408428 | NM_014787 | Hs.44896 | DnaJ (Hsp40) homolog, subfamily B, membe | 5.6 | 5.6 |
| | 442026 | AI243749 | Hs.8074 | brain-specific angiogenesis inhibitor 3 | 5.5 | 6.5 |
| | 450149 | AW969781 | Hs.132863 | Zic family member 2 (odd-paired Drosophi | 5.4 | 5.4 |
| | 414699 | AI815523 | Hs.76930 | synuclein, alpha (non A4 component of am | 5.3 | 4.5 |
| 60 | 438202 | AW169287 | Hs.22588 | ESTs | 5.3 | 5.3 |
| | 448605 | AL109678 | Hs.21597 | Homo sapiens mRNA full length insert cDN | 5.3 | 5.3 |
| | 418866 | T65754 | | gb:yc11c07.s1 Stratagene lung (937210) H | 5.3 | 3.8 |
| | 448786 | BE048842 | Hs.179075 | Homo sapiens cDNA FLJ11881 fis, clone HE | 5.2 | 5.2 |
| | 406311 | | | NM_021979; Homo sapiens heat shock 70kD | 5.2 | 11.5 |
| 65 | 443682 | AI383061 | Hs.47248 | ESTs, Highly similar to similar to Cdc14 | 5.2 | 3.3 |
| | 415666 | H72693 | | gb:yu03c11.r1 Soares fetal liver spleen | 5.2 | 5.2 |
| | 416101 | R24854 | Hs.268806 | ESTs | 5.2 | 3.3 |
| | 428508 | BE252383 | Hs.184668 | SBB131 protein | 5.2 | 4.1 |
| | 419318 | AW969742 | Hs.291005 | ESTs | 5.2 | 3.1 |
| 70 | 439238 | N47305 | Hs.302161 | ESTs | 5.1 | 5.3 |
| | 446353 | AI290919 | Hs.153661 | ESTs | 5.1 | 5.1 |
| | 412049 | N53437 | Hs.18268 | adenylate kinase 5 | 5.1 | 10.7 |
| | 437331 | AL353933 | Hs.21710 | hypothetical protein DKFZp761G0313 | 5.1 | 5.1 |
| | 413988 | M81883 | Hs.324784 | glutamate decarboxylase 1 (brain, 67kD) | 5.1 | 5.1 |
| 75 | 408068 | AW148652 | Hs.167398 | ESTs | 5.0 | 5.0 |
| | 414631 | AW970130 | Hs.65406 | ESTs | 4.9 | 4.9 |
| | 418527 | AA450386 | Hs.7149 | Homo sapiens cDNA: FLJ21950 fis, clone H | 4.9 | 4.9 |
| | 425073 | W39609 | Hs.22003 | solute carrier family 5 (neurotransmitte | 4.9 | 4.9 |
| | 427224 | AL135554 | Hs.101937 | sine oculis homeobox (Drosophila) homolo | 4.9 | 3.9 |
| | 433516 | AA595802 | Hs.33410 | ESTs, Weakly similar to T17279 hypotheti | 4.8 | 4.8 |
| 80 | 427287 | NM_014903 | Hs.174188 | KIAA0938 protein | 4.8 | 4.8 |
| | 447252 | R90916 | Hs.12449 | Homo sapiens transmembrane protein HTMP1 | 4.8 | 3.2 |
| | 424932 | R14070 | Hs.315369 | Homo sapiens cDNA: FLJ23075 fis, clone L | 4.7 | 10.2 |
| | 419643 | F06066 | Hs.91791 | chromosome 11 open reading frame 25 | 4.7 | 4.7 |

| | | | | | | |
|----|--------|-----------|-----------|--|-----|------|
| | 414949 | C15314 | Hs.323349 | ESTs | 4.7 | 3.8 |
| | 453534 | NM_014796 | Hs.33187 | KIAA0748 gene product | 4.7 | 4.7 |
| | 430537 | X82692 | Hs.2593 | phosphodiesterase 6B, cGMP-specific, rod | 4.6 | 4.6 |
| 5 | 453431 | AF094754 | Hs.32973 | glycine receptor, beta | 4.6 | 4.6 |
| | 453302 | NM_000838 | Hs.32945 | glutamate receptor, metabotropic 1 | 4.6 | 4.6 |
| | 447104 | R19085 | Hs.210706 | Homo sapiens cDNA FLJ13182 fis, clone NT | 4.6 | 4.6 |
| | 418202 | N48521 | Hs.26549 | KIAA1708 protein | 4.6 | 3.0 |
| | 419191 | U17195 | Hs.89666 | A kinase (PRKA) anchor protein 6 | 4.6 | 5.8 |
| 10 | 459080 | AW192083 | Hs.290855 | ESTs | 4.5 | 4.5 |
| | 451783 | R42554 | Hs.210862 | T-box, brain, 1 | 4.5 | 13.5 |
| | 421952 | AA300900 | Hs.98849 | ESTs, Moderately similar to AF161511 1 H | 4.4 | 11.2 |
| | 451050 | AW937420 | Hs.69662 | ESTs | 4.4 | 3.2 |
| | 423728 | AW891294 | Hs.132136 | solute carrier family 4, sodium bicarbon | 4.4 | 4.4 |
| | 447746 | AW015920 | Hs.161359 | ESTs | 4.4 | 7.9 |
| 15 | 451301 | AJ769514 | Hs.209890 | EST | 4.3 | 9.9 |
| | 452381 | H23329 | Hs.290880 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 4.3 | 4.3 |
| | 433109 | N58907 | Hs.162430 | EST | 4.3 | 4.3 |
| | 412155 | R38167 | Hs.12449 | Homo sapiens transmembrane protein HTMP1 | 4.3 | 3.9 |
| 20 | 426365 | AA376667 | Hs.10283 | RNA binding motif protein 8B | 4.3 | 27.9 |
| | 423589 | AA328082 | Hs.209569 | ESTs | 4.3 | 4.1 |
| | 432453 | AJ885537 | Hs.27172 | ESTs, Moderately similar to PC4259 ferri | 4.2 | 4.2 |
| | 420489 | AA815089 | Hs.193513 | ESTs | 4.2 | 3.9 |
| | 427457 | AW779105 | Hs.164682 | ESTs | 4.1 | 4.1 |
| 25 | 408206 | AF041853 | Hs.43670 | kinesin family member 3A | 4.1 | 11.1 |
| | 433803 | AJ823593 | Hs.27688 | ESTs | 4.1 | 4.1 |
| | 407868 | NM_000950 | Hs.40637 | proline-rich Glu (G-carboxyglutamic acid | 4.1 | 4.1 |
| | 448117 | H49129 | Hs.172982 | ESTs | 4.1 | 3.3 |
| | 442106 | AW205881 | Hs.326728 | ESTs | 4.1 | 4.1 |
| 30 | 450757 | BE081050 | Hs.31570 | ESTs, Weakly similar to KIAA1324 protein | 4.1 | 3.2 |
| | 442042 | AJ990506 | Hs.8077 | Homo sapiens mRNA; cDNA DKFZp547E184 (fr | 4.0 | 3.2 |
| | 458694 | F12832 | Hs.3610 | ESTs | 4.0 | 6.2 |
| | 452197 | AW023595 | Hs.232048 | ESTs | 4.0 | 4.0 |
| | 448583 | NM_015239 | Hs.21542 | KIAA1035 protein | 4.0 | 4.0 |
| 35 | 418940 | H17739 | Hs.288513 | Human DNA sequence from clone RPS-899C14 | 4.0 | 4.0 |
| | 442412 | R77677 | Hs.346644 | ESTs | 3.9 | 7.0 |
| | 440293 | AJ004193 | Hs.22123 | ESTs | 3.9 | 3.9 |
| | 433670 | AA604405 | | gb:nc87h09.s1 NCI_CGAP_AA1 Homo sapiens | 3.9 | 3.9 |
| 40 | 459697 | AA406062 | Hs.98002 | ESTs | 3.9 | 3.9 |
| | 429290 | AF203032 | Hs.198760 | neurofilament, heavy polypeptide (200kD) | 3.9 | 5.4 |
| | 426054 | U12431 | Hs.166109 | ELAV (embryonic lethal, abnormal vision, | 3.9 | 3.3 |
| | 424001 | W67883 | Hs.137476 | paternally expressed 10 | 3.9 | 3.9 |
| | 442676 | AJ733585 | Hs.130897 | ESTs | 3.8 | 5.4 |
| | 410240 | AL157424 | Hs.61289 | synaptotagmin 2 | 3.8 | 3.8 |
| 45 | 409339 | AB020686 | Hs.54037 | ectonucleotide pyrophosphatase/phosphodi | 3.8 | 4.6 |
| | 434998 | AW975157 | Hs.26037 | ESTs | 3.7 | 3.6 |
| | 439450 | R51613 | Hs.125304 | ESTs | 3.7 | 3.7 |
| | 455364 | H72176 | Hs.4273 | hypothetical protein FLJ13159 | 3.7 | 8.3 |
| | 400844 | | | NM_003105: Homo sapiens sortilin-related | 3.7 | 4.9 |
| 50 | 456765 | AJ497900 | Hs.33067 | ESTs | 3.7 | 3.1 |
| | 452667 | T87219 | Hs.13219 | ESTs | 3.7 | 3.7 |
| | 436773 | AW078629 | | PC4 and SFRS1 interacting protein 1 | 3.6 | 3.6 |
| | 453220 | AB033089 | Hs.32452 | Homo sapiens mRNA for KIAA1263 protein, | 3.6 | 3.6 |
| 55 | 432149 | AW614326 | Hs.133483 | ESTs, Weakly similar to T34549 probable | 3.6 | 19.9 |
| | 408119 | W26213 | Hs.101672 | ESTs, Weakly similar to T00331 hypotheti | 3.6 | 12.2 |
| | 449093 | AB035356 | Hs.22998 | neurexin 1 | 3.6 | 3.6 |
| | 429968 | U07616 | Hs.173034 | amphiphysin (Stiff-Mann syndrome with br | 3.6 | 3.6 |
| | 410011 | AB020641 | Hs.57856 | PFTAIRE protein kinase 1 | 3.6 | 15.3 |
| | 442738 | AW002370 | Hs.131055 | ESTs, Weakly similar to NPM_HUMAN NUCLEO | 3.6 | 10.0 |
| 60 | 451032 | W03692 | Hs.323079 | Homo sapiens mRNA; cDNA DKFZp564P116 (fr | 3.5 | 3.5 |
| | 449117 | AW449310 | Hs.210262 | ESTs, Weakly similar to HSS2_HUMAN HEPAR | 3.5 | 4.9 |
| | 416490 | AF090116 | Hs.79348 | regulator of G-protein signalling 7 | 3.5 | 3.5 |
| | 412266 | N59006 | Hs.26133 | ESTs | 3.5 | 12.5 |
| | 452311 | AW304029 | Hs.252744 | ESTs | 3.5 | 30.9 |
| 65 | 425649 | U30930 | Hs.158540 | UDP glycosyltransferase 8 (UDP-galactose | 3.5 | 3.5 |
| | 410224 | M55513 | Hs.150208 | potassium voltage-gated channel, shaker- | 3.5 | 38.6 |
| | 451516 | AJ800515 | Hs.12024 | ESTs | 3.4 | 3.4 |
| | 400098 | | | Eos Control | 3.4 | 6.3 |
| | 424918 | R13982 | Hs.169309 | myelin-associated oligodendrocyte basic | 3.4 | 3.4 |
| 70 | 452238 | F01811 | Hs.345757 | ESTs | 3.4 | 5.3 |
| | 417063 | N50515 | Hs.45061 | ESTs | 3.3 | 3.8 |
| | 443992 | AW022228 | Hs.322922 | ESTs | 3.3 | 3.3 |
| | 412453 | R20205 | Hs.75236 | ESTs | 3.3 | 13.1 |
| | 450561 | R49674 | Hs.25909 | ESTs | 3.3 | 3.3 |
| 75 | 415527 | F11624 | | gb:HSC22D101 normalized infant brain cDN | 3.3 | 3.3 |
| | 427386 | AW836261 | Hs.6727 | ESTs | 3.3 | 3.3 |
| | 423346 | AJ267677 | Hs.127416 | synaptotagmin 1 | 3.3 | 3.3 |
| | 431342 | AW971018 | Hs.21659 | ESTs | 3.2 | 20.1 |
| | 448533 | AL119710 | Hs.21365 | nucleosome assembly protein 1-like 3 | 3.2 | 8.0 |
| 80 | 442879 | AF032922 | Hs.8813 | synaptotagmin binding protein 3 | 3.2 | 9.6 |
| | 417284 | N62889 | Hs.107242 | Homo sapiens cDNA FLJ12965 fis, clone NT | 3.2 | 3.2 |
| | 429477 | AJ275514 | Hs.6658 | ESTs | 3.2 | 3.2 |
| | 410343 | AA084273 | Hs.76561 | ESTs, Weakly similar to S47072 finger pr | 3.2 | 3.2 |
| | 427317 | AB028955 | Hs.175780 | KIAA1032 protein | 3.2 | 5.3 |

| | | | | | | |
|----|--------|-----------|-----------|---|-----|------|
| | 408039 | AA131424 | Hs.336636 | ESTs | 3.2 | 3.2 |
| | 428976 | AL037824 | Hs.194695 | ras homolog gene family, member I | 3.2 | 17.4 |
| | 420297 | AI628272 | Hs.88323 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.2 | 4.1 |
| | 453919 | AW959912 | Hs.7076 | KIAA1705 protein | 3.2 | 3.2 |
| 5 | 428963 | AW382682 | Hs.258208 | Homo sapiens, clone MGC:15606, mRNA, com | 3.2 | 3.3 |
| | 423829 | R44107 | Hs.240905 | ESTs | 3.1 | 4.4 |
| | 424087 | N69333 | Hs.143434 | contactin 1 | 3.1 | 3.1 |
| | 419852 | AW503756 | Hs.286184 | hypothetical protein dJ55102.5 | 3.1 | 4.1 |
| | 444783 | AK001468 | Hs.62180 | anillin (Drosophila Scraps homolog), act | 3.1 | 43.2 |
| 10 | 422234 | AF119818 | Hs.113287 | discs, large (Drosophila) homolog-associ | 3.1 | 3.1 |
| | 446692 | Z44514 | | Homo sapiens mRNA for KIAA1763 protein, | 3.1 | 33.0 |
| | 437117 | AL049256 | Hs.122593 | ESTs | 3.1 | 3.8 |
| | 405819 | | | NM_002578:Homo sapiens p21 (CDKN1A)-acti | 3.1 | 13.5 |
| | 452752 | AW044058 | Hs.33578 | KIAA0820 protein | 3.1 | 13.4 |
| 15 | 416220 | N49776 | Hs.170994 | hypothetical protein MGC10945 | 3.1 | 4.5 |
| | 437380 | AL359577 | Hs.112198 | Homo sapiens mRNA; cDNA DKFZp547M073 (fr | 3.0 | 3.8 |
| | 428001 | H97428 | Hs.219907 | ESTs, Moderately similar to Transforming | 3.0 | 5.9 |
| | 445725 | AK000956 | Hs.13209 | hypothetical protein FLJ10094 | 3.0 | 3.0 |
| 20 | 447673 | AI823987 | Hs.182285 | ESTs | 3.0 | 3.0 |
| | 427283 | AL119796 | Hs.174185 | ectonucleotide pyrophosphatase/phosphodi | 3.0 | 3.0 |
| | 424724 | T06532 | Hs.287709 | Homo sapiens cDNA: FLJ22674 fis, clone H | 3.0 | 3.0 |
| | 408547 | AA574291 | Hs.57837 | ESTs | 3.0 | 4.0 |
| | 433315 | R96754 | Hs.239706 | GRB2-associated binding protein 1 | 3.0 | 3.1 |
| 25 | 439274 | AF086092 | Hs.48372 | ESTs | 3.0 | 18.3 |
| | 410765 | AI694972 | Hs.66180 | nucleosome assembly protein 1-like 2 | 3.0 | 8.0 |
| | 458268 | AA428403 | Hs.106131 | ESTs | 3.0 | 3.9 |
| | 424641 | AB001106 | Hs.151413 | glia maturation factor, beta | 3.0 | 5.6 |
| | 441869 | NM_003947 | Hs.8004 | huntingtin-associated protein interactin | 3.0 | 14.9 |
| | 442593 | R39804 | Hs.31961 | ESTs | 2.9 | 6.7 |
| 30 | 426380 | AI291267 | Hs.149990 | ESTs | 2.9 | 6.9 |
| | 428536 | AI143139 | Hs.2288 | visinin-like 1 | 2.9 | 22.1 |
| | 417417 | F05745 | Hs.89512 | ATPase, Ca transporting, plasma membrane | 2.9 | 17.1 |
| | 411379 | AI816344 | Hs.12554 | ESTs, Weakly similar to NPL4_HUMAN NUCLE | 2.9 | 11.2 |
| | 422414 | AW875237 | Hs.13701 | ESTs | 2.9 | 5.3 |
| 35 | 428186 | AW504300 | Hs.295605 | mannosidase, alpha, class 2A, member 2 | 2.9 | 3.9 |
| | 419518 | U79289 | Hs.90798 | Human clone 23695 mRNA sequence | 2.9 | 3.6 |
| | 426919 | AL041228 | | ELAV (embryonic lethal, abnormal vision, | 2.9 | 9.0 |
| | 446544 | AI631932 | Hs.7047 | ESTs, Weakly similar to Unknown [H.sapie | 2.8 | 12.4 |
| | 422411 | AW749443 | Hs.22511 | ESTs | 2.8 | 12.0 |
| 40 | 416874 | H98752 | Hs.42568 | ESTs | 2.8 | 6.0 |
| | 448902 | Z45998 | Hs.22543 | Homo sapiens mRNA; cDNA DKFZp76111912 (f | 2.8 | 21.8 |
| | 430456 | AA314998 | Hs.241503 | hypothetical protein | 2.8 | 4.7 |
| | 429859 | NM_007050 | Hs.225952 | protein tyrosine phosphatase, receptor t | 2.8 | 5.1 |
| 45 | 429656 | X05608 | Hs.211584 | neurofilament, light polypeptide (68kD) | 2.8 | 13.1 |
| | 437948 | AA772920 | Hs.303527 | ESTs | 2.8 | 24.8 |
| | 440105 | AA694010 | Hs.6932 | Homo sapiens clone 23809 mRNA sequence | 2.8 | 8.2 |
| | 414931 | AK000342 | Hs.77646 | Homo sapiens mRNA; cDNA DKFZp761M0223 (f | 2.8 | 3.4 |
| | 416530 | U62801 | Hs.79361 | kallikrein 6 (neurosin, zyme) | 2.8 | 4.4 |
| 50 | 446574 | AI310135 | Hs.335933 | ESTs | 2.8 | 3.5 |
| | 422890 | Z43784 | | ankyrin 3, node of Ranvier (ankyrin G) | 2.8 | 3.6 |
| | 410711 | AB002316 | Hs.65746 | KIAA0318 protein | 2.7 | 6.1 |
| | 422980 | N46569 | Hs.76722 | CCAAT/enhancer binding protein (C/EBP), | 2.7 | 45.2 |
| | 408554 | AA836381 | Hs.315111 | nuclear receptor co-repressor/HDAC3 comp | 2.7 | 3.7 |
| 55 | 434460 | AA478486 | Hs.3852 | KIAA0368 protein | 2.7 | 4.8 |
| | 431988 | AC002302 | Hs.77202 | protein kinase C, beta 1 | 2.7 | 10.5 |
| | 447163 | AW292770 | Hs.5542 | DnaJ (Hsp40) homolog, subfamily C, membe | 2.7 | 3.4 |
| | 437924 | AI935344 | Hs.164118 | ESTs, Weakly similar to SL51_HUMAN SODIU | 2.6 | 3.2 |
| | 424945 | AI221919 | | hypothetical protein FLJ10582 | 2.6 | 30.5 |
| 60 | 425984 | AW836277 | Hs.165636 | hypothetical protein DKFZp761C07121 | 2.6 | 29.3 |
| | 447761 | AF061573 | Hs.19492 | protocadherin 8 | 2.6 | 6.3 |
| | 425138 | H08849 | Hs.167464 | glutamate receptor, ionotropic, N-methyl | 2.6 | 4.2 |
| | 436568 | H12049 | Hs.91564 | ESTs | 2.6 | 6.8 |
| | 408065 | AW954272 | | gb:EST366342 MAGE resequences, MAGC Homo | 2.6 | 5.6 |
| 65 | 430287 | AW182459 | Hs.125759 | ESTs, Weakly similar to LEU5_HUMAN LEUKE | 2.6 | 7.6 |
| | 408777 | U71204 | Hs.47626 | Ric (Drosophila)-like, expressed in neur | 2.6 | 3.8 |
| | 420173 | AA256151 | Hs.22999 | ESTs | 2.6 | 4.1 |
| | 429550 | AW293055 | Hs.119357 | ESTs | 2.6 | 6.4 |
| | 438068 | AI927209 | Hs.306210 | Homo sapiens cDNA: FLJ23133 fis, clone L | 2.6 | 5.1 |
| 70 | 424264 | D80400 | Hs.239388 | Human DNA sequence from clone RP1-304B14 | 2.6 | 7.3 |
| | 432809 | AA565509 | Hs.131703 | ESTs | 2.6 | 9.9 |
| | 407886 | AW969688 | Hs.100826 | ESTs | 2.5 | 20.2 |
| | 445225 | AI216555 | Hs.202398 | ESTs | 2.5 | 5.5 |
| | 415257 | F03016 | Hs.27513 | ESTs | 2.5 | 8.6 |
| | 423135 | N67655 | Hs.26411 | ESTs | 2.5 | 8.2 |
| 75 | 438283 | AI458931 | Hs.37282 | ESTs | 2.5 | 7.5 |
| | 454053 | AW023006 | Hs.27172 | ESTs, Moderately similar to PC4259 ferri | 2.4 | 3.6 |
| | 443150 | AI034467 | Hs.34650 | ESTs | 2.4 | 7.6 |
| | 429956 | AI374651 | Hs.22542 | ESTs | 2.4 | 3.2 |
| | 428392 | HI0233 | Hs.2265 | secretory granule, neuroendocrine protei | 2.4 | 42.3 |
| 80 | 437268 | AI754847 | Hs.227571 | regulator of G-protein signalling 4 | 2.4 | 14.0 |
| | 426529 | AF090100 | Hs.170241 | Homo sapiens clone IMAGE 23915 | 2.4 | 5.1 |
| | 430347 | NM_002039 | Hs.239706 | GRB2-associated binding protein 1 | 2.4 | 3.2 |
| | 422949 | AA319435 | | gb:EST121657 Adrenal gland tumor Homo sap | 2.4 | 7.4 |

| | | | | | | |
|----|--------|-----------|-----------|---|-----|------|
| | 451952 | AL120173 | Hs.301663 | ESTs | | |
| | 434277 | X77748 | Hs.3786 | glutamate receptor, metabotropic 3 | 2.4 | 19.2 |
| | 422927 | AW247388 | Hs.301423 | calcium binding protein 1 (calbrain) | 2.4 | 28.5 |
| 5 | 425121 | A1797511 | Hs.154679 | synaptotagmin I | 2.4 | 3.0 |
| | 435059 | Z45270 | Hs.235873 | hypothetical protein FLJ22672 | 2.4 | 3.9 |
| | 446377 | AW014022 | Hs.170953 | ESTs | 2.4 | 4.8 |
| | 452371 | R40990 | Hs.21658 | ESTs | 2.4 | 3.3 |
| | 419103 | Z40229 | Hs.95423 | hypothetical protein FLJ23033 | 2.4 | 3.3 |
| 10 | 427658 | H61387 | Hs.30868 | nogo receptor | 2.4 | 8.4 |
| | 446100 | AW967109 | Hs.13804 | hypothetical protein DJ462023.2 | 2.4 | 3.0 |
| | 439607 | BE540565 | Hs.159460 | ESTs | 2.3 | 3.6 |
| | 412949 | AJ471639 | Hs.71913 | ESTs | 2.3 | 5.6 |
| | 419757 | AA773820 | Hs.63970 | ESTs | 2.3 | 3.7 |
| 15 | 410037 | AB020725 | Hs.58009 | KIAA0918 protein | 2.3 | 3.3 |
| | 451386 | AB029006 | Hs.26334 | spastic paraplegia 4 (autosomal dominant) | 2.3 | 12.2 |
| | 409953 | AA332277 | Hs.57691 | cadherin 18, type 2 | 2.3 | 3.1 |
| | 419629 | AB020695 | Hs.91662 | KIAA0888 protein | 2.3 | 5.5 |
| | 434792 | AA649253 | Hs.132458 | ESTs | 2.3 | 13.4 |
| 20 | 429006 | AA443143 | Hs.50929 | hypothetical protein FLJ13842 | 2.3 | 3.8 |
| | 445194 | AJ215667 | Hs.175044 | ESTs | 2.3 | 6.6 |
| | 422491 | AA338548 | Hs.117546 | neuronatin | 2.3 | 3.1 |
| | 415734 | NM_014747 | Hs.78748 | KIAA0237 gene product | 2.3 | 3.6 |
| | 434933 | R91095 | Hs.4276 | KIAA1701 protein | 2.3 | 27.4 |
| 25 | 424922 | BE386547 | Hs.217112 | hypothetical protein MGC10825 | 2.2 | 6.1 |
| | 426325 | D28114 | Hs.169309 | myelin-associated oligodendrocyte basic | 2.2 | 3.7 |
| | 424140 | Z48051 | Hs.141308 | myelin oligodendrocyte glycoprotein | 2.2 | 81.1 |
| | 418410 | AA811441 | Hs.107393 | chromosome 3 open reading frame 4 | 2.2 | 56.0 |
| | 409746 | NM_004794 | Hs.56294 | RAB33A, member RAS oncogene family | 2.2 | 3.9 |
| 30 | 439239 | AJ031540 | Hs.235331 | ESTs | 2.2 | 10.6 |
| | 450310 | N62341 | Hs.94116 | ESTs | 2.2 | 49.5 |
| | 453924 | R49295 | Hs.24886 | ESTs | 2.2 | 3.6 |
| | 411666 | AF106564 | Hs.71346 | neurofilament 3 (150kD medium) | 2.2 | 13.4 |
| | 404819 | | | NM_002688: Homo sapiens peanut (Drosophila) | 2.2 | 6.6 |
| 35 | 449568 | AL157479 | Hs.23740 | KIAA1598 protein | 2.2 | 5.8 |
| | 419271 | N34901 | Hs.238532 | ESTs | 2.2 | 3.6 |
| | 424474 | AA308883 | Hs.148680 | calcyon; D1 dopamine receptor-interactin | 2.2 | 7.5 |
| | 438208 | AL041224 | Hs.65379 | ESTs | 2.2 | 3.6 |
| | 424458 | M29273 | Hs.1780 | myelin associated glycoprotein | 2.2 | 5.8 |
| 40 | 421790 | AW896201 | Hs.22654 | sodium channel, voltage-gated, type I, a | 2.2 | 10.1 |
| | 432882 | NM_013257 | Hs.279696 | serum/glucocorticoid regulated kinase-II | 2.2 | 4.1 |
| | 419863 | AW952691 | Hs.93485 | Homo sapiens mRNA; cDNA DKFZp761D191 (tr | 2.1 | 4.2 |
| | 449277 | AA001064 | Hs.43670 | ESTs | 2.1 | 21.4 |
| | 420156 | AW449258 | Hs.6187 | ESTs | 2.1 | 8.5 |
| 45 | 452738 | AL133800 | Hs.7086 | hypothetical protein MGC12435 | 2.1 | 12.5 |
| | 410366 | AJ267589 | Hs.302689 | hypothetical protein | 2.1 | 3.5 |
| | 452106 | AJ141031 | Hs.21342 | ESTs | 2.1 | 10.4 |
| | 413409 | AJ638418 | Hs.1440 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypep | 2.1 | 3.4 |
| | 423641 | AL137256 | Hs.130489 | ATPase, aminophospholipid transporter-II | 2.1 | 9.4 |
| 50 | 410909 | AW898161 | Hs.53112 | ESTs, Moderately similar to ALU8_HUMAN A | 2.1 | 6.2 |
| | 410631 | AA086469 | Hs.47171 | ESTs | 2.1 | 12.5 |
| | 412675 | AA460716 | Hs.9788 | hypothetical protein MGC10924 similar to | 2.1 | 5.8 |
| | 448299 | AA497044 | Hs.20887 | hypothetical protein FLJ10392 | 2.1 | 3.3 |
| | 444124 | R43097 | Hs.6818 | ESTs | 2.1 | 11.5 |
| 55 | 408950 | AA707814 | Hs.14945 | long fatty acyl-CoA synthetase 2 gene | 2.1 | 9.3 |
| | 432736 | AA788898 | Hs.179902 | transporter-like protein | 2.1 | 8.5 |
| | 429024 | AJ652297 | Hs.119302 | complement-c1q tumor necrosis factor-rel | 2.1 | 4.0 |
| | 420071 | AB028985 | Hs.94806 | ATP-binding cassette, sub-family A (ABC1 | 2.1 | 3.7 |
| 60 | 408822 | AW500715 | Hs.57079 | Homo sapiens cDNA FLJ13267 fis, clone OV | 2.1 | 5.1 |
| | 424790 | AL119344 | Hs.13326 | ESTs, Weakly similar to 2004399A chromos | 2.1 | 3.0 |
| | 426814 | AF036943 | Hs.172619 | myelin transcription factor 1-like | 2.1 | 23.1 |
| | 425130 | AA448208 | Hs.99163 | ESTs | 2.1 | 14.2 |
| | 449714 | AB033015 | Hs.23941 | KIAA1189 protein | 2.1 | 3.1 |
| 65 | 439108 | AW163034 | Hs.6467 | synaptogyrin 3 | 2.0 | 7.5 |
| | 415669 | NM_005025 | Hs.78589 | serine (or cysteine) proteinase inhibitor | 2.0 | 6.9 |
| | 435040 | AJ932350 | Hs.152825 | ESTs | 2.0 | 10.2 |
| | 440152 | AB002376 | Hs.7006 | KIAA0378 protein | 2.0 | 4.7 |
| | 445102 | AW204610 | Hs.22270 | ESTs | 2.0 | 14.2 |
| | 436734 | AJ937612 | Hs.273758 | hypothetical protein FLJ23112 | 2.0 | 19.2 |
| 70 | 437414 | AW894071 | Hs.48448 | hypothetical protein DKFZp547C176 | 2.0 | 4.7 |
| | 418512 | AW498974 | | diacylglycerol kinase, zeta (104kD) | 2.0 | 6.4 |
| | 453169 | AB037815 | Hs.32156 | KIAA1394 protein | 2.0 | 7.9 |
| | 420050 | AL118615 | Hs.94653 | neurochondrin | 2.0 | 5.7 |
| | 429900 | AA460421 | Hs.30875 | ESTs | 2.0 | 6.5 |
| 75 | 432447 | X92681 | Hs.2998 | contactin 2 (axonat) | 2.0 | 4.2 |
| | 431677 | AK000496 | Hs.306989 | hypothetical protein FLJ20489 | 2.0 | 4.1 |
| | 452856 | AF034799 | Hs.30881 | protein tyrosine phosphatase, receptor I | 2.0 | 3.1 |
| | 448681 | AL109781 | Hs.21754 | Homo sapiens mRNA full length insert cDN | 2.0 | 10.7 |
| | 453754 | AW972580 | Hs.172753 | ESTs | 2.0 | 7.2 |
| 80 | 422544 | AB018259 | Hs.118140 | KIAA0716 gene product | 2.0 | 3.4 |
| | 416836 | D54745 | Hs.80247 | cholecystokinin | 2.0 | 11.8 |
| | 454048 | H05626 | Hs.6921 | ESTs | 2.0 | 6.8 |
| | 425741 | AF052152 | Hs.159412 | Homo sapiens clone 24628 mRNA sequence | 2.0 | 9.9 |
| | | | | | 2.0 | 6.5 |

TABLE 19B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

| | | | |
|----|--------|------------|--|
| 5 | Pkey | CAT Number | Accession |
| | 408065 | 103646_1 | AW954272 AJ003154 AA059300 AA046911 |
| | 415527 | 1539393_1 | F11624 Z43212 H08936 R56332 H09256 R52303 R13075 |
| 10 | 415666 | 1543492_1 | H72693 R08673 H72694 F20990 R08580 |
| | 418512 | 176394_1 | AW498974 T09332 R58460 AA350990 T33786 T30936 AA350905 T08592 T09274 AA224297 D54678 T08951 R15346 AW953188 AA350074 |
| | | | AW890649 |
| | 418866 | 179788_1 | T65754 AA229857 AA229658 |
| | 422690 | 222707_1 | Z43784 R13382 AW572911 AA449369 H17037 R19603 A1632565 AW004030 BE502530 Z25032 AA805324 AA449241 A1651825 A1264863 AW196918 |
| 15 | | | AA948267 A1953735 A1263703 AA319159 AW964436 A1903440 AW594171 A1867447 AW204071 AW956110 C15616 D81142 H17038 AW162343 |
| | | | T87230 A13 |
| | 422949 | 223184_1 | AA319435 N56456 AA319377 AW961532 T48452 AA894424 |
| | 424945 | 245223_1 | A1221919 Z19957 AA348780 AW964077 AW166028 BE540193 N94800 AA452368 N99604 A1341345 AW298800 AA724961 AA931158 A1741227 |
| 20 | | | A1806660 A1982626 D81263 D53937 D52496 AA974487 AW043854 N50483 Z39997 A1492961 A1361526 F04002 AA452141 T23551 A1472655 |
| | | | A1193667 A1341 |
| | 426919 | 273507_1 | AL041228 D62004 D61361 A1203314 A1990307 AW900295 A1018308 AW087473 AW183530 AA393346 H50055 AA935601 |
| | 433670 | 372721_1 | AA604405 BE062234 AW748386 |
| | 433921 | 377350_1 | AA618174 A1114549 R36464 R36465 |
| | 433940 | 37787_1 | H05129 N63433 A1651350 AA984734 A1368716 N40915 A1989705 F09042 T03905 R88588 AF112220 |
| 25 | 436773 | 426857_1 | AW078629 A1857375 N64357 AA731069 |
| | 446692 | 689623_1 | Z44514 A1352097 A1803984 AW235923 AW196558 A1954637 A1336983 |

TABLE 19C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 N1_position: Indicates nucleotide positions of predicted exons.

| | | | | |
|----|--------|---------|--------|---|
| 30 | Pkey | Ref | Strand | N1_position |
| | 400844 | 9188605 | Plus | 24746-24872,25035-25204 |
| | 404819 | 4678240 | Plus | 16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578 |
| | 405560 | 183148 | Plus | 5495-5655,6077-6241,6495-6692 |
| | 405819 | 4007557 | Plus | 2830-2967 |
| 35 | 406311 | 9211559 | Minus | 137114-139033 |

TABLE 20A: ABOUT 328 CNS-ENRICHED GENES SIGNIFICANTLY DOWN-REGULATED IN LOWER GRADE GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS

Table 20A lists about 328 CNS-enriched genes significantly down-regulated in lower grade glioblastoma (LGG) compared to normal adult CNS tissues. These were selected from 59680 probesets on the Affymetrix/Eos HuQ3 GeneChip array such that the ratio of "average" normal CNS to "average" LGG was greater than or equal to 2. The "average" normal CNS level was set to the 85th percentile amongst various normal CNS tissues. The "average" LGG level was set to the 85th percentile amongst various tumor samples. To enrich for CNS specific genes, the ratio of "average" CNS to "average" non-CNS normal adult tissues was calculated to be greater than or equal to 3. The "average" CNS level was set to the 85th percentile amongst various CNS tissues. The "average" normal non-CNS adult tissue level was set to the 95th percentile amongst various non-CNS normal tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratios were evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of CNS compared to LOWER GRADE GLIOBLASTOMA
 R2: Ratio of CNS compared to NON-CNS NORMAL ADULT TISSUE

| | | | | | | |
|----|--------|-----------|-----------|--|------|------|
| 45 | Pkey | ExAccn | UnigenelD | Unigene Title | R1 | R2 |
| | 425580 | L11144 | Hs.1907 | gatanin | 33.1 | 3.5 |
| | 425489 | M58594 | Hs.1905 | protactin | 24.7 | 10.5 |
| 50 | 430538 | AB032435 | Hs.242821 | differentiation-associated Na-dependent | 22.6 | 22.6 |
| | 417275 | X63578 | Hs.295449 | parvalbumin | 22.4 | 6.0 |
| | 428505 | AL035461 | Hs.2281 | chromogranin B (secretogranin 1) | 21.8 | 21.8 |
| | 408040 | A1266496 | Hs.22905 | ESTs, Weakly similar to RHG6_HUMAN RHO-G | 19.4 | 19.4 |
| 55 | 435145 | A1277259 | Hs.116631 | ESTs | 18.5 | 3.8 |
| | 407039 | X00368 | | gb:Human prolactin gene 5' region. | 18.1 | 18.1 |
| 60 | 428976 | AL037824 | Hs.194695 | ras homolog gene family, member I | 17.4 | 17.4 |
| | 409263 | AA069573 | Hs.50319 | ESTs | 16.8 | 16.8 |
| | 424645 | NM_014682 | Hs.151449 | KIAA0535 gene product | 15.1 | 15.1 |
| | 416018 | AW138239 | Hs.78977 | proprotein convertase subtilisin/kexin t | 14.0 | 14.0 |
| 65 | 405560 | AW887701 | | hypothetical protein FLJ20628 | 13.9 | 8.0 |
| | 452022 | AW072330 | Hs.293875 | ESTs | 13.8 | 13.8 |
| | 433940 | H05129 | | cyclic AMP-regulated phosphoprotein, 21 | 12.0 | 12.0 |
| | 413324 | V00571 | Hs.75294 | corticotropin releasing hormone | 12.0 | 13.2 |
| 70 | 410857 | AF063228 | Hs.65248 | dynein, cytoplasmic, intermediate polype | 11.5 | 11.5 |
| | 410330 | AW023630 | Hs.159425 | ESTs | 11.1 | 23.4 |
| 75 | 453165 | S74727 | Hs.32042 | aspartoacylase (aminoacylase 2, Canavan | 10.7 | 10.7 |
| | 420297 | A1628272 | Hs.88323 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 10.5 | 4.1 |
| | 417167 | AW206437 | Hs.4290 | ESTs | 10.4 | 10.4 |
| | 420033 | D59502 | Hs.292590 | ESTs | 10.4 | 10.4 |
| 80 | 413293 | AL047483 | Hs.302498 | GTP-binding protein homologous to Saccha | 10.0 | 10.0 |
| | 426380 | A1291267 | Hs.149990 | ESTs | 9.8 | 6.9 |
| | 410635 | D58863 | Hs.334372 | chorionic somatomammotropin hormone 1 (p | 9.5 | 6.6 |
| | 422756 | AA441787 | Hs.119689 | glycoprotein hormones, alpha polypeptide | 9.1 | 5.8 |

| | | | | | | |
|----|--------|-----------|-----------|--|-----|------|
| | 444330 | AI597655 | Hs.49265 | ESTs | | |
| | 427322 | AK002017 | Hs.176227 | hypothetical protein FLJ111155 | 9.1 | 9.1 |
| | 421633 | AF121860 | Hs.106260 | sorting nexin 10 | 8.9 | 8.9 |
| | 429095 | AB011106 | Hs.196012 | KIAA0534 protein | 8.6 | 6.7 |
| 5 | 428652 | AA584272 | Hs.336224 | transmembrane protein with EGF-like and | 8.6 | 8.6 |
| | 410309 | BE043077 | Hs.278153 | ESTs | 8.6 | 8.6 |
| | 424932 | R14070 | Hs.315369 | Homo sapiens cDNA: FLJ23075 fis, clone L | 8.5 | 8.5 |
| | 417175 | R44558 | Hs.94002 | ESTs | 8.5 | 10.2 |
| 10 | 427061 | AB032971 | Hs.173392 | KIAA1145 protein | 8.4 | 8.9 |
| | 400438 | AF185611 | Hs.115352 | Target | 8.4 | 8.4 |
| | 418207 | C14685 | Hs.34772 | ESTs | 8.3 | 5.1 |
| | 440209 | H05049 | Hs.247837 | neurexin 3 | 8.2 | 9.8 |
| | 429876 | AB028977 | Hs.225974 | KIAA1054 protein | 8.1 | 18.7 |
| 15 | 429470 | AI878901 | Hs.203862 | guanine nucleotide binding protein (G pr | 8.1 | 16.8 |
| | 430004 | U27768 | Hs.227571 | regulator of G-protein signalling 4 | 8.0 | 8.0 |
| | 436427 | AI344378 | Hs.143399 | ESTs | 7.9 | 15.7 |
| | 408814 | N62499 | Hs.176227 | hypothetical protein FLJ111155 | 7.8 | 7.8 |
| | 434367 | AB020700 | Hs.3830 | KIAA0893 protein | 7.8 | 8.6 |
| 20 | 441005 | Z41305 | Hs.303172 | Homo sapiens mRNA; cDNA DKFZp547G133 (fr | 7.7 | 5.6 |
| | 416851 | AW963951 | Hs.85618 | ESTs | 7.7 | 7.7 |
| | 429033 | NM_007374 | Hs.194756 | sine oculis homeobox (Drosophila) homolo | 7.7 | 8.5 |
| | 437073 | AI885608 | Hs.94122 | ESTs | 7.6 | 5.5 |
| | 441264 | AA927170 | Hs.23290 | ESTs | 7.5 | 7.5 |
| 25 | 450715 | AI266484 | Hs.31570 | ESTs, Weakly similar to KIAA1324 protein | 7.3 | 7.3 |
| | 415076 | NM_000857 | Hs.77890 | guanylate cyclase 1, soluble, beta 3 | 7.2 | 7.2 |
| | 410011 | AB020641 | Hs.57856 | PFTAIRE protein kinase 1 | 7.1 | 4.8 |
| | 423003 | AL120077 | Hs.122967 | ketch (Drosophila)-like 2 (Mayven) | 7.1 | 10.0 |
| | 433921 | AA618174 | | gb:ng14f01.s1 NCL_CGAP_Thy1 Homo sapiens | 7.0 | 7.0 |
| 30 | 457012 | R41480 | Hs.302754 | ESTs | 7.0 | 7.0 |
| | 445898 | AF070623 | Hs.13423 | Homo sapiens clone 24468 mRNA sequence | 6.9 | 6.9 |
| | 425352 | NM_000939 | Hs.1897 | proopiomelanocortin (adrenocorticotropin | 6.9 | 6.9 |
| | 433558 | AA833757 | Hs.201769 | ESTs, Weakly similar to T24435 hypotheti | 6.9 | 6.1 |
| | 409031 | AA376836 | Hs.288856 | ESTs | 6.9 | 6.9 |
| 35 | 419347 | C15944 | Hs.90005 | superiorcervical ganglia, neural specifi | 6.8 | 6.8 |
| | 445279 | R41900 | Hs.22245 | ESTs | 6.5 | 22.2 |
| | 437414 | AW894071 | Hs.48448 | hypothetical protein DKFZp547C176 | 6.4 | 6.4 |
| | 428414 | AL049980 | Hs.184216 | DKFZP564C152 protein | 6.4 | 6.4 |
| | 434104 | AF116691 | Hs.116459 | hypothetical protein PRO2198 | 6.4 | 6.4 |
| 40 | 443244 | AI457235 | Hs.166479 | ESTs | 6.4 | 4.0 |
| | 447761 | AF061573 | Hs.19492 | protocadherin 8 | 6.3 | 3.0 |
| | 450600 | BE079478 | Hs.24880 | ESTs | 6.3 | 6.3 |
| | 427457 | AW779105 | Hs.164682 | ESTs | 6.2 | 3.9 |
| | 416133 | NM_001683 | Hs.89512 | ATPase, Ca transporting, plasma membrane | 6.2 | 11.1 |
| 45 | 432453 | AI885537 | Hs.27172 | ESTs, Moderately similar to PC4259 ferri | 6.1 | 8.0 |
| | 432298 | AL118812 | Hs.274293 | Homo sapiens mRNA; cDNA DKFZp761G1111 (f | 6.0 | 3.9 |
| | 415114 | D60468 | Hs.94181 | ESTs | 6.0 | 15.1 |
| | 416101 | R24854 | Hs.268806 | ESTs | 6.0 | 6.0 |
| | 448958 | AB020651 | Hs.22653 | KIAA0844 protein | 5.9 | 3.3 |
| 50 | 447138 | AI439112 | Hs.93828 | ESTs, Weakly similar to 2109260A B cell | 5.9 | 5.9 |
| | 414545 | AA149287 | Hs.76605 | ESTs | 5.8 | 5.8 |
| | 424153 | AA451737 | Hs.141496 | MAGE-like 2 | 5.8 | 3.6 |
| | 424641 | AB001106 | Hs.151413 | glia maturation factor, beta | 5.7 | 5.1 |
| | 410389 | AW954049 | Hs.8177 | ESTs, Weakly similar to PIHUB6 salivary | 5.6 | 5.6 |
| 55 | 432149 | AW614326 | Hs.133483 | ESTs, Weakly similar to T34549 probable | 5.6 | 9.6 |
| | 408428 | NM_014787 | Hs.44896 | DnaJ (Hsp40) homolog, subfamily B, membe | 5.6 | 12.2 |
| | 443912 | R37257 | Hs.184780 | ESTs | 5.6 | 5.6 |
| | 442023 | AI187878 | Hs.144549 | ESTs | 5.5 | 6.1 |
| | 450642 | R39773 | Hs.7130 | copine IV | 5.5 | 5.6 |
| 60 | 439772 | AL365406 | Hs.10268 | Homo sapiens mRNA full length insert cDN | 5.4 | 5.6 |
| | 450149 | AW969781 | Hs.132863 | Zic family member 2 (odd-paired Drosophi | 5.4 | 9.8 |
| | 438202 | AW169287 | Hs.22588 | ESTs | 5.4 | 5.4 |
| | 448605 | AL109678 | Hs.21597 | Homo sapiens mRNA full length insert cDN | 5.3 | 5.3 |
| 65 | 418866 | T65754 | | gb:yc11c07.s1 Stratagene lung (937210) H | 5.3 | 5.3 |
| | 448786 | BE048842 | Hs.179075 | Homo sapiens cDNA FLJ11881 fis, clone HE | 5.3 | 3.8 |
| | 443682 | AI383061 | Hs.47248 | ESTs, Highly similar to similar to Cdc14 | 5.2 | 5.2 |
| | 415666 | H72693 | | gb:yu03c11.r1 Soares fetal liver spleen | 5.2 | 3.3 |
| | 428508 | BE252383 | Hs.184668 | S8B131 protein | 5.2 | 5.2 |
| | 446353 | AI290919 | Hs.153661 | ESTs | 5.2 | 4.1 |
| 70 | 442106 | AW205881 | Hs.326728 | ESTs | 5.1 | 5.1 |
| | 437331 | AL353933 | Hs.21710 | hypothetical protein DKFZp761G0313 | 5.1 | 3.2 |
| | 419318 | AW969742 | Hs.291005 | ESTs | 5.1 | 5.1 |
| | 408068 | AW148652 | Hs.167398 | ESTs | 5.0 | 3.1 |
| | 434149 | Z43829 | Hs.244624 | hypothetical protein MGC5469 | 5.0 | 5.0 |
| 75 | 439238 | N47305 | Hs.302161 | ESTs | 5.0 | 5.0 |
| | 414631 | AW970130 | Hs.65406 | ESTs | 4.9 | 5.3 |
| | 447104 | R19085 | Hs.210706 | Homo sapiens cDNA FLJ13182 fis, clone NT | 4.9 | 4.9 |
| | 418527 | AA450386 | Hs.7149 | Homo sapiens cDNA: FLJ21950 fis, clone H | 4.9 | 3.0 |
| 80 | 425073 | W39609 | Hs.22003 | solute carrier family 6 (neurotransmitte | 4.9 | 4.9 |
| | 433516 | AA595802 | Hs.33410 | ESTs, Weakly similar to T17279 hypotheti | 4.9 | 4.9 |
| | 427287 | NM_014903 | Hs.174188 | KIAA0938 protein | 4.8 | 4.8 |
| | 447252 | R90916 | Hs.12449 | Homo sapiens transmembrane protein HTMP1 | 4.8 | 4.8 |
| | 419643 | F06066 | Hs.91791 | chromosome 11 open reading frame 25 | 4.8 | 3.2 |
| | 414949 | C15314 | Hs.323349 | ESTs | 4.7 | 4.7 |
| | | | | | 4.7 | 3.8 |

| | | | | | | |
|----|--------|-----------|-----------|---|-----|------|
| | 429900 | AA460421 | Hs.30875 | ESTs | 4.7 | 4.2 |
| | 422949 | AA319435 | | gb:EST21657 Adrenal gland tumor Homo sap | 4.7 | 7.4 |
| | 430537 | X62692 | Hs.2593 | phosphodiesterase 6B, cGMP-specific, rod | 4.6 | 4.6 |
| | 419191 | U17195 | Hs.89666 | A kinase (PRKA) anchor protein 6 | 4.5 | 4.5 |
| 5 | 421952 | AA300900 | Hs.98849 | ESTs, Moderately similar to AF161511 1 H | 4.4 | 3.2 |
| | 406311 | | | NM_021979: Homo sapiens heat shock 70kD | 4.4 | 11.5 |
| | 451050 | AW937420 | Hs.69662 | ESTs | 4.4 | 4.4 |
| | 423728 | AW891294 | Hs.132136 | solute carrier family 4, sodium bicarbon | 4.4 | 7.9 |
| | 411498 | NM_014210 | Hs.70499 | ecotropic viral integration site 2A | 4.3 | 19.4 |
| 10 | 451301 | AI769514 | Hs.209890 | EST | 4.3 | 4.3 |
| | 452381 | H23329 | Hs.290880 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 4.3 | 4.3 |
| | 433109 | N58907 | Hs.162430 | EST | 4.3 | 3.9 |
| | 423589 | AA328082 | Hs.209569 | ESTs | 4.2 | 4.2 |
| | 427224 | AL135554 | Hs.101937 | sine oculis homeobox (Drosophila) homolo | 4.2 | 3.9 |
| 15 | 420489 | AA815089 | Hs.193513 | ESTs | 4.1 | 4.1 |
| | 408206 | AF041853 | Hs.43670 | kinesin family member 3A | 4.1 | 4.1 |
| | 418202 | N48521 | Hs.26549 | KIAA1708 protein | 4.1 | 5.8 |
| | 448117 | H49129 | Hs.172982 | ESTs | 4.1 | 4.1 |
| | 412155 | R38167 | Hs.12449 | Homo sapiens transmembrane protein HTMP1 | 4.0 | 27.9 |
| 20 | 458694 | F12832 | Hs.3610 | ESTs | 4.0 | 4.0 |
| | 452197 | AW023595 | Hs.232048 | ESTs | 4.0 | 4.0 |
| | 408547 | AA574291 | Hs.57837 | ESTs | 4.0 | 4.0 |
| | 433447 | U29195 | Hs.3281 | neuronal pentraxin II | 4.0 | 3.7 |
| | 448583 | NM_015239 | Hs.21542 | KIAA1035 protein | 4.0 | 4.0 |
| 25 | 442412 | R77677 | Hs.346644 | ESTs | 3.9 | 3.9 |
| | 440293 | AI004193 | Hs.22123 | ESTs | 3.9 | 3.9 |
| | 426365 | AA376667 | Hs.10283 | RNA binding motif protein 8B | 3.9 | 4.1 |
| | 400844 | | | NM_003105: Homo sapiens sortilin-related | 3.9 | 3.1 |
| 30 | 426054 | U12431 | Hs.166109 | ELAV (embryonic lethal, abnormal vision, | 3.9 | 3.9 |
| | 429290 | AF203032 | Hs.198760 | neurofilament, heavy polypeptide (200kD) | 3.8 | 3.3 |
| | 408777 | U71204 | Hs.47626 | Ric (Drosophila)-like, expressed in neur | 3.8 | 3.8 |
| | 442676 | AI733585 | Hs.130897 | ESTs | 3.8 | 3.8 |
| | 414699 | AI815523 | Hs.76930 | synuclein, alpha (non A4 component of am | 3.8 | 4.5 |
| 35 | 436476 | AA326108 | Hs.33829 | bHLH protein DEC2 | 3.8 | 3.3 |
| | 434998 | AW975157 | Hs.26037 | ESTs | 3.7 | 3.7 |
| | 412049 | N53437 | Hs.18268 | adenylate kinase 5 | 3.7 | 10.7 |
| | 416220 | N49776 | Hs.170994 | hypothetical protein MGC10946 | 3.7 | 4.5 |
| | 459697 | AA406062 | Hs.98002 | ESTs | 3.7 | 5.4 |
| | 435648 | H24347 | Hs.27524 | ESTs | 3.7 | 8.1 |
| 40 | 442042 | AI990506 | Hs.8077 | Homo sapiens mRNA; cDNA DKFZp547E184 (fr | 3.7 | 6.2 |
| | 456765 | AI497900 | Hs.33067 | ESTs | 3.7 | 3.7 |
| | 434933 | R91095 | Hs.4276 | KIAA1701 protein | 3.6 | 6.1 |
| | 419518 | U79289 | Hs.90798 | Human clone 23695 mRNA sequence | 3.6 | 3.6 |
| | 452667 | T87219 | Hs.13219 | ESTs | 3.6 | 3.6 |
| 45 | 436773 | AW078629 | | PC4 and SFRS1 interacting protein 1 | 3.6 | 3.6 |
| | 408119 | W26213 | Hs.101672 | ESTs, Weakly similar to T00331 hypotheti | 3.6 | 3.6 |
| | 453534 | NM_014796 | Hs.33187 | KIAA0748 gene product | 3.6 | 4.7 |
| | 449093 | AB035356 | Hs.22998 | neurexin 1 | 3.6 | 3.6 |
| 50 | 442738 | AW002370 | Hs.131055 | ESTs, Weakly similar to NPM_HUMAN NUCLEO | 3.5 | 3.5 |
| | 447746 | AW015920 | Hs.161359 | ESTs | 3.5 | 9.9 |
| | 449117 | AW449310 | Hs.210262 | ESTs, Weakly similar to HSS2_HUMAN HEPAR | 3.5 | 3.5 |
| | 447750 | AI422234 | Hs.143434 | contactin 1 | 3.5 | 9.8 |
| | 453590 | AF150278 | Hs.33578 | KIAA0820 protein | 3.5 | 22.3 |
| 55 | 409339 | AB020686 | Hs.54037 | ectonucleotide pyrophosphatase/phosphodi | 3.5 | 3.6 |
| | 410240 | AL157424 | Hs.61289 | synaptotagmin 2 | 3.5 | 4.6 |
| | 410224 | M55513 | Hs.150208 | potassium voltage-gated channel, shaker- | 3.4 | 3.4 |
| | 400098 | | | Eos Control | 3.4 | 3.4 |
| | 450181 | H05254 | Hs.201198 | ESTs | 3.4 | 7.2 |
| 60 | 459080 | AW192083 | Hs.290855 | ESTs | 3.4 | 13.5 |
| | 417063 | N50515 | Hs.45061 | ESTs | 3.3 | 3.3 |
| | 424918 | R13982 | Hs.169309 | myelin-associated oligodendrocyte basic | 3.3 | 5.3 |
| | 453431 | AF094754 | Hs.32973 | glycine receptor, beta | 3.3 | 4.6 |
| | 412453 | R20205 | Hs.75236 | ESTs | 3.3 | 3.3 |
| | 450561 | R49674 | Hs.25909 | ESTs | 3.3 | 3.3 |
| 65 | 415527 | F11624 | | gb:HSC2ZD101 normalized infant brain cDN | 3.3 | 3.3 |
| | 426968 | U07616 | Hs.173034 | amphiphysin (Stiff-Mann syndrome with br | 3.3 | 15.3 |
| | 427386 | AW836261 | Hs.6727 | ESTs | 3.3 | 3.3 |
| | 424001 | W67883 | Hs.137476 | paternally expressed 10 | 3.2 | 5.4 |
| 70 | 439450 | R51613 | Hs.125304 | ESTs | 3.2 | 8.3 |
| | 442879 | AF032922 | Hs.8813 | syntactin binding protein 3 | 3.2 | 3.2 |
| | 417284 | N62889 | Hs.107242 | Homo sapiens cDNA FLJ12965 fis, clone NT | 3.2 | 3.2 |
| | 410343 | AA084273 | Hs.76561 | ESTs, Weakly similar to S47072 finger pr | 3.2 | 3.2 |
| | 410909 | AW898161 | Hs.53112 | ESTs, Moderately similar to ALU8_HUMAN A | 3.2 | 12.5 |
| | 453919 | AW959912 | Hs.7076 | KIAA1705 protein | 3.2 | 3.2 |
| 75 | 424087 | N69333 | Hs.143434 | contactin 1 | 3.1 | 3.1 |
| | 428963 | AW382682 | Hs.258208 | Homo sapiens, clone MGC:15606, mRNA, com | 3.1 | 3.3 |
| | 419852 | AW503756 | Hs.266184 | hypothetical protein dJ55102.5 | 3.1 | 4.1 |
| | 422234 | AF119818 | Hs.113287 | discs, large (Drosophila) homolog-associ | 3.1 | 3.1 |
| 80 | 423829 | R44107 | Hs.240905 | ESTs | 3.1 | 4.4 |
| | 443297 | AI049864 | Hs.133029 | ESTs | 3.1 | 3.1 |
| | 453302 | NM_000838 | Hs.32945 | glutamate receptor, metabotropic 1 | 3.1 | 4.6 |
| | 405819 | | | NM_002578: Homo sapiens p21 (CDKN1A)-acti | 3.1 | 13.5 |
| | 445725 | AK000956 | Hs.13209 | hypothetical protein FLJ10094 | 3.0 | 3.0 |

| | | | | | | |
|----|--------|-----------|-----------|--|-----|------|
| | 447673 | AI823987 | Hs.182285 | ESTs | | |
| | 433670 | AA604405 | | gb:nc87h09.s1 NC1_CGAP_AA1 Homo sapiens | 3.0 | 3.0 |
| | 450757 | BE081050 | Hs.31570 | ESTs, Weakly similar to KIAA1324 protein | 3.0 | 3.9 |
| 5 | 424724 | T06532 | Hs.287709 | Homo sapiens cDNA: FLJ22674 fs, clone H | 3.0 | 3.2 |
| | 433315 | R96754 | Hs.239706 | GRB2-associated binding protein 1 | 3.0 | 3.0 |
| | 451032 | W03692 | Hs.323079 | Homo sapiens mRNA: cDNA DKFZp564P116 (fr | 3.0 | 3.1 |
| | 423346 | AI267677 | Hs.127416 | synaptojanin 1 | 3.0 | 4.9 |
| | 439274 | AF086092 | Hs.48372 | ESTs | 3.0 | 20.1 |
| 10 | 425649 | U03930 | Hs.158540 | UDP glycosyltransferase 8 (UDP-galactose | 3.0 | 18.3 |
| | 441869 | NM_003947 | Hs.8004 | huntingtin-associated protein interactin | 2.9 | 38.6 |
| | 407868 | NM_000950 | Hs.40637 | proline-rich Gla (G-carboxyglutamic acid | 2.9 | 14.9 |
| | 410765 | AI694972 | Hs.66180 | nucleosome assembly protein 1-like 2 | 2.9 | 3.3 |
| | 428001 | H97428 | Hs.219907 | ESTs, Moderately similar to Transforming | 2.9 | 8.0 |
| 15 | 448533 | AL119710 | Hs.21365 | nucleosome assembly protein 1-like 3 | 2.8 | 5.9 |
| | 425130 | AA448208 | Hs.99163 | ESTs | 2.8 | 9.6 |
| | 408554 | AA836381 | Hs.315111 | nuclear receptor co-repressor/HDAC3 comp | 2.8 | 3.1 |
| | 452238 | F01811 | Hs.345757 | ESTs | 2.8 | 3.7 |
| | 446544 | AI631932 | Hs.7047 | ESTs, Weakly similar to Unknown (H.sapie | 2.8 | 3.8 |
| 20 | 433803 | AI823593 | Hs.27688 | ESTs | 2.8 | 12.4 |
| | 407728 | AW071502 | Hs.175931 | ESTs | 2.8 | 4.1 |
| | 414931 | AK000342 | Hs.77646 | Homo sapiens mRNA: cDNA DKFZp761M0223 (f | 2.7 | 10.2 |
| | 410711 | AB002316 | Hs.65746 | KIAA0318 protein | 2.7 | 3.4 |
| | 452738 | AL133800 | Hs.7086 | hypothetical protein MGC12435 | 2.7 | 6.1 |
| 25 | 451516 | AI800515 | Hs.12024 | ESTs | 2.7 | 3.5 |
| | 454053 | AW023006 | Hs.27172 | ESTs, Moderately similar to PC4259 ferri | 2.7 | 6.3 |
| | 450474 | AW872844 | Hs.117494 | ESTs | 2.7 | 3.6 |
| | 422414 | AW875237 | Hs.13701 | ESTs | 2.7 | 7.2 |
| | 428186 | AW504300 | Hs.295605 | mannosidase, alpha, class 2A, member 2 | 2.7 | 5.3 |
| 30 | 431342 | AW971018 | Hs.21659 | ESTs | 2.7 | 3.9 |
| | 423449 | AI497900 | Hs.33067 | ESTs | 2.7 | 8.0 |
| | 427283 | AL119796 | Hs.174185 | ectonucleotide pyrophosphatase/phosphodi | 2.6 | 14.5 |
| | 426919 | AL041228 | | ELAV (embryonic lethal, abnormal vision, | 2.6 | 3.0 |
| | 437117 | AL049256 | | ESTs | 2.6 | 9.0 |
| 35 | 422491 | AA338548 | Hs.122593 | neuronatin | 2.6 | 3.8 |
| | 438068 | AI927209 | Hs.306210 | Homo sapiens cDNA: FLJ23133 fs, clone L | 2.6 | 3.6 |
| | 432809 | AA565509 | Hs.131703 | ESTs | 2.6 | 5.1 |
| | 433551 | AI985544 | Hs.12450 | protocadherin 9 | 2.5 | 9.9 |
| | 444783 | AK001468 | Hs.62180 | anillin (Drosophila Scraps homolog), act | 2.5 | 18.1 |
| 40 | 417417 | F05745 | Hs.89512 | ATPase, Ca transporting, plasma membrane | 2.5 | 43.2 |
| | 413554 | AA319146 | Hs.75426 | secretogranin II (chromogranin C) | 2.5 | 17.1 |
| | 448902 | Z45998 | Hs.22543 | Homo sapiens mRNA: cDNA DKFZp761I1912 (f | 2.5 | 5.7 |
| | 442910 | AI365130 | Hs.11307 | ESTs, Weakly similar to T19326 hypotheti | 2.5 | 21.8 |
| | 423135 | N67655 | Hs.26411 | ESTs | 2.5 | 14.5 |
| 45 | 452311 | AW304029 | Hs.252744 | ESTs | 2.5 | 8.2 |
| | 418940 | HI7739 | Hs.288513 | Human DNA sequence from clone RP5-899C14 | 2.5 | 3.5 |
| | 432882 | NM_013257 | Hs.279696 | serum/lytucocorticoid regulated kinase-6 | 2.5 | 7.0 |
| | 422411 | AW749443 | Hs.22511 | ESTs | 2.5 | 4.2 |
| | 451386 | AB029006 | Hs.26334 | spastic paraplegia 4 (autosomal dominant | 2.5 | 12.0 |
| 50 | 404819 | | | NM_002688*:Homo sapiens peanut (Drosophi | 2.4 | 3.1 |
| | 429656 | X05608 | Hs.211584 | neurofilament, light polypeptide (68kD) | 2.4 | 5.8 |
| | 431988 | AC002302 | Hs.77202 | protein kinase C, beta 1 | 2.4 | 13.1 |
| | 411379 | AI816344 | Hs.12554 | ESTs, Weakly similar to NPL4_HUMAN NUCLE | 2.4 | 10.5 |
| | 422980 | N46569 | Hs.76722 | CCAAT/enhancer binding protein (CEBP), | 2.4 | 11.2 |
| 55 | 429859 | NM_007050 | Hs.225952 | protein tyrosine phosphatase, receptor t | 2.4 | 45.2 |
| | 430287 | AW182459 | Hs.125759 | ESTs, Weakly similar to LEU5_HUMAN LEUKE | 2.4 | 5.1 |
| | 422890 | Z43784 | | ankyrin 3, node of Ranvier (ankyrin G) | 2.4 | 7.6 |
| | 427658 | H61387 | Hs.30868 | nogo receptor | 2.4 | 3.6 |
| | 446100 | AW967109 | Hs.13804 | hypothetical protein dJ462023.2 | 2.4 | 3.0 |
| 60 | 412266 | N59006 | Hs.26133 | ESTs | 2.3 | 3.6 |
| | 435059 | Z45270 | Hs.235873 | hypothetical protein FLJ22672 | 2.3 | 30.9 |
| | 420173 | AA256151 | Hs.22999 | ESTs | 2.3 | 4.8 |
| | 452371 | R40990 | Hs.21658 | ESTs | 2.3 | 4.1 |
| | 430456 | AA314998 | Hs.241503 | hypothetical protein | 2.3 | 3.3 |
| 65 | 409953 | AA332277 | Hs.57691 | cadherin 18, type 2 | 2.3 | 4.7 |
| | 429006 | AA443143 | Hs.50929 | hypothetical protein FLJ13842 | 2.3 | 5.5 |
| | 445194 | AI215667 | Hs.175044 | ESTs | 2.3 | 6.6 |
| | 428392 | H10233 | Hs.2265 | secretory granule, neuroendocrine protei | 2.3 | 3.1 |
| | 434460 | AA478486 | Hs.3852 | KIAA0368 protein | 2.3 | 42.3 |
| 70 | 416490 | AF090116 | Hs.79348 | regulator of G-protein signalling 7 | 2.3 | 4.8 |
| | 437924 | AI935344 | Hs.164118 | ESTs, Weakly similar to SLS1_HUMAN SODIU | 2.3 | 12.5 |
| | 418738 | AW388633 | Hs.6682 | solute carrier family 7, (cationic amino | 2.3 | 3.2 |
| | 424945 | AI221919 | | hypothetical protein FLJ10582 | 2.2 | 16.9 |
| | 416530 | U62801 | Hs.79361 | kalikrein 6 (neurosin, zyme) | 2.2 | 30.5 |
| 75 | 422927 | AW247388 | Hs.301423 | calcium binding protein 1 (calbrain) | 2.2 | 4.4 |
| | 438831 | BE263273 | Hs.6439 | synapsin II | 2.2 | 3.0 |
| | 449078 | AK001256 | Hs.22975 | KIAA1576 protein | 2.2 | 3.4 |
| | 410631 | AA086469 | Hs.47171 | ESTs | 2.2 | 16.1 |
| | 419271 | N34901 | Hs.238532 | ESTs | 2.2 | 5.8 |
| 80 | 452752 | AW044058 | Hs.33578 | KIAA0820 protein | 2.2 | 7.5 |
| | 446574 | AI310135 | Hs.339933 | ESTs | 2.2 | 13.4 |
| | 452106 | AI141031 | Hs.21342 | ESTs | 2.2 | 3.5 |
| | 415910 | U20350 | Hs.78913 | chemokine (C-X3-C) receptor 1 | 2.2 | 3.4 |
| | 444458 | BE041526 | Hs.31746 | hypothetical protein DKFZp547F072 | 2.2 | 28.9 |
| | | | | | 2.2 | 7.7 |

| | | | | | | |
|----|--------------|---|--|--|-----|------|
| 5 | 446692 | Z44514 | Hs.198416 | Homo sapiens mRNA for KIAA1763 protein, | 2.2 | 33.0 |
| | 412788 | AA120960 | Hs.96423 | ESTs | 2.2 | 8.5 |
| | 419103 | Z40229 | Hs.148680 | hypothetical protein FLJ23033 | 2.2 | 8.4 |
| | 424474 | AA308883 | Hs.148680 | calcyon; D1 dopamine receptor-interactin | 2.2 | 3.6 |
| | 451783 | R42554 | Hs.210852 | T-box, brain, 1 | 2.1 | 11.2 |
| | 434792 | AA649253 | Hs.132458 | ESTs | 2.1 | 3.8 |
| | 424922 | BE386547 | Hs.217112 | hypothetical protein MGC10825 | 2.1 | 3.7 |
| | 455364 | H72176 | Hs.4273 | hypothetical protein FLJ13159 | 2.1 | 4.9 |
| 10 | 413988 | M81883 | Hs.324784 | glutamate decarboxylase 1 (brain, 67kD) | 2.1 | 5.1 |
| | 452744 | AI267652 | Hs.246107 | Homo sapiens mRNA; cDNA DKFZp434E082 (fr | 2.1 | 3.6 |
| | 443150 | AI034467 | Hs.344650 | ESTs | 2.1 | 7.6 |
| | 453220 | AB033089 | Hs.32452 | Homo sapiens mRNA for KIAA1263 protein, | 2.1 | 19.9 |
| | 420050 | AL118615 | Hs.94653 | neurochondrin | 2.1 | 6.5 |
| 15 | 408449 | NM_004408 | Hs.166161 | dynamitin 1 | 2.1 | 5.1 |
| | 423641 | AL137256 | Hs.130489 | ATPase, aminophospholipid transporter-li | 2.1 | 6.2 |
| | 430347 | NM_002039 | Hs.239706 | GRB2-associated binding protein 1 | 2.1 | 3.2 |
| | 449568 | AL157479 | Hs.23740 | KIAA1598 protein | 2.1 | 3.6 |
| | 412675 | AA460716 | Hs.9788 | hypothetical protein MGC10924 similar to | 2.1 | 3.3 |
| 20 | 429550 | AW293055 | Hs.119357 | ESTs | 2.1 | 6.4 |
| | 446782 | AI653048 | Hs.144006 | ESTs | 2.1 | 9.0 |
| | 453924 | R49295 | Hs.24886 | ESTs | 2.1 | 13.4 |
| | 437948 | AA772920 | Hs.303527 | ESTs | 2.1 | 24.8 |
| | 451952 | AL120173 | Hs.301663 | ESTs | 2.0 | 19.2 |
| 25 | 453754 | AW972580 | Hs.172753 | ESTs | 2.0 | 3.4 |
| | 448765 | R15337 | Hs.21958 | Homo sapiens mRNA; cDNA DKFZp547D086 (fr | 2.0 | 3.9 |
| | 447163 | AW292770 | Hs.5542 | DnaJ (Hsp40) homolog, subfamily C, membe | 2.0 | 3.4 |
| | 448299 | AA497044 | Hs.20887 | hypothetical protein FLJ10392 | 2.0 | 11.5 |
| | 411666 | AF106564 | Hs.71346 | neurofilament 3 (150kD medium) | 2.0 | 6.6 |
| 30 | 424458 | M29273 | Hs.1780 | myelin associated glycoprotein | 2.0 | 10.1 |
| | 434277 | X77748 | Hs.3786 | glutamate receptor, metabotropic 3 | 2.0 | 28.5 |
| | 440152 | AB002376 | Hs.7006 | KIAA0378 protein | 2.0 | 14.2 |
| | 429956 | AI374651 | Hs.22542 | ESTs | 2.0 | 3.2 |
| | 450590 | AI701507 | Hs.273740 | ESTs | 2.0 | 3.8 |
| 35 | 429024 | AI652297 | Hs.119302 | complement-c1q tumor necrosis factor-rel | 2.0 | 3.7 |
| | 430643 | AW970065 | Hs.287425 | MEGF10 protein | 2.0 | 4.1 |
| | 415734 | NM_014747 | Hs.78748 | KIAA0237 gene product | 2.0 | 27.4 |
| | 419757 | AA773820 | Hs.63970 | ESTs | 2.0 | 3.3 |
| | 421264 | AL039123 | Hs.103042 | microtubule-associated protein 1B | 2.0 | 23.8 |
| 40 | 439607 | BE540565 | Hs.159460 | ESTs | 2.0 | 5.6 |
| | 435624 | AF218942 | Hs.24889 | formin 2 | 2.0 | 12.2 |
| | 425121 | AI797511 | Hs.154679 | synaptotagmin I | 2.0 | 3.9 |
| | 431677 | AK000496 | Hs.306989 | hypothetical protein FLJ20489 | 2.0 | 3.1 |
| | 442593 | R38804 | Hs.31961 | ESTs | 2.0 | 6.7 |
| 45 | 410366 | AI267589 | Hs.302689 | hypothetical protein | 2.0 | 10.4 |
| | 426575 | M74826 | Hs.170808 | glutamate decarboxylase 2 (pancreatic is | 2.0 | 4.6 |
| | 452856 | AF034799 | Hs.30881 | protein tyrosine phosphatase, receptor I | 2.0 | 10.7 |
| | 437380 | AL359577 | Hs.112198 | Homo sapiens mRNA; cDNA DKFZp547M073 (fr | 2.0 | 3.8 |
| | 424893 | AW295112 | Hs.153648 | Homo sapiens cDNA FLJ13303 fis, clone OV | 2.0 | 3.8 |
| 50 | 436734 | AI937612 | Hs.273758 | hypothetical protein FLJ23112 | 2.0 | 4.7 |
| | 422544 | AB018259 | Hs.118140 | KIAA0716 gene product | 2.0 | 11.8 |
| | 440105 | AA694010 | Hs.6932 | Homo sapiens clone Z3809 mRNA sequence | 2.0 | 8.2 |
| | 425741 | AF052152 | Hs.159412 | Homo sapiens clone 24628 mRNA sequence | 2.0 | 6.5 |
| | 450310 | N62341 | Hs.94116 | ESTs | 2.0 | 3.6 |
| 55 | TABLE 20B: | | | | | |
| | Pkey: | Unique Eos probeset identifier number | | | | |
| | CAT number: | Gene cluster number | | | | |
| | Accession: | Genbank accession numbers | | | | |
| 60 | Pkey | CAT Number | Accession | | | |
| | 415527 | 1539393_1 | F11624 Z43212 H08936 R56332 H09256 R52303 R13075 | | | |
| | 415666 | 1543492_1 | H72693 R08673 H72694 F20990 R08580 | | | |
| | 418866 | 179788_1 | T65754 AA229857 AA229658 | | | |
| 65 | 422890 | 222707_1 | Z43784 R13382 AW572911 AA449369 H17037 R19603 AI632565 AW004030 BE502530 Z25032 AA805324 AA449241 AI651825 AI264863 AW196918 | | | |
| | | | AA948267 AI953735 AI263703 AA319159 AW964436 AI903440 AW594171 AI857447 AW204071 AW956110 C15616 D81142 H17038 AW162343 | | | |
| | | | T87230 AI3 | | | |
| | 422949 | 223184_1 | AA319435 N56456 AA319377 AW961532 T48452 AA894424 | | | |
| | 424945 | 245223_1 | AI221919 Z19967 AA348780 AW964077 AW166028 BE540193 N94800 AA452368 N99604 AI341345 AW298800 AA724961 AA931158 AI741227 | | | |
| 70 | | | AI806660 AI982626 D81263 D53937 D52496 AA974487 AW043854 N50483 Z39997 AI492961 AI361526 F04002 AA452141 T23551 AI472655 | | | |
| | | | AI193667 AI341 | | | |
| | 426919 | 273507_1 | AL041228 D82004 D61361 AI203314 AI990307 AW900295 AI018308 AW087473 AW183530 AA393346 H50055 AA935601 | | | |
| | 433670 | 372721_1 | AA604405 BE052234 AW748386 | | | |
| | 433921 | 377350_1 | AA518174 AI114549 R36464 R36465 | | | |
| | 433940 | 37787_1 | H05129 N63433 AI651350 AA984734 AI368716 N40915 AI989705 F09042 T03905 R88588 AF112220 | | | |
| 75 | 436773 | 426857_1 | AW078629 AI857375 N64357 AA731069 | | | |
| | 446692 | 689623_1 | Z44514 AI352097 AI803984 AW235923 AW196558 AI954637 AI336983 | | | |
| 80 | TABLE 20C: | | | | | |
| | Pkey: | Unique number corresponding to an Eos probeset | | | | |
| | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA | | | | |
| | Strand: | sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. | | | | |
| | NT_position: | Indicates DNA strand from which exons were predicted. | | | | |
| | | Indicates nucleotide positions of predicted exons. | | | | |

| | | | | |
|--|--------|---------|--------|---|
| | Pkey | Ref | Strand | Nt_position |
| | 400844 | 9188605 | Plus | 24746-24872,25035-25204 |
| | 404819 | 4578240 | Plus | 16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578 |
| | 405560 | 183148 | Plus | 5495-5655,6077-6241,6495-6692 |
| | 405819 | 4007557 | Plus | 2830-2967 |
| | 406311 | 9211559 | Minus | 137114-139033 |

TABLE 21A: ABOUT 410 GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA MULTIFORMA COMPARED TO NORMAL ADULT CNS
 Table 21A lists about 410 genes significantly down-regulated in glioblastoma multiforma (GBM) compared to normal adult CNS tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal CNS to "average" GBM was greater than or equal to 2. The "average" normal CNS level was set to the 75th percentile amongst various normal CNS tissues. The "average" GBM level was set to the 95th percentile amongst various tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probe identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of CNS to GLIOBLASTOMA MULTIFORMA

| | | | | | |
|--|--------|-----------|-----------|--|------|
| | Pkey | ExAccn | UnigenID | Unigene Title | R1 |
| | 417275 | X63578 | Hs.295449 | parvalbumin | 18.6 |
| | 428505 | AL035461 | Hs.2281 | chromogranin B (secretogranin 1) | 13.8 |
| | 415672 | N53097 | Hs.193579 | ESTs | 13.5 |
| | 459080 | AW192083 | Hs.290855 | ESTs | 12.9 |
| | 432298 | AL118812 | Hs.274293 | Homo sapiens mRNA; cDNA DKFZp761G1111 (f | 11.7 |
| | 400302 | N48056 | Hs.1915 | folate hydrolase (prostate-specific memb | 10.9 |
| | 418318 | U47732 | Hs.84072 | transmembrane 4 superfamily member 3 | 10.1 |
| | 424645 | NM_014682 | Hs.151449 | KIAA0535 gene product | 8.2 |
| | 415274 | AF001548 | Hs.78344 | myosin, heavy polypeptide 11, smooth mus | 7.5 |
| | 413324 | V00571 | Hs.75294 | coricotropin releasing hormone | 7.5 |
| | 417167 | AW206437 | Hs.4290 | ESTs | 7.3 |
| | 422728 | AW937826 | Hs.103262 | ESTs, Weakly similar to ZN91_HUMAN ZINC | 6.8 |
| | 410330 | AW023630 | Hs.159425 | ESTs | 6.5 |
| | 450590 | AI701507 | Hs.273740 | ESTs | 6.5 |
| | 453165 | S74727 | Hs.32042 | aspartoacylase (aminoacylase 2, Canavan | 6.5 |
| | 454076 | AW204712 | Hs.61957 | ESTs | 6.5 |
| | 419956 | AL137939 | Hs.40096 | ESTs | 6.3 |
| | 416851 | AW963951 | Hs.85618 | ESTs | 6.3 |
| | 428874 | W32133 | Hs.194366 | transferrin (prealbumin, amyloidosis I | 6.0 |
| | 409743 | N48721 | Hs.183506 | hypothetical protein FLJ14213 | 5.9 |
| | 449078 | AK001256 | Hs.22975 | KIAA1576 protein | 5.6 |
| | 448072 | AI459306 | Hs.24908 | ESTs | 5.6 |
| | 412622 | AW664708 | Hs.171959 | ESTs | 5.6 |
| | 428414 | AL049980 | Hs.184216 | DKFZP564C152 protein | 5.5 |
| | 427322 | AK002017 | Hs.176227 | hypothetical protein FLJ11155 | 5.5 |
| | 411498 | NM_014210 | Hs.70499 | ecotropic viral integration site 2A | 5.4 |
| | 453344 | BE349075 | Hs.44571 | ESTs | 5.4 |
| | 441790 | AW294909 | Hs.132208 | ESTs | 5.3 |
| | 443037 | AW500305 | Hs.8906 | syntactin 7 | 5.3 |
| | 445529 | H14421 | Hs.180513 | ATP-binding cassette, sub-family A (ABC1 | 5.2 |
| | 447750 | AI422234 | Hs.143434 | contactin 1 | 5.2 |
| | 444409 | AI792140 | Hs.49265 | ESTs | 5.2 |
| | 409031 | AA376836 | Hs.288856 | ESTs | 5.1 |
| | 453220 | AB033089 | Hs.32452 | Homo sapiens mRNA for KIAA1263 protein, | 5.0 |
| | 452022 | AW072330 | Hs.293875 | ESTs | 4.9 |
| | 408428 | NM_014787 | Hs.44896 | DnaJ (Hsp40) homolog, subfamily B, membe | 4.8 |
| | 444922 | AI921750 | Hs.144871 | Homo sapiens cDNA FLJ13752 fis, clone PL | 4.8 |
| | 443622 | AI911527 | Hs.11805 | ESTs | 4.8 |
| | 442023 | AI187878 | Hs.144549 | ESTs | 4.7 |
| | 445618 | H79667 | Hs.237642 | Homo sapiens cDNA FLJ12052 fis, clone HE | 4.6 |
| | 429611 | AI889077 | Hs.211388 | Homo sapiens BAC clone CTB-60N22 from 7q | 4.5 |
| | 414290 | AI568801 | Hs.71721 | ESTs | 4.4 |
| | 450715 | AI266484 | Hs.31570 | ESTs, Weakly similar to KIAA1324 protein | 4.4 |
| | 428508 | BE252383 | Hs.184668 | SBB131 protein | 4.4 |
| | 425649 | U30930 | Hs.158540 | UDP glycosyltransferase 8 (UDP-galactose | 4.3 |
| | 459247 | N46243 | Hs.110373 | ESTs, Highly similar to T42626 secreted | 4.3 |
| | 434064 | AL049045 | Hs.180758 | hypothetical protein PRO0082 | 4.3 |
| | 414602 | AW630088 | Hs.76550 | Homo sapiens mRNA; cDNA DKFZp564B1264 (f | 4.3 |
| | 416133 | NM_001683 | Hs.89512 | ATPase, Ca transporting, plasma membrane | 4.3 |
| | 426471 | M22440 | Hs.170009 | transforming growth factor, alpha | 4.2 |
| | 409231 | AA446644 | Hs.692 | GA733-2 antigen; epithelial glycoprotein | 4.2 |
| | 448958 | AB020651 | Hs.22653 | KIAA0844 protein | 4.2 |
| | 410657 | AF063228 | Hs.65248 | dynein, cytoplasmic, intermediate polype | 4.1 |
| | 447138 | AI439112 | Hs.93828 | ESTs, Weakly similar to 2109260A B cell | 4.1 |
| | 440736 | D56919 | Hs.265848 | myomegalin | 4.1 |
| | 407245 | X90568 | Hs.172004 | titin | 4.1 |
| | 441976 | AA428403 | Hs.106131 | ESTs | 4.1 |
| | 450642 | R39773 | Hs.7130 | copine IV | 4.1 |
| | 432799 | NM_016161 | Hs.278960 | alpha-1,4-N-acetylglucosaminyltransferas | 4.0 |
| | 428465 | AW970976 | Hs.293653 | ESTs | 4.0 |
| | 407868 | NM_000950 | Hs.40637 | proline-rich Gla (G-carboxyglutamic acid | 4.0 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| 5 | 433558 | AA833757 | Hs.201769 | ESTs, Weakly similar to T24435 hypothe | 4.0 |
| | 429470 | A1878901 | Hs.203862 | guanine nucleotide binding protein (G pr | 4.0 |
| | 415666 | H72693 | | gb:yu03c11.1 Soares fetal liver spleen | 3.9 |
| | 407988 | N47760 | Hs.285107 | hypothetical protein FLJ13397 | 3.9 |
| | 427061 | AB032971 | Hs.173392 | KIAA1145 protein | 3.9 |
| 10 | 430261 | AA305127 | Hs.237225 | hypothetical protein HT023 | 3.9 |
| | 440624 | AF017987 | Hs.7306 | secreted frizzled-related protein 1 | 3.8 |
| | 431668 | AW969610 | Hs.151179 | ESTs | 3.8 |
| | 446692 | Z44514 | | Homo sapiens mRNA for KIAA1763 protein, | 3.8 |
| | 408739 | W01556 | Hs.238797 | ESTs, Moderately similar to I38022 hypot | 3.8 |
| 15 | 426716 | NM_006379 | Hs.171921 | sema domain, immunoglobulin domain (Ig), | 3.8 |
| | 450103 | R08665 | Hs.17244 | hypothetical protein FLJ13605 | 3.7 |
| | 426775 | AA384564 | Hs.3628 | ESTs | 3.7 |
| | 403469 | | | Target Exon | 3.7 |
| | 450181 | H05254 | Hs.201198 | ESTs | 3.7 |
| 20 | 438202 | AW169287 | Hs.22588 | ESTs | 3.7 |
| | 445279 | R41900 | Hs.22245 | ESTs | 3.7 |
| | 422546 | AB007969 | Hs.301478 | KIAA0500 protein | 3.7 |
| | 435712 | AA694607 | Hs.176956 | ESTs | 3.6 |
| | 417620 | R02530 | Hs.191198 | ESTs | 3.6 |
| 25 | 421952 | AA300900 | Hs.98849 | ESTs, Moderately similar to AF161511 H | 3.6 |
| | 453655 | AW960427 | Hs.342874 | transforming growth factor, beta recepto | 3.6 |
| | 426365 | AA376667 | Hs.10283 | RNA binding motif protein 88 | 3.6 |
| | 416982 | J05401 | Hs.80691 | creatine kinase, mitochondrial 2 (sarcom | 3.6 |
| | 438086 | AA336519 | Hs.83623 | nuclear receptor subfamily 1, group I, m | 3.6 |
| 30 | 424704 | A1263293 | Hs.152096 | cytochrome P450, subfamily IIJ (arachido | 3.6 |
| | 414631 | AW970130 | Hs.65406 | ESTs | 3.6 |
| | 453698 | AA037615 | Hs.42746 | ESTs | 3.6 |
| | 438704 | A1435060 | Hs.32825 | ESTs | 3.5 |
| | 437073 | A1885608 | Hs.94122 | ESTs | 3.5 |
| 35 | 434460 | AA478486 | Hs.3852 | KIAA0368 protein | 3.5 |
| | 414541 | BE293116 | Hs.76392 | aldehyde dehydrogenase 1 family, member | 3.5 |
| | 423665 | BE167153 | Hs.24380 | ESTs | 3.5 |
| | 446390 | AA233393 | Hs.14992 | hypothetical protein FLJ11151 | 3.5 |
| | 441264 | AA927170 | Hs.23290 | ESTs | 3.5 |
| 40 | 433629 | R13140 | Hs.13359 | ESTs | 3.5 |
| | 411811 | AW864370 | | gb:PM4-SN0016-100500-004-h09 SN0016 Homo | 3.5 |
| | 410140 | AL134435 | Hs.247837 | neurexin 3 | 3.4 |
| | 415114 | D60468 | Hs.94181 | ESTs | 3.4 |
| | 455649 | BE065051 | | gb:RC1-BT0313-110500-017-c04 BT0313 Homo | 3.4 |
| 45 | 433670 | AA604405 | | gb:nc87h09.s1 NCI_CGAP_AA1 Homo sapiens | 3.4 |
| | 417175 | R44558 | Hs.94002 | ESTs | 3.4 |
| | 427176 | AW381569 | Hs.40334 | ESTs | 3.4 |
| | 448519 | AW175665 | Hs.278695 | Homo sapiens prostein mRNA, complete cds | 3.4 |
| | 457012 | R41480 | Hs.302754 | ESTs | 3.3 |
| 50 | 405354 | | | CX000321:gil6671579[ref]NP_031518.1 ari | 3.3 |
| | 445872 | A1681573 | Hs.288671 | Homo sapiens cDNA FLJ11997 fis, clone HE | 3.3 |
| | 433803 | A1823593 | Hs.27688 | ESTs | 3.3 |
| | 449017 | AW002425 | Hs.224142 | ESTs | 3.3 |
| | 414545 | AA149287 | Hs.76605 | ESTs | 3.3 |
| 55 | 409010 | A1648675 | Hs.103441 | Homo sapiens, Similar to RIKEN cDNA 1700 | 3.3 |
| | 426158 | NM_001982 | Hs.199067 | v-erb-b2 avian erythroblastic leukemia v | 3.3 |
| | 422411 | AW749443 | Hs.22511 | ESTs | 3.3 |
| | 428850 | AA934975 | Hs.185076 | ESTs | 3.3 |
| | 406922 | S70284 | Hs.119597 | gb:stearyl-CoA desaturase [human, adipo | 3.2 |
| 60 | 429556 | AW139399 | Hs.98988 | ESTs | 3.2 |
| | 434104 | AF116691 | Hs.116459 | hypothetical protein PRQ2198 | 3.2 |
| | 427229 | A1799751 | Hs.5635 | ESTs | 3.2 |
| | 444458 | BE041526 | Hs.31746 | hypothetical protein DKFZp547F072 | 3.2 |
| | 433328 | AW298159 | Hs.23644 | ESTs, Weakly similar to S65824 reverse t | 3.2 |
| 65 | 412786 | AW900654 | Hs.285729 | ESTs, Weakly similar to unnamed protein | 3.2 |
| | 440808 | AK001339 | Hs.7432 | hypothetical protein FLJ10477 | 3.2 |
| | 442117 | AW664964 | Hs.128899 | ESTs; hypothetical protein for IMAGE:447 | 3.1 |
| | 429876 | AB028977 | Hs.225974 | KIAA1054 protein | 3.1 |
| | 450757 | BE081050 | Hs.31570 | ESTs, Weakly similar to KIAA1324 protein | 3.1 |
| 70 | 414327 | BE408145 | Hs.185254 | ESTs, Weakly similar to T24435 hypothei | 3.1 |
| | 459399 | BE407712 | Hs.153998 | creatine kinase, mitochondrial 1 (ubiqui | 3.1 |
| | 433582 | BE548749 | Hs.148016 | ESTs | 3.1 |
| | 452752 | AW044058 | Hs.33578 | KIAA0820 protein | 3.0 |
| | 439165 | AA029517 | Hs.95162 | KCNQ1 overlapping transcript 1 | 3.0 |
| 75 | 409403 | AA668224 | Hs.6634 | Homo sapiens cDNA: FLJ22547 fis, clone H | 3.0 |
| | 422414 | AW875237 | Hs.13701 | ESTs | 3.0 |
| | 407173 | T64349 | | gb:yc10d08.s1 Stratagene lung (937210) H | 3.0 |
| | 448583 | NM_015239 | Hs.21542 | KIAA1035 protein | 3.0 |
| | 429043 | A1824977 | Hs.145319 | ESTs | 3.0 |
| 80 | 452990 | AA887428 | Hs.246970 | mitogen-activated protein kinase kinase | 3.0 |
| | 412258 | AA376768 | Hs.324841 | hypothetical protein FLJ22622 | 3.0 |
| | 429968 | AA322503 | Hs.227011 | G-substrate | 3.0 |
| | 434348 | BE393191 | Hs.181795 | putative b,b-carotene-9',10'-dioxygenase | 2.9 |
| | 427115 | AW972853 | Hs.112237 | ESTs | 2.9 |
| | 430538 | AB032435 | Hs.242821 | differentiation-associated Na-dependent | 2.9 |
| | 449561 | A1022240 | Hs.17924 | ESTs, Moderately similar to ALU1_HUMAN A | 2.9 |
| | 405403 | | | Target Exon | 2.9 |

| | | | | | |
|----|--------|----------|-----------|--|-----|
| | 452197 | AW023595 | Hs.232048 | ESTs | |
| | 437357 | AL359559 | Hs.331666 | Homo sapiens mRNA; cDNA DKFZp76202215 (f | 2.9 |
| | 436427 | AI344378 | Hs.143399 | ESTs | 2.9 |
| 5 | 417787 | R14948 | Hs.23883 | ESTs | 2.9 |
| | 439272 | AA832474 | Hs.25851 | ESTs | 2.9 |
| | 454247 | AJ243950 | Hs.46735 | deafness locus associated putative guani | 2.9 |
| | 415839 | R40611 | Hs.94694 | ESTs | 2.9 |
| | 408814 | N62499 | Hs.176227 | hypothetical protein FLJ11155 | 2.9 |
| 10 | 408468 | AI909712 | Hs.93837 | phosphatidylinositol transfer protein, m | 2.9 |
| | 431304 | BE157283 | | gb:RC4-HT0373-130200-011-a03 HT0373 Homo | 2.9 |
| | 410240 | AL157424 | Hs.61289 | synaptojanin 2 | 2.9 |
| | 444783 | AK001468 | Hs.62180 | anillin (Drosophila Scraps homolog), act | 2.9 |
| | 408438 | AB011180 | Hs.100960 | KIAA0608 protein | 2.8 |
| 15 | 458793 | N80159 | Hs.121849 | microtubule-associated proteins 1A/1B li | 2.8 |
| | 429788 | U87791 | Hs.221040 | HBS1 (S. cerevisiae)-like | 2.8 |
| | 424264 | D80400 | Hs.239388 | Human DNA sequence from clone RP1-304B14 | 2.8 |
| | 433109 | N58907 | Hs.162430 | EST | 2.8 |
| | 427974 | BE093023 | Hs.188767 | ESTs | 2.8 |
| 20 | 432266 | AK000385 | Hs.274222 | hypothetical protein FLJ20378 | 2.8 |
| | 414764 | AW013887 | Hs.31522 | ESTs | 2.8 |
| | 411918 | AW876354 | | gb:PM4-PT0019-141299-009-F08 PT0019 Homo | 2.8 |
| | 404563 | | | Target Exon | 2.8 |
| 25 | 446468 | AI765890 | Hs.16341 | MAWD binding protein | 2.8 |
| | 444755 | AA431791 | Hs.113823 | ClpX (caseinolytic protease X, E. coli) | 2.8 |
| | 445898 | AF070623 | Hs.13423 | Homo sapiens clone 24468 mRNA sequence | 2.7 |
| | 427283 | AL119796 | Hs.174185 | ectonucleotide pyrophosphatase/phosphodi | 2.7 |
| | 400138 | | | Eos Control | 2.7 |
| 30 | 458676 | AI692464 | Hs.202263 | ESTs | 2.7 |
| | 459697 | AA406062 | Hs.98002 | ESTs | 2.7 |
| | 444420 | AI148157 | Hs.146766 | ESTs | 2.7 |
| | 430371 | D87466 | Hs.240112 | KIAA0276 protein | 2.7 |
| | 449117 | AW449310 | Hs.210262 | ESTs, Weakly similar to HSS2_HUMAN HEPAR | 2.7 |
| | 424994 | AW954525 | | gb:EST366595 MAGE resequences, MAGE Homo | 2.7 |
| 35 | 400339 | X57131 | Hs.248209 | H2A histone family, member F, pseudogene | 2.7 |
| | 417494 | AI369494 | Hs.222137 | ESTs | 2.7 |
| | 427166 | AA431576 | Hs.99154 | ESTs | 2.7 |
| | 404746 | | | CX000138"gi 7512767 pir T12477 hypothe | 2.7 |
| 40 | 411361 | AW839073 | | gb:CM2-L70066-030100-109-d06 L70066 Homo | 2.7 |
| | 428358 | AA993222 | Hs.101915 | Stargardt disease 3 (autosomal dominant) | 2.7 |
| | 406625 | Y13647 | Hs.119597 | stearoyl-CoA desaturase (delta-9-desatur | 2.7 |
| | 416101 | R24854 | Hs.268806 | ESTs | 2.7 |
| | 404606 | | | Target Exon | 2.7 |
| 45 | 433921 | AA618174 | | gb:nq14f01.s1 NCL_CGAP_Thy1 Homo sapiens | 2.7 |
| | 414272 | AI651603 | Hs.46988 | ESTs | 2.7 |
| | 418047 | R37633 | Hs.4847 | ESTs | 2.7 |
| | 421089 | AB037771 | Hs.101799 | KIAA1350 protein | 2.7 |
| | 412244 | AW948175 | | gb:RC0-MT0013-280300-021-c10 MT0013 Homo | 2.7 |
| | 432434 | AL161977 | Hs.2994 | PCTAIRE protein kinase 3 | 2.6 |
| 50 | 424153 | AA451737 | Hs.141496 | MAGE-like 2 | 2.6 |
| | 427189 | H82453 | Hs.5635 | ESTs | 2.6 |
| | 454454 | AW612264 | Hs.131705 | ESTs | 2.6 |
| | 426747 | AA535210 | Hs.171995 | kallikrein 3, (prostate specific antigen | 2.6 |
| 55 | 456791 | H05202 | Hs.133968 | FGF receptor activating protein 1 | 2.6 |
| | 405715 | | | ENSP00000005198" Mixed lineage kinase ML | 2.6 |
| | 425494 | N55540 | Hs.78026 | ESTs, Weakly similar to similar to ankyr | 2.6 |
| | 430865 | AJ073424 | Hs.5232 | HSPC125 protein | 2.6 |
| | 435767 | H73505 | Hs.117874 | ESTs | 2.6 |
| | 410119 | F07841 | Hs.13926 | ESTs | 2.6 |
| 60 | 432146 | AW081072 | Hs.115960 | KIAA0939 protein | 2.6 |
| | 448871 | BE616709 | Hs.159265 | kruppel-related zinc finger protein hckr | 2.6 |
| | 414516 | AI307802 | Hs.135560 | ESTs, Weakly similar to T43458 hypothesi | 2.6 |
| | 429477 | AI275514 | Hs.6658 | ESTs | 2.6 |
| | 400269 | | | Eos Control | 2.5 |
| 65 | 443692 | AW022228 | Hs.322922 | ESTs | 2.5 |
| | 451926 | AW134519 | Hs.96125 | Homo sapiens, Similar to clone FLB3816, | 2.5 |
| | 435145 | AI277259 | Hs.116631 | ESTs | 2.5 |
| | 420309 | AW043637 | Hs.21766 | ESTs, Weakly similar to ALU5_HUMAN ALU S | 2.5 |
| | 449709 | BE410592 | Hs.23918 | hypothetical protein PP5395 | 2.5 |
| 70 | 416530 | U62801 | Hs.79361 | kallikrein-6 (neurosin, zyme) | 2.5 |
| | 411678 | AI907114 | Hs.71465 | squalene epoxidase | 2.5 |
| | 408119 | W26213 | Hs.101672 | ESTs, Weakly similar to T00331 hypothesi | 2.5 |
| | 436624 | T64297 | | fatty acid binding protein 1, liver | 2.5 |
| | 458268 | AA428403 | Hs.106131 | ESTs | 2.5 |
| 75 | 451336 | AI264643 | Hs.3610 | ESTs | 2.5 |
| | 456924 | AI631510 | Hs.196956 | ESTs, Highly similar to match to EST AA3 | 2.5 |
| | 455040 | AW852286 | | gb:QV0-CT0225-100400-187-d08 CT0225 Homo | 2.5 |
| | 420033 | D59502 | Hs.292590 | ESTs | 2.5 |
| | 448786 | BE048842 | Hs.179075 | Homo sapiens cDNA FLJ11881 fis, clone HE | 2.5 |
| 80 | 432251 | AW972983 | Hs.232165 | polycythemia rubra vera 1; cell surface | 2.5 |
| | 408206 | AF041853 | Hs.43670 | kinesin family member 3A | 2.5 |
| | 440205 | T86950 | Hs.105448 | ESTs, Weakly similar to B34087 hypothesi | 2.5 |
| | 442138 | AA445973 | Hs.13303 | Homo sapiens cDNA: FLJ21784 fis, clone H | 2.5 |
| | 420912 | AW853156 | Hs.90787 | ESTs | 2.4 |

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|----|--------|-----------|-----------|--|-----|
| | 439180 | AI393742 | Hs.199057 | v-erb-b2 avian erythroblastic leukemia v | 2.4 |
| | 421025 | AW958975 | Hs.29387 | Homo sapiens cDNA FLJ13226 fis, clone OV | 2.4 |
| | 439973 | AI733308 | Hs.124663 | ESTs | 2.4 |
| 5 | 446847 | T51454 | Hs.82845 | Homo sapiens cDNA: FLJ21930 fis, clone H | 2.4 |
| | 414672 | AI218038 | Hs.48504 | ESTs, Moderately similar to ALU5_HUMAN A | 2.4 |
| | 451522 | BE565817 | Hs.26498 | hypothetical protein FLJ21657 | 2.4 |
| | 433068 | NM_006456 | Hs.288215 | sialyltransferase | 2.4 |
| | 446520 | AA128808 | Hs.179902 | transporter-like protein | 2.4 |
| 10 | 423803 | NM_005709 | Hs.132945 | PDZ-73 protein | 2.4 |
| | 407978 | AW385129 | Hs.41717 | phosphodiesterase 1A, calmodulin-depende | 2.4 |
| | 425907 | AA365752 | Hs.155965 | ESTs | 2.4 |
| | 433819 | AW511097 | Hs.112765 | ESTs | 2.4 |
| | 446066 | AI343931 | Hs.149383 | ESTs | 2.4 |
| 15 | 430573 | AA744550 | Hs.136345 | ESTs | 2.4 |
| | 444992 | R37658 | Hs.21375 | ESTs | 2.4 |
| | 434975 | AA657884 | Hs.314413 | ESTs | 2.4 |
| | 458227 | Z40670 | Hs.181340 | ESTs | 2.4 |
| | 443244 | AI457235 | Hs.156479 | ESTs | 2.4 |
| 20 | 432408 | N39127 | | ESTs, Weakly similar to A46010 X-linked | 2.4 |
| | 401600 | BE247275 | | U5 snRNP-specific protein, 116 kD | 2.3 |
| | 419066 | Z98492 | Hs.6975 | PRO1073 protein | 2.3 |
| | 424823 | NM_006226 | Hs.153322 | phospholipase C, epsilon | 2.3 |
| | 402124 | | | NM_031891:Homo sapiens cadherin 20, type | 2.3 |
| 25 | 416678 | N80448 | Hs.269106 | ESTs | 2.3 |
| | 444897 | AW137088 | Hs.144857 | ESTs | 2.3 |
| | 425111 | BE018485 | Hs.30977 | ESTs, Weakly similar to B34087 hypothesi | 2.3 |
| | 400536 | | | NM_000681*:Homo sapiens adrenergic, alph | 2.3 |
| | 427544 | AI767152 | Hs.181400 | ESTs, Weakly similar to I78885 serine/th | 2.3 |
| 30 | 459511 | AI142379 | | gb:gg64c01.r1 Soares_testis_NHT Homo sap | 2.3 |
| | 415111 | R39039 | Hs.279041 | EST | 2.3 |
| | 433331 | AI738815 | Hs.117323 | ESTs | 2.3 |
| | 440293 | AI004193 | Hs.22123 | ESTs | 2.3 |
| | 411770 | NM_014278 | Hs.71992 | heat shock protein (hsp110 family) | 2.3 |
| 35 | 416964 | D87467 | Hs.80620 | guanine nucleotide exchange factor for R | 2.3 |
| | 419386 | AA236867 | | ESTs, Weakly similar to I38022 hypothesi | 2.3 |
| | 402493 | AI743260 | | mannosidase, alpha, class 1A, member 1 | 2.3 |
| | 401783 | | | NM_003771*:Homo sapiens keratin, hair, a | 2.3 |
| | 420548 | AA278246 | Hs.920 | ESTs | 2.3 |
| 40 | 419763 | AI039691 | Hs.127486 | ESTs | 2.3 |
| | 421750 | AK000768 | Hs.107872 | hypothetical protein FLJ20761 | 2.3 |
| | 406023 | | | Target Exon | 2.3 |
| | 454024 | AA993527 | Hs.293907 | hypothetical protein FLJ23403 | 2.3 |
| | 401586 | | | Target Exon | 2.3 |
| 45 | 404091 | | | Target Exon | 2.3 |
| | 456773 | AI038192 | Hs.129764 | EGF-like repeats and discoidin I-like do | 2.3 |
| | 414106 | BE300325 | Hs.77135 | RNA binding protein | 2.3 |
| | 454288 | BE222648 | Hs.241432 | ESTs, Highly similar to c380A1.1b [H.sap | 2.3 |
| | 441879 | AI521936 | Hs.107149 | novel protein similar to archaeal, yeast | 2.3 |
| 50 | 424724 | T06532 | Hs.287709 | Homo sapiens cDNA: FLJ22674 fis, clone H | 2.3 |
| | 415692 | N51935 | Hs.47374 | Homo sapiens cDNA FLJ13561 fis, clone PL | 2.3 |
| | 416282 | R86664 | Hs.167257 | brain link protein-1 | 2.2 |
| | 404659 | | | ENSP00000239999*:HYPOTHETICAL 34.7 kDa P | 2.2 |
| 55 | 429956 | AI374651 | Hs.22542 | ESTs | 2.2 |
| | 429670 | L01087 | Hs.211593 | protein kinase C, theta | 2.2 |
| | 429655 | U48959 | Hs.211582 | myosin, light polypeptide kinase | 2.2 |
| | 458921 | AI682088 | Hs.79375 | holocarboxylase synthetase (biotin-[prop | 2.2 |
| | 436463 | H06502 | Hs.6656 | ESTs | 2.2 |
| | 408994 | AW299520 | Hs.43052 | ESTs | 2.2 |
| 60 | 413303 | AW836130 | Hs.75277 | hypothetical protein FLJ13910 | 2.2 |
| | 418154 | BE165866 | | nuclear receptor subfamily 1, group I, m | 2.2 |
| | 418407 | AL044818 | Hs.84928 | nuclear transcription factor Y, beta | 2.2 |
| | 422907 | AI879263 | Hs.77273 | Human glucose transporter pseudogene | 2.2 |
| | 446377 | AW014022 | Hs.170953 | ESTs | 2.2 |
| 65 | 429290 | AF203032 | Hs.198760 | neurofilament, heavy polypeptide (200kD) | 2.2 |
| | 449714 | AB033015 | Hs.23941 | KIAA1189 protein | 2.2 |
| | 408480 | AI350337 | Hs.164568 | fibroblast growth factor 7 (keratinocyte | 2.2 |
| | 410066 | AL117664 | Hs.58419 | DKFZP586L2024 protein | 2.2 |
| | 410912 | AW810224 | | gb:MR4-ST0125-021199-017-e07 ST0125 Homo | 2.2 |
| 70 | 447163 | AW292770 | Hs.5542 | DnaJ (Hsp40) homolog, subfamily C, membe | 2.2 |
| | 421709 | AA159394 | Hs.107056 | CED-6 protein | 2.2 |
| | 403728 | | | Target Exon | 2.2 |
| | 453359 | AA448787 | Hs.24872 | ESTs | 2.2 |
| | 411379 | AI816344 | Hs.12554 | ESTs, Weakly similar to NPL4_HUMAN NUCLE | 2.2 |
| 75 | 413427 | U31120 | Hs.845 | interleukin 13 | 2.2 |
| | 409028 | AB014513 | Hs.49998 | Z-band alternatively spliced PDZ-motif | 2.2 |
| | 413924 | AL119964 | Hs.75616 | setadin-1 | 2.2 |
| | 403463 | | | Target Exon | 2.2 |
| 80 | 408068 | AW148652 | Hs.167398 | ESTs | 2.2 |
| | 407819 | R42185 | Hs.102720 | ESTs | 2.2 |
| | 414203 | BE262170 | Hs.78629 | ATPase, Na ⁺ transporting, beta 1 polypep | 2.2 |
| | 448045 | AJ297436 | Hs.20166 | prostate stem cell antigen | 2.2 |
| | 449835 | AW979300 | Hs.293813 | ESTs | 2.2 |
| | 458547 | AW204314 | Hs.170784 | ESTs | 2.2 |

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|----|--------|-----------|-----------|---|-----|
| | 414276 | BE297862 | | gb:601174780F1 NIH_MGC_17 Homo sapiens c | 2.2 |
| | 427493 | H09037 | | Target CAT | 2.2 |
| | 458441 | AW842283 | Hs.288232 | cyclin I | 2.1 |
| 5 | 410705 | BE004107 | | gb:CM0-BN0102-150300-288-112 BN0102 Homo | 2.1 |
| | 444647 | H14718 | Hs.11506 | Human clone 23589 mRNA sequence | 2.1 |
| | 405502 | | | C7000609*:gij628012ipin]A53933 myosin I | 2.1 |
| | 400818 | | | Target Exon | 2.1 |
| | 435059 | Z45270 | Hs.235873 | hypothetical protein FLJ22672 | 2.1 |
| 10 | 426559 | AB001914 | Hs.170414 | paired basic amino acid cleaving system | 2.1 |
| | 445200 | AA084460 | Hs.12409 | somatostatin | 2.1 |
| | 453396 | AW162768 | Hs.22620 | ESTs | 2.1 |
| | 443819 | AB033076 | Hs.9873 | likely homolog of rat kinase D-interacti | 2.1 |
| | 401929 | | | C17001690:gi6005701jref]NP_009099.1] AT | 2.1 |
| 15 | 451032 | W03692 | Hs.323079 | Homo sapiens mRNA; cDNA DKFZp564P116 (fr | 2.1 |
| | 433862 | D86960 | Hs.3610 | KIAA0205 gene product | 2.1 |
| | 458694 | F12832 | Hs.3610 | ESTs | 2.1 |
| | 417063 | N50515 | Hs.45061 | ESTs | 2.1 |
| | 416935 | AA190712 | | gb:zp87109.r1 Stratagene HeLa cell s3 93 | 2.1 |
| 20 | 414446 | AA147534 | Hs.142019 | ESTs, Weakly similar to 1207289A reverse | 2.1 |
| | 434681 | AA642402 | Hs.59142 | ESTs | 2.1 |
| | 413835 | A1272727 | Hs.249163 | fatty acid hydroxylase | 2.1 |
| | 426137 | AL040683 | Hs.167031 | DKFZP566D133 protein | 2.1 |
| | 424481 | R19453 | Hs.1787 | proteolipid protein 1 (Pelizaeus-Merzbac | 2.1 |
| 25 | 454339 | AW381980 | | gb:QV4-HT0316-091199-028-d05 HT0316 Homo | 2.1 |
| | 407786 | AA687538 | Hs.38972 | tetraspan 1 | 2.1 |
| | 421296 | NM_002666 | Hs.103253 | perlepin | 2.1 |
| | 444200 | AA327113 | Hs.149057 | ESTs | 2.1 |
| | 409339 | AB020686 | Hs.54037 | ectonucleotide pyrophosphatase/phosphodi | 2.1 |
| 30 | 418410 | AA811441 | Hs.107393 | chromosome 3 open reading frame 4 | 2.1 |
| | 414759 | AW295157 | Hs.47587 | ESTs | 2.1 |
| | 449511 | AI436187 | Hs.296261 | guanine nucleotide binding protein (G pr | 2.1 |
| | 451606 | AA018791 | Hs.7945 | AIE-75 binding protein protein | 2.1 |
| | 437924 | AI935344 | Hs.164118 | ESTs, Weakly similar to SL51_HUMAN SODIU | 2.1 |
| 35 | 449119 | AI631195 | Hs.232193 | ESTs | 2.1 |
| | 431568 | AW972316 | Hs.283703 | ESTs | 2.1 |
| | 447932 | AA837474 | Hs.20021 | vesicle-associated membrane protein 1 (s | 2.1 |
| | 433516 | AA595802 | Hs.33410 | ESTs, Weakly similar to T17279 hypotheti | 2.1 |
| | 441987 | AW452234 | Hs.128293 | ESTs | 2.1 |
| 40 | 414055 | AW818687 | Hs.5366 | hypothetical protein FLJ21522 | 2.1 |
| | 445066 | BE178734 | Hs.197422 | ESTs | 2.1 |
| | 455546 | AW994075 | | gb:RC3-BN0036-090200-011-g06 BN0036 Homo | 2.1 |
| | 413607 | T64741 | | gb:yc4B11.r1 Stratagene liver (937224) | 2.1 |
| | 456401 | W28146 | | gb:43f11 Human retina cDNA randomly prim | 2.1 |
| 45 | 407341 | AA918886 | Hs.204918 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 2.0 |
| | 425055 | AW961959 | Hs.96940 | ESTs | 2.0 |
| | 426917 | AA913814 | Hs.172854 | DKFZP586B0923 protein | 2.0 |
| | 419647 | AA348947 | Hs.91816 | hypothetical protein | 2.0 |
| | 412266 | N59006 | Hs.26133 | ESTs | 2.0 |
| 50 | 449658 | AI964033 | Hs.195730 | ESTs, Weakly similar to CTXN RAT CORTEXI | 2.0 |
| | 424505 | AA446131 | Hs.124918 | KIAA1795 protein | 2.0 |
| | 438219 | AI916151 | Hs.257194 | ESTs | 2.0 |
| | 425068 | AL048716 | Hs.154387 | KIAA0103 gene product | 2.0 |
| | 412949 | AJ471639 | Hs.71913 | ESTs | 2.0 |
| 55 | 418866 | T65754 | | gb:yc11c07.s1 Stratagene lung (937210) H | 2.0 |
| | 445071 | AI280246 | Hs.149504 | ESTs | 2.0 |
| | 456529 | AF014643 | Hs.100072 | connexin46.6 | 2.0 |
| | 406475 | | | C15000508*:gij2558825]gb]AAC53387.1] (AF | 2.0 |
| 60 | 429656 | X05608 | Hs.211584 | neurofilament, light polypeptide (68kd) | 2.0 |
| | 431542 | H63010 | Hs.5740 | ESTs | 2.0 |
| | 452625 | AA724771 | Hs.61425 | ESTs | 2.0 |
| | 410378 | R23324 | Hs.41693 | DnaJ (Hsp40) homolog, subfamily B, membe | 2.0 |
| | 409767 | AW501470 | | gb:U1-HF-BP0p-ajd-b-03-0-UI.r1 NIH_MGC_5 | 2.0 |
| | 446873 | AI554439 | Hs.30724 | ESTs | 2.0 |
| 65 | 453938 | AF082569 | Hs.36794 | D-type cyclin-interacting protein 1 | 2.0 |
| | 423605 | AF047826 | Hs.129887 | cadherin 19, type 2 | 2.0 |
| | 420061 | AW024937 | Hs.29410 | ESTs | 2.0 |
| | 439559 | AW364675 | Hs.173921 | ESTs, Weakly similar to Z109260A B cell | 2.0 |
| | 449901 | AI674072 | | gb:wd15h01.x1 Soares_NFL_T_GBC_S1 Homo s | 2.0 |
| 70 | 428304 | AI743177 | Hs.98422 | ESTs | 2.0 |
| | 432278 | AL137506 | Hs.274256 | hypothetical protein FLJ23563 | 2.0 |
| | 458480 | AI792298 | | p30 OBC protein | 2.0 |
| | 404559 | | | Target Exon | 2.0 |
| | 445831 | NM_006055 | Hs.13351 | LanC (bacterial tetracycline synthetase c | 2.0 |
| 75 | 427523 | BE242779 | Hs.179526 | upregulated by 1,25-dihydroxyvitamin D-3 | 2.0 |
| | 413055 | AV655701 | Hs.75183 | cytochrome P450, subfamily IIE (ethanol- | 2.0 |
| | 444904 | AW452054 | Hs.161139 | ESTs | 2.0 |
| | 443713 | AI082810 | Hs.204934 | ESTs | 2.0 |
| | 448743 | AB032962 | Hs.21896 | KIAA1136 protein | 2.0 |
| 80 | 428186 | AW504300 | Hs.295605 | mannosidase, alpha, class 2A, member 2 | 2.0 |
| | 448770 | AA326683 | Hs.21992 | likely ortholog of mouse variant polyade | 2.0 |
| | 453994 | BE180964 | Hs.165590 | ribosomal protein S13 | 2.0 |
| | 420290 | AW977318 | Hs.194480 | ESTs | 2.0 |
| | 431467 | N71831 | Hs.256398 | Homo sapiens mRNA; cDNA DKFZp434E0528 (f | 2.0 |

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|----|--------------|---|---|---|-----|
| 5 | 447965 | AW292577 | Hs.94445 | ESTs | 2.0 |
| | 423073 | BE252922 | Hs.123119 | MAD (mothers against decapentaplegic, Dr | 2.0 |
| | 459256 | AW967468 | Hs.99821 | hypothetical protein FLJ14547 | 2.0 |
| | 411906 | AW875765 | | gb:CV2-PT0012-020500-186-a08 PT0012 Homo | 2.0 |
| | 441984 | AB037763 | Hs.8059 | synaptotagmin IV | 2.0 |
| | 437900 | AI763301 | Hs.107331 | ESTs | 2.0 |
| | 436092 | AI345995 | Hs.127383 | ESTs | 2.0 |
| | 416529 | AW009370 | Hs.115772 | ESTs | 2.0 |
| 10 | 414320 | U13616 | Hs.75893 | ankyrin 3, node of Ranvier (ankyrin G) | 2.0 |
| | 444749 | AI190672 | Hs.65926 | ESTs | 2.0 |
| | 446277 | AI284218 | Hs.159204 | ESTs | 2.0 |
| | 452550 | AA026735 | Hs.326048 | Homo sapiens mRNA; cDNA DKFp434M0420 (f | 2.0 |
| | 445725 | AK000956 | Hs.13209 | hypothetical protein FLJ10094 | 2.0 |
| 15 | 409265 | T78737 | Hs.321062 | ESTs | 2.0 |
| | 426736 | AA431615 | Hs.130722 | ESTs | 2.0 |
| | 447098 | AI939409 | Hs.157803 | ESTs | 2.0 |
| | 403582 | | | Target Exon | 2.0 |
| 20 | TABLE 21B: | | | | |
| | Pkey: | Unique Eos probeset identifier number | | | |
| | CAT number: | Gene cluster number | | | |
| | Accession: | Genbank accession numbers | | | |
| 25 | Pkey | CAT Number | Accession | | |
| | 409767 | 1154015_1 | AW501470 AW502931 AW499500 | | |
| | 410705 | 1217235_1 | BE004107 BE004105 AW901093 AW797879 AW901094 AW797881 AW797880 BE004108 | | |
| | 410912 | 1265543_1 | AW810224 AW810337 AW810295 AW810333 AW810335 AW810296 AW816053 | | |
| | 411361 | 1240611_1 | AW839073 AW839234 AW839230 AW878302 AW839109 AW843897 | | |
| 30 | 411811 | 1259427_1 | AW864370 AW864319 AW864504 | | |
| | 411906 | 1265204_1 | AW875765 H50294 AW875444 | | |
| | 411918 | 1265807_1 | AW876354 AW876179 AW876318 AW876290 AW876234 AW876125 AW876199 AW876198 | | |
| | 412244 | 1284692_1 | AW948175 AW947637 AW902869 AW947537 AW947531 AW947532 AW947530 | | |
| | 413607 | 1379911_1 | T64741 BE158393 BE152805 | | |
| 35 | 414276 | 1432115_1 | BE297862 | | |
| | 415666 | 1543492_1 | H72693 R08673 H72694 F20990 R08580 | | |
| | 416935 | 163179_1 | AA190712 AA190665 AA252564 | | |
| | 418154 | 17249_1 | BE165866 BE165832 AA319621 AA401166 AI811901 H78857 X56199 R93797 AW896675 AA401072 AW374411 H52942 AW896685 AA348138 | | |
| 40 | | | AI399764 AA010244 W90159 N90874 AA339496 AW967136 W38705 AA029093 AW444647 BE175700 AV651656 AV651847 AA332039 AV649227 | | |
| | | | AV649164 AV649491 N87956 AA332262 BE001561 H75493 BE218742 AA333298 AA095633 AA091968 M78602 T05342 W17094 AA126501 | | |
| | | | AW374665 AI452905 AW316900 AI185080 AI202928 AI651843 AA693541 AI681019 AV658257 AV658133 BE045335 BE089546 AA300830 AA361376 | | |
| | | | BE218739 AW207622 AA765340 AW612733 BE348741 AI806054 AI871553 AA808552 AI500693 AW342032 AA147066 | | |
| | 418866 | 179788_1 | T65754 AA229857 AA229658 | | |
| | 419386 | 184356_1 | AA236867 AA237066 AA354236 AW957759 H08961 | | |
| 45 | 424994 | 245786_1 | AW954525 AI372685 AA349501 AI372687 H10564 | | |
| | 427493 | 279541_2 | H09037 AW974937 AA657521 H86138 H86513 H09016 AA404410 AA404454 | | |
| | 431304 | 331286_1 | BE157283 BE157287 AA502438 | | |
| | 432408 | 346286_2 | N39127 F20776 AI082691 AA865520 F36964 F33894 | | |
| | 433670 | 372721_1 | AA604405 BE062234 AW748386 | | |
| 50 | 433921 | 377350_1 | AA618174 AI114549 R36464 R36465 | | |
| | 436624 | 4237_5 | T64297 AA894931 NM_001443 M10050 AW843109 AI698516 T53219 T48785 T64166 AA706930 R29613 T55913 T56518 T64679 R29666 M10617 | | |
| | | | AI768596 AA101894 W90338 AI742193 AW752206 AA099433 T53220 AW082135 AW272775 T29562 T55862 AI343047 AI345671 T68235 T68121 | | |
| | | | AW842284 | | |
| | 446692 | 689623_1 | Z44514 AI352097 AI803984 AW235923 AW196558 AI954637 AI336983 | | |
| 55 | 449901 | 818599_1 | AI674072 BE268487 | | |
| | 454339 | 1122972_1 | AW381980 BE152244 BE152235 BE152238 BE152232 | | |
| | 455040 | 1250028_1 | AW852286 AW851934 AW852096 AW852274 | | |
| | 455546 | 1324614_1 | AW994075 AW994386 | | |
| | 455649 | 1348708_1 | BE065051 BE155165 BE064764 BE155231 BE064648 BE064671 BE064636 | | |
| 60 | 456401 | 1844649_2 | W28146 W28187 | | |
| | 458480 | 59843_1 | AI792298 H14121 AI375113 AA960851 AA744592 AV648739 AI298360 AW293609 | | |
| 65 | TABLE 21C: | | | | |
| | Pkey: | Unique number corresponding to an Eos probeset | | | |
| | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA | | | |
| | | sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. | | | |
| | Strand: | Indicates DNA strand from which exons were predicted. | | | |
| | Nt_position: | Indicates nucleotide positions of predicted exons. | | | |
| 70 | Pkey | Ref | Strand | Nt_position | |
| | 400536 | 9797380 | Minus | 170994-172025 | |
| | 400818 | 8569994 | Plus | 172644-172765,173085-173200 | |
| | 401586 | 9838242 | Minus | 93974-94099 | |
| | 401600 | 4388746 | Minus | 27363-27518,28727-28891,29526-29731 | |
| 75 | 401783 | 7249190 | Plus | 139369-139827,140509-140591,140834-140990,141496-141657,141757-141882,142063-142283 | |
| | 401929 | 3810670 | Minus | 3167-3286,4216-4310 | |
| | 402124 | 4033680 | Plus | 164206-164459 | |
| | 402493 | 9797670 | Minus | 205146-205240,205428-205542 | |
| | 403463 | 9929538 | Plus | 102596-102879 | |
| 80 | 403469 | 9929739 | Minus | 4831-7707 | |
| | 403582 | 8101185 | Plus | 18308-18458 | |
| | 403728 | 7534291 | Minus | 34481-34671 | |
| | 404091 | 7684554 | Minus | 82121-83229 | |
| | 404559 | 8748893 | Minus | 73499-73651,89575-89739 | |

| | | | |
|--------|---------|-------|-----------------------------|
| 404563 | 9838310 | Plus | 100136-100343 |
| 404606 | 9212936 | Minus | 22310-23269 |
| 404659 | 9797068 | Minus | 65026-67930 |
| 404746 | 7219894 | Minus | 32643-32834 |
| 405354 | 2642452 | Plus | 52213-53089 |
| 405403 | 6850244 | Minus | 37491-37670,40951-41031 |
| 405502 | 9211311 | Minus | 50360-50584 |
| 405715 | 4156209 | Plus | 26293-26706 |
| 406023 | 8272661 | Plus | 205623-205936 |
| 406475 | 9797684 | Plus | 125417-125563,128052-128180 |

TABLE 22A: ABOUT 301 GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS

Table 22A lists about 301 genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal CNS to "average" glioblastoma was greater than or equal to 2. The "average" normal CNS level was set to the 75th percentile amongst various normal CNS tissues. The "average" glioblastoma level was set to the 95th percentile amongst various tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exempt Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of CNS to GLIOBLASTOMA

| Pkey | ExAccn | UnigenelD | Unigene Title | R1 |
|--------|-----------|-----------|--|------|
| 418318 | U47732 | Hs.84072 | transmembrane 4 superfamily member 3 | 10.1 |
| 445529 | H14421 | Hs.180513 | ATP-binding cassette, sub-family A (ABC1 | 9.4 |
| 415274 | AF001548 | Hs.78344 | myosin, heavy polypeptide 11, smooth mus | 7.5 |
| 417167 | AW206437 | Hs.4290 | ESTs | 7.3 |
| 453165 | S74727 | Hs.32042 | aspartoacylase (aminoacylase 2, Canavan | 6.5 |
| 454076 | AW204712 | Hs.61957 | ESTs | 6.3 |
| 417275 | X63578 | Hs.295449 | parvalbumin | 6.2 |
| 412636 | NM_004415 | | desmoplakin (DPI, DPTI) | 6.0 |
| 409743 | N48721 | Hs.183506 | hypothetical protein FLJ14213 | 5.9 |
| 424645 | NM_014682 | Hs.151449 | KIAA0535 gene product | 5.6 |
| 427322 | AK002017 | Hs.176227 | hypothetical protein FLJ11155 | 5.5 |
| 446390 | AA233393 | Hs.14992 | hypothetical protein FLJ11151 | 5.2 |
| 444409 | AI792140 | Hs.49265 | ESTs | 5.2 |
| 409031 | AA376836 | Hs.288856 | ESTs | 5.1 |
| 408428 | NM_014787 | Hs.44896 | DnaJ (Hsp40) homolog, subfamily B, membe | 4.8 |
| 428414 | AL049980 | Hs.184216 | DKFZP564C152 protein | 4.8 |
| 428874 | W32133 | Hs.194366 | transferrin (prealbumin, amyloidosis I | 4.6 |
| 420605 | BE391491 | Hs.99291 | HSPC156 protein | 4.6 |
| 445618 | H79667 | Hs.237642 | Homo sapiens cDNA FLJ12052 fis, clone HE | 4.6 |
| 450715 | AI266484 | Hs.31570 | ESTs, Weakly similar to KIAA1324 protein | 4.4 |
| 428508 | BE252383 | Hs.184668 | SBB131 protein | 4.4 |
| 434064 | AL049045 | Hs.180758 | hypothetical protein PRO0082 | 4.3 |
| 410330 | AW023630 | Hs.159425 | ESTs | 4.2 |
| 426471 | M22440 | Hs.170009 | transforming growth factor, alpha | 4.2 |
| 409231 | AA446644 | Hs.692 | GA733-2 antigen; epithelial glycoprotein | 4.2 |
| 448958 | AB020651 | Hs.22653 | KIAA0844 protein | 4.2 |
| 428465 | AW970976 | Hs.293653 | ESTs | 4.0 |
| 429470 | AI878901 | Hs.203852 | guanine nucleotide binding protein (G pr | 4.0 |
| 432298 | AL118812 | Hs.274293 | Homo sapiens mRNA; cDNA DKFZp761G1111 (I | 3.9 |
| 427061 | AB032971 | Hs.173392 | KIAA1145 protein | 3.9 |
| 430261 | AA305127 | Hs.237225 | hypothetical protein HT023 | 3.9 |
| 435145 | AI277259 | Hs.116631 | ESTs | 3.8 |
| 416101 | R24854 | Hs.268806 | ESTs | 3.8 |
| 426716 | NM_006379 | Hs.171921 | sema domain, immunoglobulin domain (Ig), | 3.8 |
| 438202 | AW169287 | Hs.22588 | ESTs | 3.8 |
| 433558 | AA833757 | Hs.201769 | ESTs, Weakly similar to T24435 hypothei | 3.7 |
| 419956 | AL137939 | Hs.40096 | ESTs | 3.7 |
| 430573 | AA744550 | Hs.136345 | ESTs | 3.7 |
| 422546 | AB007969 | Hs.301478 | KIAA0500 protein | 3.7 |
| 453344 | BE349075 | Hs.44571 | ESTs | 3.6 |
| 417620 | R02530 | Hs.191198 | ESTs | 3.6 |
| 421952 | AA300900 | Hs.98849 | ESTs, Moderately similar to AF161511.1 H | 3.6 |
| 414631 | AW970130 | Hs.65406 | ESTs | 3.6 |
| 437073 | AI885608 | Hs.94122 | ESTs | 3.5 |
| 441264 | AA927170 | Hs.23290 | ESTs | 3.5 |
| 433629 | R13140 | Hs.13359 | ESTs | 3.5 |
| 415114 | D60468 | Hs.94181 | ESTs | 3.4 |
| 411770 | NM_014278 | Hs.71992 | heat shock protein (hsp110 family) | 3.4 |
| 415666 | H72693 | | gb:yu03c11.1 Soares fetal liver spleen | 3.4 |
| 416851 | AW963951 | Hs.85618 | ESTs | 3.4 |
| 443037 | AW500305 | Hs.8906 | syntaxin 7 | 3.4 |
| 449511 | AI436187 | Hs.296261 | guanine nucleotide binding protein (G pr | 3.4 |
| 427176 | AW381569 | Hs.40334 | ESTs | 3.4 |
| 438704 | AI435060 | Hs.32825 | ESTs | 3.3 |
| 417175 | R44558 | Hs.94002 | ESTs | 3.3 |
| 430865 | AI073424 | Hs.5232 | HSPC125 protein | 3.3 |
| 457012 | R41480 | Hs.302754 | ESTs | 3.3 |
| 405354 | | | CX000321:gi 6671579 ref NP_031518.1 an | 3.3 |
| 432799 | NM_016161 | Hs.278960 | alpha-1,4-N-acetylglucosaminyltransferas | 3.3 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 429876 | AB028977 | Hs.225974 | KIAA1054 protein | 3.3 |
| | 434348 | BE393191 | Hs.181795 | putative b,b-carotene-9,10'-dioxygenase | 3.3 |
| | 441071 | D79550 | Hs.7149 | Homo sapiens cDNA: FLJ21950 fis, clone H | 3.3 |
| 5 | 445279 | R41900 | Hs.22245 | ESTs | 3.2 |
| | 414541 | BE293116 | Hs.76392 | aldehyde dehydrogenase 1 family, member | 3.2 |
| | 448072 | AI459306 | Hs.24908 | ESTs | 3.2 |
| | 402429 | | | Target Exon | 3.2 |
| | 433328 | AW298159 | Hs.23644 | ESTs, Weakly similar to S65824 reverse t | 3.2 |
| 10 | 400138 | | | Eos Control | 3.1 |
| | 414327 | BE408145 | Hs.185254 | ESTs, Weakly similar to T24435 hypotheti | 3.1 |
| | 459399 | BE407712 | Hs.153998 | creatine kinase, mitochondrial 1 (ubiqui | 3.1 |
| | 433582 | BE548749 | Hs.148016 | ESTs | 3.1 |
| | 434104 | AF116691 | Hs.116459 | hypothetical protein PRO2198 | 3.0 |
| 15 | 404606 | | | Target Exon | 3.0 |
| | 407173 | T64349 | | gb:yc10d08.s1 Stratagene lung (937210) H | 3.0 |
| | 415672 | N53097 | Hs.193579 | ESTs | 3.0 |
| | 448583 | NM_015239 | Hs.21542 | KIAA1035 protein | 3.0 |
| | 429043 | AI824977 | Hs.145319 | ESTs | 3.0 |
| 20 | 439165 | AA029517 | Hs.95162 | KCNQ1 overlapping transcript 1 | 2.9 |
| | 449561 | AI022240 | Hs.17924 | ESTs, Moderately similar to ALU1_HUMAN A | 2.9 |
| | 436427 | AI344378 | Hs.143399 | ESTs | 2.9 |
| | 405403 | | | Target Exon | 2.9 |
| | 452197 | AW023595 | Hs.232048 | ESTs | 2.9 |
| 25 | 437357 | AL359559 | Hs.331666 | Homo sapiens mRNA: cDNA DKFZp76202215 (I | 2.9 |
| | 439272 | AA832474 | Hs.25851 | ESTs | 2.9 |
| | 415839 | R40611 | Hs.94694 | ESTs | 2.9 |
| | 411906 | AW875765 | | gb:QV2-PT0012-020500-186-a08 PT0012 Homo | 2.9 |
| | 409403 | AA668224 | Hs.6634 | Homo sapiens cDNA: FLJ22547 fis, clone H | 2.9 |
| 30 | 412258 | AA376768 | Hs.324841 | hypothetical protein FLJ22622 | 2.8 |
| | 435836 | AW292532 | Hs.343667 | homolog of yeast long chain polyunsatura | 2.8 |
| | 433109 | N58907 | Hs.162430 | EST | 2.8 |
| | 404563 | | | Target Exon | 2.8 |
| | 427974 | BE093023 | Hs.188767 | ESTs | 2.8 |
| 35 | 413324 | V00571 | Hs.75294 | corticotropin releasing hormone | 2.7 |
| | 409263 | AA089573 | Hs.50319 | ESTs | 2.7 |
| | 454247 | AJ243950 | Hs.46735 | deafness locus associated putative guani | 2.7 |
| | 449180 | AI633836 | Hs.195649 | ESTs | 2.7 |
| | 416004 | D11880 | Hs.299254 | Homo sapiens cDNA: FLJ23597 fis, clone L | 2.7 |
| 40 | 424994 | AW954525 | | gb:EST366595 MAGC resequences, MAGC Homo | 2.7 |
| | 430371 | D87466 | Hs.240112 | KIAA0276 protein | 2.7 |
| | 449117 | AW449310 | Hs.210262 | ESTs, Weakly similar to HSS2_HUMAN HEPAR | 2.7 |
| | 451007 | H38108 | Hs.32759 | ESTs | 2.7 |
| | 414502 | AL133721 | Hs.224680 | ESTs | 2.7 |
| 45 | 458793 | N80159 | Hs.121849 | microtubule-associated proteins 1A/1B li | 2.7 |
| | 459053 | AI807052 | Hs.210361 | ESTs | 2.7 |
| | 427229 | AI799751 | Hs.5635 | ESTs | 2.7 |
| | 425649 | U30930 | Hs.158540 | UDP glycosyltransferase 8 (UDP-galactose | 2.7 |
| | 444922 | AI921750 | Hs.144871 | Homo sapiens cDNA FLJ13752 fis, clone PL | 2.7 |
| 50 | 433921 | AA618174 | | gb:ncq14f01.s1 NCL_CGAP_Thy1 Homo sapiens | 2.7 |
| | 414272 | AI651603 | Hs.46988 | ESTs | 2.7 |
| | 418047 | R37633 | Hs.4847 | ESTs | 2.7 |
| | 421089 | AB037771 | Hs.101799 | KIAA1350 protein | 2.7 |
| | 416498 | U33632 | Hs.79351 | potassium channel, subfamily K, member 1 | 2.6 |
| 55 | 414290 | AI568801 | Hs.71721 | ESTs | 2.6 |
| | 433703 | AA210863 | Hs.3532 | nemo-like kinase | 2.6 |
| | 408739 | W01556 | Hs.238797 | ESTs, Moderately similar to I38022 hypot | 2.6 |
| | 414602 | AW630088 | Hs.76550 | Homo sapiens mRNA: cDNA DKFZp56481264 (I | 2.6 |
| | 422137 | AJ236885 | Hs.112180 | zinc finger protein 148 (pH2-52) | 2.6 |
| 60 | 442023 | AI187878 | Hs.144549 | ESTs | 2.6 |
| | 421709 | AA159394 | Hs.107056 | CED-6 protein | 2.6 |
| | 426747 | AA535210 | Hs.171995 | kallikrein 3, (prostate specific antigen | 2.6 |
| | 412244 | AW948175 | | gb:RC0-MT0013-280300-021-c10 MT0013 Homo | 2.6 |
| | 419386 | AA236867 | | ESTs, Weakly similar to I38022 hypotheti | 2.6 |
| 65 | 423665 | BE167153 | Hs.24380 | ESTs | 2.6 |
| | 430320 | BE245290 | Hs.239218 | uncharacterized hypothalamus protein HCD | 2.6 |
| | 408468 | AI909712 | Hs.93837 | phosphatidylinositol transfer protein, m | 2.6 |
| | 410657 | AF063228 | Hs.65248 | dynein, cytoplasmic, intermediate polype | 2.6 |
| | 448871 | BE616709 | Hs.159265 | kruppel-related zinc finger protein hckr | 2.6 |
| 70 | 414516 | AI307802 | Hs.135560 | ESTs, Weakly similar to T43458 hypotheti | 2.6 |
| | 459080 | AW192083 | Hs.290855 | ESTs | 2.5 |
| | 455040 | AW852286 | | gb:QV0-CT0225-100400-187-d08 CT0225 Homo | 2.5 |
| | 435712 | AA694607 | Hs.176956 | ESTs | 2.5 |
| | 431662 | AA513406 | Hs.152307 | ESTs | 2.5 |
| 75 | 435902 | AA701867 | Hs.297726 | ESTs | 2.5 |
| | 436624 | T64297 | | fatty acid binding protein 1, liver | 2.5 |
| | 443155 | R54485 | Hs.23772 | ESTs | 2.5 |
| | 439183 | AW970600 | Hs.303261 | ESTs | 2.5 |
| | 426365 | AA376667 | Hs.10283 | RNA binding motif protein 8B | 2.5 |
| 80 | 420033 | D59502 | Hs.292590 | ESTs | 2.5 |
| | 408438 | AB011180 | Hs.100960 | KIAA0608 protein | 2.5 |
| | 440205 | T86950 | Hs.105448 | ESTs, Weakly similar to B34087 hypotheti | 2.5 |
| | 448786 | BE048842 | Hs.179075 | Homo sapiens cDNA FLJ11881 fis, clone HE | 2.5 |
| | 432251 | AW972983 | Hs.232165 | polycythemia rubra vera 1; cell surface | 2.5 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 427115 | AW972853 | Hs.112237 | ESTs | |
| | 433670 | AA604405 | | gb:nc087h09.s1 NCI_CGAP_AA1 Homo sapiens | 2.4 |
| | 452022 | AW072330 | Hs.293875 | ESTs | 2.4 |
| 5 | 408814 | N62499 | Hs.176227 | hypothetical protein FLJ11155 | 2.4 |
| | 403469 | | | Target Exon | 2.4 |
| | 450374 | AA397540 | Hs.60293 | Homo sapiens clone 122482 unknown mRNA | 2.4 |
| | 451926 | AW134519 | Hs.96125 | Homo sapiens, Similar to clone FLB3816, | 2.4 |
| | 443622 | AJ911527 | Hs.11805 | ESTs | 2.4 |
| 10 | 456791 | H05202 | Hs.133968 | FGF receptor activating protein 1 | 2.4 |
| | 414672 | AJ218038 | Hs.48504 | ESTs, Moderately similar to ALU5_HUMAN A | 2.4 |
| | 451522 | BE565817 | Hs.26498 | hypothetical protein FLJ21657 | 2.4 |
| | 422414 | AW875237 | Hs.13701 | ESTs | 2.4 |
| | 425383 | D83407 | Hs.156007 | Down syndrome critical region gene 1-lik | 2.4 |
| 15 | 438086 | AA335519 | Hs.83623 | nuclear receptor subfamily 1, group 1, m | 2.4 |
| | 410240 | AL157424 | Hs.61289 | synaptotagmin 2 | 2.4 |
| | 432408 | N39127 | | ESTs, Weakly similar to A46010 X-linked | 2.4 |
| | 458227 | Z40570 | Hs.181340 | ESTs | 2.4 |
| | 431325 | AW026751 | Hs.5794 | ESTs, Weakly similar to 2109260A B cell | 2.4 |
| 20 | 401600 | BE247275 | | U5 snRNP-specific protein, 116 kD | 2.4 |
| | 422963 | M79141 | Hs.13234 | ESTs | 2.3 |
| | 444897 | AW137088 | Hs.144857 | ESTs | 2.3 |
| | 418207 | C14685 | Hs.34772 | ESTs | 2.3 |
| | 445071 | AJ280246 | Hs.149504 | ESTs | 2.3 |
| 25 | 407868 | NM_000950 | | proline-rich Gla (G-carboxyglutamic acid | 2.3 |
| | 433331 | AJ738815 | Hs.117323 | ESTs | 2.3 |
| | 440293 | AJ004193 | Hs.22123 | ESTs | 2.3 |
| | 428850 | AA934975 | Hs.185076 | ESTs | 2.3 |
| | 401783 | | | NM_003771*:Homo sapiens keratin, hair, a | 2.3 |
| 30 | 419763 | AJ039691 | Hs.127486 | ESTs | 2.3 |
| | 416018 | AW138239 | Hs.78977 | proprotein convertase subtilisin/kexin 1 | 2.3 |
| | 420912 | AW853156 | Hs.90787 | ESTs | 2.3 |
| | 442097 | AW015799 | Hs.128474 | ESTs | 2.3 |
| | 425907 | AA365752 | Hs.155965 | ESTs | 2.3 |
| 35 | 404091 | | | Target Exon | 2.3 |
| | 414106 | BE300325 | Hs.77135 | RNA binding protein | 2.3 |
| | 454288 | BE222648 | Hs.241432 | ESTs, Highly similar to c380A1.1b [H.sap | 2.3 |
| | 441040 | AW449782 | Hs.178803 | ESTs | 2.3 |
| | 424724 | T06532 | Hs.287709 | Homo sapiens cDNA: FLJ22674 fis, clone H | 2.3 |
| 40 | 441879 | AJ521936 | Hs.107149 | novel protein similar to archaeal, yeast | 2.3 |
| | 407988 | N47760 | Hs.285107 | hypothetical protein FLJ13397 | 2.2 |
| | 452420 | BE564871 | Hs.29463 | centrin, EF-hand protein, 3 (CDC31 yeast | 2.2 |
| | 458676 | AJ692464 | Hs.202263 | ESTs | 2.2 |
| | 418407 | AL044818 | Hs.84928 | nuclear transcription factor Y, beta | 2.2 |
| 45 | 453938 | AF082569 | Hs.36794 | D-type cyclin-interacting protein 1 | 2.2 |
| | 407978 | AW385129 | Hs.41717 | phosphodiesterase 1A, calmodulin-depende | 2.2 |
| | 420548 | AA278246 | Hs.920 | ESTs | 2.2 |
| | 422907 | AJ879263 | Hs.77273 | Human glucose transporter pseudogene | 2.2 |
| | 446351 | AW444551 | Hs.35380 | x 001 protein | 2.2 |
| 50 | 442117 | AW664964 | Hs.128899 | ESTs; hypothetical protein for IMAGE:447 | 2.2 |
| | 429598 | AA811257 | Hs.269710 | ESTs | 2.2 |
| | 408480 | AJ350337 | Hs.164568 | fibroblast growth factor 7 (keratinocyte | 2.2 |
| | 411361 | AW839073 | | gb:CM2-LT0066-030100-109-d06 LT0066 Homo | 2.2 |
| | 459697 | AA406062 | Hs.98002 | ESTs | 2.2 |
| 55 | 409856 | AW502082 | | gb:U1-HF-BR0p-ajq-g-04-0-U1.r1 NIH_MGC_5 | 2.2 |
| | 444760 | AJ796296 | Hs.208062 | ESTs | 2.2 |
| | 443258 | AF169301 | Hs.9098 | sulfate transporter 1 | 2.2 |
| | 428206 | AB020643 | Hs.183006 | KIAA0836 protein | 2.2 |
| | 410119 | F07841 | Hs.13926 | ESTs | 2.2 |
| 60 | 413427 | U31120 | Hs.845 | interleukin 13 | 2.2 |
| | 438021 | AV653790 | Hs.324275 | WW domain-containing protein 1 | 2.2 |
| | 428652 | AA584272 | Hs.336224 | transmembrane protein with EGF-like and | 2.2 |
| | 429655 | U48959 | Hs.211582 | myosin, light polypeptide kinase | 2.2 |
| | 424153 | AA451737 | Hs.141496 | MAGE-like 2 | 2.2 |
| 65 | 413303 | AW836130 | Hs.75277 | hypothetical protein FLJ13910 | 2.2 |
| | 427287 | NM_014903 | Hs.174188 | KIAA0938 protein | 2.2 |
| | 449658 | AJ964033 | Hs.195730 | ESTs, Weakly similar to CTXN RAT CORTEXI | 2.2 |
| | 441984 | AB037763 | Hs.8059 | synaptotagmin IV | 2.2 |
| | 449709 | BE410592 | Hs.23918 | hypothetical protein PPS395 | 2.2 |
| 70 | 408068 | AW148652 | Hs.167398 | ESTs | 2.2 |
| | 407819 | R42185 | Hs.102720 | ESTs | 2.2 |
| | 414203 | BE262170 | Hs.78629 | ATPase, Na ⁺ transporting, beta 1 polypep | 2.2 |
| | 454339 | AW381980 | | gb:QV4-HT0316-091199-028-d05 HT0316 Homo | 2.2 |
| | 448045 | AJ297436 | Hs.20166 | prostate stem cell antigen | 2.2 |
| 75 | 458480 | AJ792298 | | p30 DBC protein | 2.2 |
| | 449835 | AW979300 | Hs.293813 | ESTs | 2.2 |
| | 458547 | AW204314 | Hs.170784 | ESTs | 2.2 |
| | 411678 | AJ907114 | Hs.71465 | squalene epoxidase | 2.2 |
| | 444783 | AK001468 | Hs.62180 | anilin (Drosophila Scraps homolog), act | 2.1 |
| 80 | 424632 | AB014523 | Hs.151406 | KIAA0623 gene product | 2.1 |
| | 449901 | AJ674072 | | gb:wd15h01.x1 Soares_NFL_T_GBC_S1 Homo s | 2.1 |
| | 431583 | AL042613 | Hs.262476 | S-adenosylmethionine decarboxylase 1 | 2.1 |
| | 410538 | AW753115 | | gb:PM0-CT0248-131099-001-h12 CT0248 Homo | 2.1 |
| | 426775 | AA384564 | Hs.3628 | ESTs | 2.1 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 433862 | D86960 | Hs.3610 | KIAA0205 gene product | 2.1 |
| | 458694 | F12832 | Hs.3610 | ESTs | 2.1 |
| | 417063 | N50515 | Hs.45061 | ESTs | 2.1 |
| 5 | 416935 | AA190712 | | gb:zfp8709.r1 Stratagene HeLa cell s3 93 | 2.1 |
| | 436489 | AJ272269 | Hs.121429 | zinc-binding protein Rbccc728 | 2.1 |
| | 431128 | AI203545 | Hs.296169 | S-phase response (cyclin-related) | 2.1 |
| | 442310 | AF033199 | Hs.8198 | zinc finger protein 204 | 2.1 |
| | 432434 | AL161977 | Hs.2994 | PCTAIRE protein kinase 3 | 2.1 |
| 10 | 400339 | X57131 | Hs.248209 | H2A histone family, member F, pseudogene | 2.1 |
| | 432266 | AK000385 | Hs.274222 | hypothetical protein FLJ20378 | 2.1 |
| | 414759 | AW295157 | Hs.47587 | ESTs | 2.1 |
| | 438219 | AI916151 | Hs.257194 | ESTs | 2.1 |
| | 451336 | AI264643 | Hs.3610 | ESTs | 2.1 |
| 15 | 430538 | AB032435 | Hs.242821 | differentiation-associated Na-dependent | 2.1 |
| | 413493 | BE144444 | | gb:MR0-HT0168-141199-002-009 HT0168 Homo | 2.1 |
| | 428501 | AL041162 | Hs.98587 | ESTs | 2.1 |
| | 431568 | AW972316 | Hs.283703 | ESTs | 2.1 |
| | 456177 | NM_012391 | Hs.79414 | prostate epithelium-specific Ets transcr | 2.1 |
| 20 | 441976 | AA428403 | Hs.106131 | ESTs | 2.1 |
| | 421311 | N71848 | Hs.283609 | hypothetical protein PRO2032 | 2.1 |
| | 428358 | AA993222 | Hs.101915 | Slargard disease 3 (autosomal dominant) | 2.1 |
| | 439973 | AI733308 | Hs.124663 | ESTs | 2.1 |
| | 446185 | AI279191 | Hs.149454 | ESTs, Weakly similar to DSR6_HUMAN DOWN | 2.1 |
| 25 | 451606 | AA018791 | Hs.7945 | AIE-75 binding protein protein | 2.1 |
| | 433516 | AA595802 | Hs.33410 | ESTs, Weakly similar to T17279 hypotheti | 2.1 |
| | 441987 | AW452234 | Hs.128293 | ESTs | 2.1 |
| | 457140 | AI279960 | Hs.178140 | ESTs | 2.1 |
| | 414055 | AW818687 | Hs.5366 | hypothetical protein FLJ21522 | 2.1 |
| 30 | 445066 | BE178734 | Hs.197422 | ESTs | 2.1 |
| | 459265 | AJ003616 | | gb:AJ003616 Selected chromosome 21 cDNA | 2.0 |
| | 425337 | AA355442 | Hs.169054 | ESTs | 2.0 |
| | 409339 | AB020686 | Hs.54037 | ectonucleotide pyrophosphatase/phosphodi | 2.0 |
| | 453023 | AW028733 | Hs.31439 | serine protease inhibitor, Kunitz type, | 2.0 |
| 35 | 425055 | AW961959 | Hs.96940 | ESTs | 2.0 |
| | 425068 | AL048716 | Hs.154387 | KIAA0103 gene product | 2.0 |
| | 444700 | NM_003645 | Hs.11729 | fatty acid-Coenzyme A ligase, very long- | 2.0 |
| | 424823 | NM_006226 | Hs.153322 | phospholipase C, epsilon | 2.0 |
| | 450103 | R08665 | Hs.17244 | hypothetical protein FLJ13605 | 2.0 |
| 40 | 448519 | AW175665 | Hs.278695 | Homo sapiens protein mRNA, complete cds | 2.0 |
| | 440808 | AK001339 | Hs.7432 | hypothetical protein FLJ10477 | 2.0 |
| | 429968 | AA322503 | Hs.227011 | G-substrate | 2.0 |
| | 429290 | AF203032 | Hs.198760 | neurofilament, heavy polypeptide (200kD) | 2.0 |
| | 433068 | NM_006456 | Hs.288215 | sialyltransferase | 2.0 |
| 45 | 416982 | J05401 | Hs.80691 | creatine kinase, mitochondrial 2 (sarcom | 2.0 |
| | 423479 | NM_014326 | Hs.129208 | death-associated protein kinase 2 | 2.0 |
| | 407341 | AA918886 | Hs.204918 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 2.0 |
| | 452625 | AA724771 | Hs.61425 | ESTs | 2.0 |
| | 410378 | R23324 | Hs.41693 | DnaJ (Hsp40) homolog, subfamily B, membe | 2.0 |
| 50 | 409767 | AW501470 | | gb:U1-HF-BP0p-ajd-b-03-0-UI.r1 NIH_MGC_5 | 2.0 |
| | 415925 | HD9474 | Hs.202341 | Homo sapiens cDNA: FLJ23573 fis, clone L | 2.0 |
| | 405670 | | | C20006277:gi12034653 gb AAG45951.1 AF22 | 2.0 |
| | 408206 | AF041853 | Hs.43670 | kinesin family member 3A | 2.0 |
| | 458660 | AI299739 | Hs.99601 | hypothetical protein FLJ12553 | 2.0 |
| 55 | 432278 | AL137506 | Hs.274256 | hypothetical protein FLJ23563 | 2.0 |
| | 404559 | | | Target Exon | 2.0 |
| | 403728 | | | Target Exon | 2.0 |
| | 413055 | AV655701 | Hs.75183 | cytochrome P450, subfamily IIE (ethanol- | 2.0 |
| 60 | 407786 | AA687538 | Hs.38972 | tetraspan 1 | 2.0 |
| | 413266 | BE300352 | | gb:600944231F1 NIH_MGC_17 Homo sapiens c | 2.0 |
| | 453994 | BE180964 | Hs.165590 | ribosomal protein S13 | 2.0 |
| | 451583 | AI653797 | Hs.24133 | ESTs | 2.0 |
| | 443244 | AI457235 | Hs.166479 | ESTs | 2.0 |
| | 453396 | AW162768 | Hs.22620 | ESTs | 2.0 |
| 65 | 415694 | AW194301 | Hs.339283 | Human DNA sequence from clone RP1-187J11 | 2.0 |
| | 459511 | AI142379 | | gb:ag64c01.r1 Soares_letis_NHT Homo sap | 2.0 |
| | 450757 | BE081050 | Hs.31570 | ESTs, Weakly similar to KIAA1324 protein | 2.0 |
| | 451032 | W03692 | Hs.323079 | Homo sapiens mRNA; cDNA DKFZp564P116 (fr | 2.0 |
| | 440509 | BE410132 | Hs.134202 | ESTs, Weakly similar to T17279 hypotheti | 2.0 |
| 70 | 444647 | H14718 | Hs.11506 | Human clone Z3589 mRNA sequence | 2.0 |
| | 447932 | AA837474 | Hs.20021 | vesicle-associated membrane protein 1 (s | 2.0 |
| | 444749 | AI190672 | Hs.65926 | ESTs | 2.0 |
| | 446277 | AI284218 | Hs.159204 | ESTs | 2.0 |
| | 452550 | AA026735 | Hs.326048 | Homo sapiens mRNA; cDNA DKFZp434M0420 (f | 2.0 |
| 75 | 453843 | D25215 | Hs.35804 | hect domain and RLD 3 | 2.0 |
| | 445725 | AK000956 | Hs.13209 | hypothetical protein FLJ10094 | 2.0 |
| | 409265 | T78737 | Hs.321062 | ESTs | 2.0 |

TABLE 22B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey CAT Number Accession

| | | | |
|----|--------|-----------|---|
| 5 | 409767 | 1154015_1 | AW501470 AW502931 AW499500 |
| | 409856 | 1156268_1 | AW502082 AW502979 AW502807 AW501876 |
| | 410538 | 1207341_1 | AW753115 AW753113 R45779 |
| | 411361 | 1240611_1 | AW839073 AW839234 AW839230 AW878302 AW839109 AW843897 |
| | 411906 | 1265204_1 | AW875765 H50294 AW875444 |
| | 412244 | 1284692_1 | AW948175 AW947637 AW902869 AW947537 AW947531 AW947532 AW947530 |
| | 412636 | 13165_1 | NM_004415 AL031058 M77830 BE149760 AW752599 AW848723 AW376697 AW376817 AW376699 AW848371 AW376782 AW848789 AW361413 |
| 10 | | | AW849074 AW997139 AW799304 AW799309 BE077020 BE077017 BE185187 AW997196 BE156621 BE179915 BE006561 BE143155 AW890985 |
| | | | BE002107 AW103521 AA857316 AW383133 BE011378 AW170253 BE185750 AW886475 BE160433 J05211 BE082576 BE082584 BE004047 |
| | | | AW607238 AW377700 AW377699 BE082526 BE082505 BE082507 BE082514 AW178000 AW177933 AJ905935 AW747877 AW748114 BE148516 |
| | | | AW265328 AW847678 AW847688 AW365151 AW365148 AW365153 AW365156 AW365175 AW365157 AW365154 AW068840 BE005272 AW365145 |
| | | | BE001925 BE182166 BE144243 BE001923 AJ951766 AJ434518 BE184920 BE184933 AJ284090 BE184941 AW804674 BE184924 C04715 W39488 |
| 15 | | | AW995615 BE184948 BE159646 AW606653 AA098991 AA131128 AA337270 AA340777 AW384371 AA852212 R58704 AW366566 AW364859 |
| | | | AA025851 AA025852 AA455100 AA719958 AW352220 AW996245 BE165351 BE073467 AA377127 AW890264 AW609750 AW391912 AW849690 |
| | | | T87267 AW853812 AA852213 W74149 BE009090 AA056401 H91011 AW368529 AW390272 C18467 AW674920 N57176 AA026480 AW576767 |
| | | | H3284 AA026863 AW177787 AA026654 AW177786 BE092134 BE092137 BE092136 AW177784 AJ022862 BE091653 AW376811 AW848592 |
| 20 | | | AA040018 BE185331 BE182164 AA368564 AW951576 T29918 AA131077 W95048 W25458 AW205789 H90899 N29754 W32490 R20904 BE167181 |
| | | | BE167165 N84767 H27408 H30146 AJ190590 C03378 AJ554403 AJ205263 AA128470 AJ392926 AF139065 AW370813 AW370827 AW798417 |
| | | | AW798780 AW798883 AW798569 R33557 AA149190 C03029 AW177783 AA088866 AW370829 AA247685 BE002273 AJ760816 AJ439101 AW879451 |
| | | | AJ702424 AJ417612 AJ306554 AJ686869 AJ568892 AW190555 AJ571075 AJ220573 AA056527 AJ471874 AJ304772 AW517828 AJ915596 AJ627383 |
| | | | AJ270345 AW021347 AW166807 AW105614 AJ346078 AA552300 W95070 AJ494069 AJ911702 AA149191 AA026864 AJ830049 AJ887258 AW780435 |
| 25 | | | AJ910434 AJ819984 AJ858282 AJ078449 AJ025932 AJ860584 AJ635878 AA026047 AA703232 D12062 AW192085 AA658154 AW514597 AW591892 |
| | | | T87181 AA782066 AW243815 AW150038 AW268383 AW004633 AJ927207 AA782109 AW473233 AJ804485 AW169216 AJ572669 AA602182 |
| | | | AW015480 AW771865 AJ270027 AA961816 AA283207 AJ076962 AJ498487 AJ348053 AJ783914 H44405 AW799118 AA128330 AA515500 AA918281 |
| | | | W02156 AJ905927 AA022701 W38382 R20795 T77861 AW860878 |
| 30 | 413266 | 1356260_1 | BE300352 BE299274 BE075351 BE297444 |
| | 413493 | 1373555_1 | BE144444 BE144430 |
| | 415666 | 1543492_1 | H72693 R08673 H72694 F20990 R08580 |
| | 416935 | 163179_1 | AA190712 AA190665 AA252564 |
| | 419386 | 184356_1 | AA236867 AA237066 AA354236 AW957759 H08961 |
| | 424994 | 245786_1 | AW954525 AJ372685 AA349501 AJ372687 H10564 |
| | 432408 | 346286_2 | N39127 F20776 AJ082691 AA865520 F36964 F33894 |
| 35 | 433670 | 372721_1 | AA604405 BE062234 AW748386 |
| | 433921 | 377350_1 | AA618174 AJ114549 R36464 R36465 |
| | 436624 | 4237_5 | T64297 AA894931 NM_001443 M10050 AW843109 AJ698516 T53219 T48785 T64166 AA706930 R29613 T55913 T56518 T64679 R29666 M10617 |
| 40 | 449901 | 818599_1 | AJ785996 AA101894 W90338 AJ742193 AW752206 AA099433 T53220 AW082135 AW272775 T29562 T55862 AJ343047 AJ345671 T68235 T68121 |
| | 454339 | 1122972_1 | AW842284 |
| | 455040 | 1250028_1 | AJ674072 BE268487 |
| | 458480 | 59843_1 | AW381980 BE152244 BE152235 BE152238 BE152232 |
| | 459265 | 966590_1 | AW852286 AW851934 AW852096 AW852274 |
| | | | AJ792298 H14121 AJ375113 AA960851 AA744592 AV648739 AJ298360 AW293609 |
| | | | AJ003616 AJ003654 AJ003617 |

| | | | |
|----|--------------|---|--|
| 45 | TABLE 22C: | | |
| | Pkey: | Unique number corresponding to an Eos probeset | |
| | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. | |
| 50 | Strand: | Indicates DNA strand from which exons were predicted. | |
| | NL_position: | Indicates nucleotide positions of predicted exons. | |

| | | | | |
|----|--------|---------|--------|---|
| 55 | Pkey | Ref | Strand | NL_position |
| | 401600 | 4388746 | Minus | 27363-27518,28727-28891,29526-29731 |
| | 401783 | 7249190 | Plus | 139369-139827,140509-140591,140834-140990,141496-141657,141757-141882,142063-142283 |
| | 402429 | 9796372 | Minus | 57622-57793,59282-59402,59624-59827 |
| | 403469 | 9929739 | Minus | 4831-7707 |
| | 403728 | 7534291 | Minus | 34481-34671 |
| | 404091 | 7684554 | Minus | 82121-83229 |
| 60 | 404559 | 8748893 | Minus | 73499-73651,89575-89739 |
| | 404563 | 9838310 | Plus | 100136-100343 |
| | 404606 | 9212936 | Minus | 22310-23269 |
| | 405354 | 2642452 | Plus | 52213-53089 |
| | 405403 | 6850244 | Minus | 37491-37670,40951-41031 |
| 65 | 405670 | 4662655 | Plus | 96543-96870 |

| | | | |
|----|---|--|--|
| 70 | TABLE 23A: ABOUT 441 GENES SIGNIFICANTLY DOWN-REGULATED IN LOWER GRADE GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS | | |
| | Table 23A lists about 441 genes significantly down-regulated in lower grade glioblastoma (LGG) compared to normal adult CNS tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal CNS to "average" LGG was greater than or equal to 2.5. The "average" normal CNS level was set to the 75th percentile amongst various normal CNS tissues. The "average" LGG level was set to the 95th percentile amongst various tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated. | | |

| | | | |
|----|----------------|---|--|
| 75 | Pkey: | Unique Eos probeset identifier number | |
| | ExAccn: | Exemplar Accession number, Genbank accession number | |
| | UnigenelD: | Unigene number | |
| | Unigene Title: | Unigene gene title | |
| | R1: | Ratio of CNS to LOWER GRADE GLIOBLASTOMA | |

| | | | | | |
|----|--------|----------|-----------|--|------|
| 80 | Pkey | ExAccn | UnigenelD | Unigene Title | R1 |
| | 415388 | AF018081 | Hs.78409 | collagen, type XVIII, alpha 1 | 10.3 |
| | 418318 | U47732 | Hs.84072 | transmembrane 4 superfamily member 3 | 10.1 |
| | 445529 | H14421 | Hs.180513 | ATP-binding cassette, sub-family A (ABC1 | 9.9 |
| | 417433 | BE270266 | Hs.82128 | ST4 oncofetal trophoblast glycoprotein | 7.8 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 422746 | NM_004484 | Hs.119651 | glypican 3 | 7.7 |
| | 448362 | AA641767 | Hs.21015 | hypothetical protein DKFZp564L0864 simil | 7.7 |
| | 430573 | AA744550 | Hs.136345 | ESTs | 7.6 |
| 5 | 415274 | AF001548 | Hs.78344 | myosin, heavy polypeptide 11, smooth mus | 7.5 |
| | 419290 | AI128114 | Hs.112885 | spinal cord-derived growth factor-B | 7.4 |
| | 424670 | W61215 | Hs.116651 | epithelial V-like antigen 1 | 7.3 |
| | 417167 | AW206437 | Hs.4290 | ESTs | 7.3 |
| | 416018 | AW138239 | Hs.78977 | proprotein convertase subtilisin/kexin 1 | 7.3 |
| 10 | 424632 | AB014523 | Hs.151406 | KIAA0623 gene product | 6.9 |
| | 453165 | S74727 | Hs.32042 | aspartoacylase (aminoacylase 2, Canavan | 6.5 |
| | 411770 | NM_014278 | Hs.71992 | heat shock protein (hsp110 family) | 6.5 |
| | 439272 | AA832474 | Hs.25851 | ESTs | 6.5 |
| | 414831 | M31158 | Hs.77439 | protein kinase, cAMP-dependent, regulato | 6.4 |
| 15 | 454076 | AW204712 | Hs.61957 | ESTs | 6.3 |
| | 446390 | AA233393 | Hs.14992 | hypothetical protein FLJ11151 | 6.3 |
| | 430865 | AI073424 | Hs.5232 | HSPC125 protein | 6.3 |
| | 434064 | AL049045 | Hs.180758 | hypothetical protein PRO0082 | 6.2 |
| | 417458 | NM_005655 | Hs.82173 | TGFB inducible early growth response | 6.1 |
| 20 | 412636 | NM_004415 | | desmoplakin (DPI, DPH) | 6.0 |
| | 409743 | N48721 | Hs.183506 | hypothetical protein FLJ14213 | 5.9 |
| | 430998 | AF128847 | Hs.204038 | indolethylamine N-methyltransferase | 5.8 |
| | 434725 | AK000796 | Hs.4104 | hypothetical protein | 5.6 |
| | 417175 | R44558 | Hs.94002 | ESTs | 5.6 |
| 25 | 417275 | X63578 | Hs.295449 | parvalbumin | 5.5 |
| | 427322 | AK002017 | Hs.176227 | hypothetical protein FLJ11155 | 5.5 |
| | 431009 | BE149762 | Hs.48956 | gap junction protein, beta 6 (connexin 3 | 5.4 |
| | 420297 | AI628272 | Hs.88323 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 5.4 |
| | 412472 | AW975398 | Hs.293836 | ESTs | 5.4 |
| 30 | 443258 | AF169301 | Hs.9098 | sulfate transporter 1 | 5.3 |
| | 427210 | BE396283 | Hs.173987 | eukaryotic translation initiation factor | 5.3 |
| | 442064 | AI422867 | Hs.88594 | ESTs | 5.2 |
| | 438868 | AW246243 | Hs.334800 | hypothetical protein FLJ20974 | 5.2 |
| | 444409 | AI792140 | Hs.49265 | ESTs | 5.2 |
| 35 | 442310 | AF033199 | Hs.8198 | zinc finger protein 204 | 5.1 |
| | 409031 | AA376836 | Hs.288856 | ESTs | 5.1 |
| | 438460 | AB020702 | Hs.6224 | KIAA0895 protein | 5.1 |
| | 411939 | AI365585 | Hs.146246 | ESTs | 5.0 |
| | 448429 | D17408 | Hs.21223 | calponin 1, basic, smooth muscle | 5.0 |
| 40 | 413293 | AL047483 | Hs.302498 | GTP-binding protein homologous to Saccha | 5.0 |
| | 408968 | AI652236 | Hs.49376 | hypothetical protein FLJ20644 | 5.0 |
| | 443491 | AW499665 | Hs.9456 | SWI/SNF related, matrix associated, acti | 4.9 |
| | 448960 | AF006513 | Hs.22670 | chromodomain helicase DNA binding protei | 4.9 |
| | 416101 | R24854 | Hs.268806 | ESTs | 4.9 |
| 45 | 433558 | AA833757 | Hs.201769 | ESTs, Weakly similar to T24435 hypotheti | 4.9 |
| | 424645 | NM_014682 | Hs.151449 | KIAA0535 gene product | 4.8 |
| | 437679 | NM_014214 | Hs.5753 | inositol(myo)-1(or 4)-monophosphatase 2 | 4.8 |
| | 408428 | NM_014787 | Hs.44896 | OnaJ (Hsp40) homolog, subfamily B, membe | 4.8 |
| | 414502 | AL133721 | Hs.224680 | ESTs | 4.8 |
| 50 | 442572 | AI001922 | Hs.135121 | hypothetical protein FLJ22415 | 4.8 |
| | 412700 | BE222433 | Hs.239208 | ESTs, Weakly similar to I38022 hypotheti | 4.8 |
| | 422603 | BE242587 | Hs.118551 | hematopoietically expressed homeobox | 4.8 |
| | 420605 | BE391491 | Hs.99291 | HSPC156 protein | 4.7 |
| | 422482 | AI439905 | Hs.344476 | gb:ti57g08.x1 NCI_CGAP_Lym12 Homo sapien | 4.7 |
| 55 | 416636 | N32536 | Hs.42645 | solute carrier family 16 (monocarboxylic | 4.7 |
| | 409263 | AA069573 | Hs.50319 | ESTs | 4.7 |
| | 410657 | AF063228 | Hs.65248 | dynein, cytoplasmic, intermediate polype | 4.6 |
| | 457216 | AA452554 | Hs.283697 | ESTs, Weakly similar to A41796 neural re | 4.6 |
| | 433423 | BE407127 | Hs.8997 | heat shock 70kD protein 1A | 4.6 |
| 60 | 449901 | AI674072 | | gb:wd15h01.x1 Soares_NFL_T_GBC_S1 Homo s | 4.6 |
| | 445618 | H79667 | Hs.237642 | Homo sapiens cDNA FLJ12052 fs, clone HE | 4.6 |
| | 431582 | F07136 | Hs.261828 | G protein-coupled receptor kinase 7 | 4.5 |
| | 424675 | NM_005512 | Hs.151641 | glycoprotein A repetitions predominant | 4.5 |
| | 449511 | AI436187 | Hs.296261 | guanine nucleotide binding protein (G pr | 4.5 |
| 65 | 401600 | BE247275 | | U5 snRNP-specific protein, 116 kD | 4.5 |
| | 447135 | T58148 | | gb:yb98g06.s1 Stratagene lung (937210) H | 4.5 |
| | 426689 | BE245550 | Hs.171825 | basic helix-loop-helix domain containing | 4.4 |
| | 429598 | AA811257 | Hs.269710 | ESTs | 4.4 |
| | 428206 | AB020643 | Hs.183006 | KIAA0836 protein | 4.4 |
| 70 | 450715 | AI266484 | Hs.31570 | ESTs, Weakly similar to KIAA1324 protein | 4.4 |
| | 428508 | BE252383 | Hs.184668 | SBB131 protein | 4.4 |
| | 435145 | AI277259 | Hs.116631 | ESTs | 4.4 |
| | 405670 | | | C2000627*:gj12034653[gb]AAG45951.1[AF22 | 4.4 |
| | 442321 | AF207664 | Hs.8230 | a disintegrin-like and metalloprotease (| 4.3 |
| 75 | 427670 | BE612888 | Hs.180224 | myosin regulatory light chain | 4.3 |
| | 428465 | AW970976 | Hs.293653 | ESTs | 4.3 |
| | 449180 | AI633836 | Hs.195649 | ESTs | 4.3 |
| | 402364 | AV653231 | | CCAAT/enhancer binding protein (C/EBP), | 4.3 |
| | 426471 | M22440 | Hs.170009 | transforming growth factor, alpha | 4.2 |
| 80 | 419386 | AA236867 | | ESTs, Weakly similar to I38022 hypotheti | 4.2 |
| | 441408 | AI733249 | Hs.126897 | ESTs | 4.2 |
| | 419631 | AW188117 | Hs.303154 | popeye protein 3 | 4.2 |
| | 409231 | AA446644 | Hs.692 | GA733-2 antigen; epithelial glycoprotein | 4.2 |
| | 448958 | AB020651 | Hs.22653 | KIAA0844 protein | 4.2 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| 5 | 421878 | AA299652 | Hs.111496 | Homo sapiens cDNA FLJ11643 fis, clone HE | 4.2 |
| | 422278 | AF072873 | Hs.114218 | frizzled (Drosophila) homolog 6 | 4.2 |
| | 459053 | AI807052 | Hs.210361 | ESTs | 4.1 |
| | 450600 | BE079478 | Hs.24880 | ESTs | 4.1 |
| | 415839 | R40611 | Hs.94694 | ESTs | 4.1 |
| 10 | 450374 | AA397540 | Hs.60293 | Homo sapiens clone 122482 unknown mRNA | 4.1 |
| | 422270 | AF114494 | Hs.114062 | protein tyrosine phosphatase-like (prol) | 4.1 |
| | 405674 | | | NM_022775:Homo sapiens hypothetical prot | 4.1 |
| | 453906 | AW444952 | Hs.257054 | ESTs | 4.1 |
| | 419318 | AW969742 | Hs.291005 | ESTs | 4.1 |
| 15 | 456382 | NM_001126 | Hs.90011 | adenylosuccinate synthase | 4.0 |
| | 435902 | AA701867 | Hs.297726 | ESTs | 4.0 |
| | 449483 | AK001971 | Hs.23607 | hypothetical protein FLJ11109 | 4.0 |
| | 434228 | Z42047 | Hs.283978 | Homo sapiens PRO2751 mRNA, complete cds | 4.0 |
| | 403890 | | | CS002036*gi10241574 emb CAC09416.1 (A | 4.0 |
| 20 | 429470 | AI878901 | Hs.203862 | guanine nucleotide binding protein (G pr | 4.0 |
| | 409856 | AW502082 | | gb:U1-HF-BR0p-ajq-g-04-0-U1.r1 NM_MGC_5 | 4.0 |
| | 443682 | AI383061 | Hs.47248 | ESTs, Highly similar to similar to Cdc14 | 4.0 |
| | 420230 | AL034344 | Hs.284186 | forkhead box C1 | 4.0 |
| | 410509 | AW840743 | | gb:QV1-CN0002-080300-102-f07 CN0002 Homo | 4.0 |
| 25 | 428414 | AL049980 | Hs.184216 | DKFZP564C152 protein | 3.9 |
| | 400138 | | | Eos Control | 3.9 |
| | 451522 | BE565817 | Hs.26498 | hypothetical protein FLJ21657 | 3.9 |
| | 436521 | AW203986 | Hs.213003 | ESTs | 3.9 |
| | 401507 | | | C15000810*gi11131272 sp P79331 ATS2_BO | 3.9 |
| 30 | 449785 | AI225235 | Hs.288300 | hypothetical protein FLJ23231 | 3.9 |
| | 434815 | AF155582 | Hs.46744 | core1 UDP-galactose-4-epimerase | 3.9 |
| | 411906 | AW875765 | | gb:QV2-PT0012-020500-186-a08 PT0012 Homo | 3.9 |
| | 440509 | BE410132 | Hs.134202 | ESTs, Weakly similar to T17279 hypotheti | 3.9 |
| | 427061 | AB032971 | Hs.173392 | KIAA1145 protein | 3.9 |
| 35 | 430261 | AA305127 | Hs.237225 | hypothetical protein HT023 | 3.9 |
| | 449658 | AI964033 | Hs.195730 | ESTs, Weakly similar to CTXN RAT CORTEX | 3.9 |
| | 429876 | AB028977 | Hs.225974 | KIAA1054 protein | 3.8 |
| | 410330 | AW023630 | Hs.159425 | ESTs | 3.8 |
| | 431369 | BE184455 | Hs.251754 | secretory leukocyte protease inhibitor (| 3.8 |
| 40 | 437659 | AB007944 | Hs.5737 | KIAA0475 gene product | 3.8 |
| | 438171 | AW976507 | Hs.293515 | ESTs | 3.8 |
| | 418394 | AF132818 | Hs.84728 | Kruppel-like factor 5 (intestinal) | 3.8 |
| | 405586 | | | NM_000299:Homo sapiens plakophilin 1 (ec | 3.8 |
| | 432298 | AL118812 | Hs.274293 | Homo sapiens mRNA; cDNA DKFZp761G1111 (f | 3.8 |
| 45 | 426716 | NM_006379 | Hs.171921 | sema domain, immunoglobulin domain (Ig), | 3.8 |
| | 438202 | AW169287 | Hs.22588 | ESTs | 3.8 |
| | 404606 | | | Target Exon | 3.8 |
| | 425329 | AI961644 | Hs.145444 | Homo sapiens cDNA FLJ11494 fis, clone HE | 3.8 |
| | 407604 | AW191962 | Hs.288061 | collagen, type VIII, alpha 2 | 3.8 |
| 50 | 416498 | U33632 | Hs.79351 | potassium channel, subfamily K, member 1 | 3.7 |
| | 430868 | W93178 | Hs.5232 | HSPC125 protein | 3.7 |
| | 457008 | AA410446 | Hs.112011 | ESTs, Weakly similar to unknown [H.sapie | 3.7 |
| | 458660 | AI299739 | Hs.99601 | hypothetical protein FLJ12553 | 3.7 |
| | 408732 | AL117490 | Hs.47225 | Ras-associated protein Rap1 | 3.7 |
| 55 | 436281 | AW411194 | Hs.85195 | myeloid leukemia factor 1 | 3.7 |
| | 413493 | BE144444 | | gb:MR0-HT0168-141199-002-f09 HT0168 Homo | 3.7 |
| | 418407 | AL044818 | Hs.84928 | nuclear transcription factor Y, beta | 3.7 |
| | 445797 | AI253414 | | gb:aq14f04.x1 Stanley Frontal NS pool 2 | 3.7 |
| | 457121 | AI743770 | Hs.180513 | ESTs, Weakly similar to KIAA0822 protein | 3.6 |
| 60 | 417620 | R02530 | Hs.191198 | ESTs | 3.6 |
| | 421952 | AA300900 | Hs.98849 | ESTs, Moderately similar to AF161511 1 H | 3.6 |
| | 454247 | AJ243950 | Hs.46735 | deafness locus associated putative guani | 3.6 |
| | 431662 | AA513406 | Hs.152307 | ESTs | 3.6 |
| | 426908 | AW815163 | Hs.172851 | arginase, type II | 3.6 |
| 65 | 438519 | AI186033 | Hs.147025 | ESTs, Weakly similar to C57785 zinc fing | 3.6 |
| | 415606 | W70022 | | gb:zd51e10.r1 Soares_fetal_heart_NbHH19W | 3.6 |
| | 444859 | AW449137 | Hs.157487 | ESTs | 3.6 |
| | 414631 | AW970130 | Hs.65406 | ESTs | 3.6 |
| | 428897 | AJ245719 | Hs.194385 | hypothetical protein FLJ20234 | 3.5 |
| 70 | 437073 | AI885608 | Hs.94122 | ESTs | 3.5 |
| | 427287 | NM_014903 | Hs.174188 | KIAA0938 protein | 3.5 |
| | 415927 | AL120168 | Hs.78919 | Kell blood group precursor (McLeod pheno | 3.5 |
| | 450235 | AA007512 | Hs.17538 | ESTs | 3.5 |
| | 447263 | AW965667 | Hs.322406 | hypothetical protein FLJ14494 | 3.5 |
| 75 | 419440 | AB020689 | Hs.90419 | KIAA0882 protein | 3.5 |
| | 427254 | AL121523 | Hs.97774 | ESTs | 3.5 |
| | 434348 | BE393191 | Hs.181795 | putative b,b-carotene-9',10'-dioxygenase | 3.5 |
| | 441264 | AA927170 | Hs.23290 | ESTs | 3.5 |
| | 433629 | R13140 | Hs.13359 | ESTs | 3.5 |
| 80 | 446494 | AA463276 | Hs.288906 | VW Domain-Containing Gene | 3.5 |
| | 441585 | AJ760755 | Hs.202383 | ESTs | 3.5 |
| | 438704 | AI435060 | Hs.32825 | ESTs | 3.5 |
| | 445279 | R41900 | Hs.22245 | ESTs | 3.4 |
| | 415114 | D60468 | Hs.94181 | ESTs | 3.4 |
| | 449561 | AI022240 | Hs.17924 | ESTs, Moderately similar to ALU1_HUMAN A | 3.4 |
| | 452420 | BE564871 | Hs.29463 | centrin, EF-hand protein, 3 (CDC31 yeast | 3.4 |
| | 416517 | AA775987 | Hs.79357 | proteasome (prosome, macropain) 26S subu | 3.4 |

| | | | | | |
|----|--------|---------------|-----------|--|-----|
| | 441134 | W29092 | Hs.346950 | cellular retinoic acid-binding protein 1 | 3.4 |
| | 427176 | AW381569 | Hs.40334 | ESTs | 3.4 |
| | 415668 | AW957684 | Hs.306814 | hypothetical protein FLJ21889 | 3.4 |
| | 450928 | AJ744417 | | gb:tr10h12.x1 NCI_CGAP_Ov23 Homo sapiens | 3.4 |
| 5 | 457012 | R41480 | Hs.302754 | ESTs | 3.3 |
| | 405354 | | | CX000321:gij6671579[ref]NP_031518.1 ari | 3.3 |
| | 408855 | T83061 | Hs.319946 | Homo sapiens mRNA for KIAA1727 protein, | 3.3 |
| | 418525 | AW450369 | Hs.86937 | ESTs | 3.3 |
| | 420174 | AJ824144 | Hs.23912 | ESTs | 3.3 |
| 10 | 437124 | AA554458 | Hs.279860 | KIAA0666 protein | 3.3 |
| | 419211 | BE270817 | Hs.37617 | ESTs, Weakly similar to A53933 myosin I | 3.3 |
| | 424335 | AW021508 | Hs.28170 | ESTs | 3.3 |
| | 453344 | BE349075 | Hs.44571 | ESTs | 3.3 |
| 15 | 428065 | AJ634046 | Hs.157313 | ESTs | 3.3 |
| | 417248 | AA329449 | Hs.247302 | twisted gastrulation | 3.3 |
| | 429415 | NM_002593 | Hs.202097 | procollagen C-endopeptidase enhancer | 3.3 |
| | 411393 | AW797437 | Hs.69771 | B-factor, perlecan | 3.3 |
| | 406976 | M60299 | | gb:Human alpha-1 collagen type II gene, | 3.3 |
| | 441071 | D79550 | Hs.7149 | Homo sapiens cDNA: FLJ21950 fis, clone H | 3.3 |
| 20 | 414327 | BE408145 | Hs.185254 | ESTs, Weakly similar to T24435 hypotheti | 3.3 |
| | 433703 | AA210863 | Hs.3532 | nemo-like kinase | 3.3 |
| | 418880 | N87353 | Hs.89421 | CBF1 interacting corepressor | 3.3 |
| | 445947 | AW612084 | Hs.298494 | ESTs | 3.3 |
| 25 | 437334 | AL353947 | Hs.283760 | hypothetical protein DKFZp761N1814 | 3.3 |
| | 434795 | BE620794 | Hs.4147 | translocating chain-associating membrane | 3.2 |
| | 400127 | | | Eos Control | 3.2 |
| | 414602 | AW630088 | Hs.76550 | Homo sapiens mRNA: cDNA DKFZp564B1264 (f | 3.2 |
| | 402429 | | | Target Exon | 3.2 |
| 30 | 428595 | AI355647 | Hs.189999 | purinergic receptor (family A group 5) | 3.2 |
| | 427699 | AW965076 | Hs.180378 | hypothetical protein 669 | 3.2 |
| | 403442 | | | Target Exon | 3.2 |
| | 419272 | AA663904 | Hs.89862 | TNFRSF1A-associated via death domain | 3.2 |
| | 456614 | AV653110 | Hs.106650 | hypothetical protein FLJ20533 | 3.2 |
| 35 | 407581 | R48402 | Hs.173508 | P3ECSL | 3.2 |
| | 412633 | AF001691 | Hs.74304 | periplakin | 3.2 |
| | 433328 | AW298159 | Hs.23644 | ESTs, Weakly similar to S65824 reverse t | 3.2 |
| | 449294 | AJ651786 | Hs.195045 | ESTs | 3.1 |
| | 442799 | AJ564739 | Hs.68505 | ESTs | 3.1 |
| 40 | 434045 | AJ065133 | Hs.152316 | hypothetical protein PRO0971 | 3.1 |
| | 409403 | AA668224 | Hs.6634 | Homo sapiens cDNA: FLJ22547 fis, clone H | 3.1 |
| | 420033 | D59502 | Hs.292590 | ESTs | 3.1 |
| | 422137 | AJ236885 | Hs.112180 | zinc finger protein 148 (pH2-52) | 3.1 |
| | 444760 | AJ796296 | Hs.208062 | ESTs | 3.1 |
| 45 | 403488 | | | ENSP00000201948:KARYOPHERIN BETA2B HOMOL | 3.1 |
| | 411359 | H86088 | Hs.22635 | ESTs | 3.1 |
| | 443037 | AW500305 | Hs.8906 | syntaxin 7 | 3.1 |
| | 407127 | R45970 | Hs.236349 | EST | 3.1 |
| | 416851 | AW963951 | Hs.85618 | ESTs | 3.1 |
| 50 | 416838 | D84109 | Hs.80248 | RNA-binding protein gene with multiple s | 3.1 |
| | 443030 | R68048 | Hs.9238 | hypothetical protein FLJ23516 | 3.1 |
| | 410389 | AW954049 | Hs.8177 | ESTs, Weakly similar to PIHUB6 salivary | 3.1 |
| | 459399 | BE407712 | Hs.153998 | creatine kinase, mitochondrial 1 (ubiqui | 3.1 |
| | 433582 | BE548749 | Hs.148016 | ESTs | 3.1 |
| 55 | 431128 | AJ203545 | Hs.296169 | S-phase response (cyclin-related) | 3.1 |
| | 420411 | AJ581085 | Hs.24678 | sphingosine-1-phosphatase | 3.1 |
| | 459584 | AJ910884 | Hs.346429 | ESTs | 3.1 |
| | 449883 | AJ004464 | Hs.344156 | gb:ot56e06.s1 Soares_testis_NHT Homo sap | 3.1 |
| | 445320 | AA503887 | Hs.167011 | Homo sapiens cDNA: FLJ21362 fis, clone C | 3.1 |
| 60 | 410786 | AW803340 | | gb:IL2-UM0079-090300-050-D02 UM0079 Homo | 3.1 |
| | 418207 | C14685 | Hs.34772 | ESTs | 3.0 |
| | 420521 | AJ915734 | Hs.87298 | ESTs | 3.0 |
| | 425890 | H24530 | Hs.273294 | hypothetical protein FLJ20069 | 3.0 |
| | 416749 | AW068550.comp | Hs.79732 | fibulin 1 | 3.0 |
| 65 | 412258 | AA376768 | Hs.324841 | hypothetical protein FLJ22622 | 3.0 |
| | 407173 | T64349 | | gb:yc10d08.s1 Stratagene lung (937210) H | 3.0 |
| | 415672 | N53097 | Hs.193579 | ESTs | 3.0 |
| | 448583 | NM_015239 | Hs.21542 | KIAA1035 protein | 3.0 |
| | 429043 | AJ824977 | Hs.145319 | ESTs | 3.0 |
| 70 | 404091 | | | Target Exon | 3.0 |
| | 406085 | | | Target Exon | 3.0 |
| | 438825 | BE327427 | Hs.79953 | ESTs | 3.0 |
| | 457441 | BE467737 | Hs.146125 | ESTs | 3.0 |
| | 403512 | | | C3000579:gij12643308[sp]Q9Y4K1 AIM1_HUM | 3.0 |
| 75 | 416866 | AA297356 | Hs.80324 | serine/threonine protein phosphatase cat | 3.0 |
| | 439877 | H39685 | Hs.250700 | tryptase beta 1 | 3.0 |
| | 441984 | AB037763 | Hs.8059 | synaptotagmin IV | 3.0 |
| | 436765 | AB028952 | Hs.5307 | synaptopodin | 3.0 |
| | 445071 | AJ280246 | Hs.149504 | ESTs | 3.0 |
| 80 | 404333 | | | C7001735:gij7768636[dbj]BAA95483.1 (AB | 3.0 |
| | 422907 | AJ879263 | Hs.77273 | Human glucose transporter pseudogene | 3.0 |
| | 413266 | BE300352 | | gb:600944231F1 NIH_MGC_17 Homo sapiens c | 3.0 |
| | 429393 | AA383024 | Hs.201603 | Homo sapiens mRNA: cDNA DKFZp434D0917 (f | 3.0 |
| | 415337 | Z44881 | Hs.9012 | ESTs, Weakly similar to S26650 DNA-bind | 3.0 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 415044 | AA419108 | Hs.77840 | annexin A4 | 2.9 |
| | 403469 | | | Target Exon | 2.9 |
| | 416928 | AA190573 | Hs.85902 | ESTs, Weakly similar to MCHU calmodulin | 2.9 |
| 5 | 430195 | AW969308 | Hs.188594 | ESTs | 2.9 |
| | 458544 | A631036 | Hs.196843 | ESTs | 2.9 |
| | 440667 | BE076969 | Hs.7337 | hypothetical protein FLJ10936 | 2.9 |
| | 424641 | AB001106 | Hs.151413 | gla maturation factor, beta | 2.9 |
| | 428820 | AA436187 | Hs.172631 | integrin, alpha M (complement component | 2.9 |
| 10 | 405403 | | | Target Exon | 2.9 |
| | 452197 | AW023595 | Hs.232048 | ESTs | 2.9 |
| | 437357 | AL359559 | Hs.331666 | Homo sapiens mRNA; cDNA DKFZp76202215 (f | 2.9 |
| | 423479 | NM_014326 | Hs.129208 | death-associated protein kinase 2 | 2.9 |
| | 404559 | | | Target Exon | 2.9 |
| 15 | 406270 | | | Target Exon | 2.9 |
| | 422190 | H17399 | Hs.11506 | Human clone 23589 mRNA sequence | 2.9 |
| | 431300 | AA502346 | | gb:ne26b03.s1 NCI_CGAP_Co3 Homo sapiens | 2.9 |
| | 420286 | A1796395 | Hs.111377 | ESTs | 2.9 |
| | 422964 | AW439476 | Hs.256895 | ESTs | 2.9 |
| 20 | 431583 | AL042613 | Hs.262476 | S-adenosylmethionine decarboxylase 1 | 2.9 |
| | 428595 | AB037795 | Hs.186547 | KIAA1374 protein | 2.9 |
| | 402198 | | | NM_024323:Homo sapiens hypothetical prot | 2.9 |
| | 416246 | U47413 | Hs.79101 | cyclin G1 | 2.9 |
| | 427593 | AK001132 | Hs.179752 | Homo sapiens cDNA FLJ10270 fis, clone HE | 2.9 |
| 25 | 446351 | AW444551 | Hs.35380 | x 001 protein | 2.9 |
| | 440432 | A239637 | Hs.202653 | ESTs, Weakly similar to T14267 Xln prote | 2.9 |
| | 446525 | AW967069 | Hs.211556 | hypothetical protein MGC5487 | 2.8 |
| | 400965 | | | C11002190:gij12737279[ref]XP_012163.1j | 2.8 |
| | 436489 | AJ272269 | Hs.121429 | zinc-binding protein Rboc728 | 2.8 |
| 30 | 458793 | N80159 | Hs.121849 | microtubule-associated proteins 1A/18 fi | 2.8 |
| | 406810 | U82275 | Hs.94498 | leukocyte immunoglobulin-like receptor, | 2.8 |
| | 445577 | N40696 | Hs.137064 | cytoplasmic polyadenylation element bind | 2.8 |
| | 428874 | W32133 | Hs.194366 | transferrin (prealbumin, amyloidosis 1 | 2.8 |
| | 418745 | AW882645 | Hs.88044 | sprouty (Drosophila) homolog 1 (antagoni | 2.8 |
| 35 | 433095 | AK001092 | Hs.302480 | Homo sapiens cDNA FLJ10230 fis, clone HE | 2.8 |
| | 425580 | L11144 | Hs.1907 | galanin | 2.8 |
| | 416233 | AA176633 | | gb:zp13g01.s1 Stratagene fetal retina 93 | 2.8 |
| | 438219 | AF16151 | Hs.257194 | ESTs | 2.8 |
| 40 | 404661 | | | C9000306:gij12737280[ref]XP_006682.2j k | 2.8 |
| | 435836 | AW292532 | Hs.343667 | homolog of yeast long chain polyunsatura | 2.8 |
| | 423665 | BE167153 | Hs.24380 | ESTs | 2.8 |
| | 430320 | BE245290 | Hs.239218 | uncharacterized hypothalamus protein HCD | 2.8 |
| | 401783 | | | NM_003771*:Homo sapiens keratin, hair, a | 2.8 |
| | 423837 | AW937063 | Hs.275150 | gb:PM3-DT0037-231299-001-g11 DT0037 Homo | 2.8 |
| 45 | 447271 | AL041747 | Hs.170261 | ESTs | 2.8 |
| | 438913 | AI380429 | Hs.172445 | ESTs | 2.8 |
| | 441962 | AW972542 | Hs.289008 | Homo sapiens cDNA: FLJ21814 fis, clone H | 2.8 |
| | 444385 | BE278964 | Hs.11085 | CGI-111 protein | 2.8 |
| | 432278 | AL137506 | Hs.274256 | hypothetical protein FLJ23563 | 2.8 |
| 50 | 415666 | H72693 | | gb:yu03c11.r1 Soares fetal liver spleen | 2.8 |
| | 452345 | AA293279 | Hs.29173 | hypothetical protein FLJ20515 | 2.8 |
| | 445898 | AF070623 | Hs.13423 | Homo sapiens clone 24468 mRNA sequence | 2.8 |
| | 439556 | AI623752 | Hs.163603 | ESTs | 2.8 |
| | 405474 | | | NM_001093*:Homo sapiens acetyl-Coenzyme | 2.8 |
| 55 | 426208 | AI370379 | Hs.132216 | ESTs | 2.8 |
| | 419461 | AI452601 | Hs.288869 | nuclear receptor subfamily 2, group F, m | 2.8 |
| | 428501 | AL041162 | Hs.98587 | ESTs | 2.8 |
| | 413427 | U31120 | Hs.845 | interleukin 13 | 2.8 |
| | 433109 | N58907 | Hs.162430 | EST | 2.8 |
| 60 | 427974 | BE093023 | Hs.188767 | ESTs | 2.8 |
| | 455040 | AW852286 | | gb:QV0-CT0225-100400-187-d08 CT0225 Homo | 2.8 |
| | 453994 | BE180964 | Hs.165590 | ribosomal protein S13 | 2.8 |
| | 459171 | AW967801 | Hs.64783 | ESTs, Weakly similar to T42705 hypotheti | 2.8 |
| | 404845 | | | C22000163:gij10242166[gb]AAG15318.1jAF2 | 2.8 |
| 65 | 408182 | AA047854 | | gb:z49g04.r1 Soares retina N2b4HR Homo | 2.8 |
| | 427111 | AA351026 | Hs.173594 | serine (or cysteine) proteinase inhibitor | 2.7 |
| | 414541 | BE293116 | Hs.76392 | aldehyde dehydrogenase 1 family, member | 2.7 |
| | 432815 | Z30045 | Hs.293676 | ESTs | 2.7 |
| | 404036 | | | Target Exon | 2.7 |
| 70 | 418157 | W99382 | Hs.283709 | lipopolysaccharide specific response-7 p | 2.7 |
| | 426403 | NM_000361 | Hs.2030 | thrombomodulin | 2.7 |
| | 439659 | AW970780 | Hs.59483 | Homo sapiens cDNA FLJ14471 fis, clone MA | 2.7 |
| | 443932 | AW888222 | Hs.9973 | tensin | 2.7 |
| | 444930 | BE185536 | Hs.301183 | molecule possessing ankyrin repeats indu | 2.7 |
| 75 | 419269 | AA235838 | | gb:zs41b04.s1 Soares_NhHMPu_S1 Homo sapi | 2.7 |
| | 416004 | D11880 | Hs.299254 | Homo sapiens cDNA: FLJ23597 fis, clone L | 2.7 |
| | 430371 | D87466 | Hs.240112 | KIAA0276 protein | 2.7 |
| | 449117 | AW449310 | Hs.210262 | ESTs, Weakly similar to HSS2_HUMAN HEPAR | 2.7 |
| | 451007 | H38108 | Hs.32759 | ESTs | 2.7 |
| 80 | 421202 | AF193339 | Hs.102506 | eukaryotic translation initiation factor | 2.7 |
| | 406308 | | | NM_025192:Homo sapiens hypothetical prot | 2.7 |
| | 413208 | BE071799 | | gb:RC0-BT0522-071299-011-b10 BT0522 Homo | 2.7 |
| | 421420 | AI024236 | Hs.123296 | ESTs, Weakly similar to PEC1_HUMAN PLATE | 2.7 |
| | 445693 | AW800444 | Hs.76507 | LPS-induced TNF-alpha factor | 2.7 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 452351 | AA025647 | | gb:ze85d01.r1 Soares_fetal_heart_NbHH19W | 2.7 |
| | 410538 | AW753115 | | gb:PM0-CT0248-131099-001-h12 CT0248 Homo | 2.7 |
| | 448072 | AA459306 | Hs.24908 | ESTs | 2.7 |
| 5 | 420912 | AW853156 | Hs.90787 | ESTs | 2.7 |
| | 453830 | AA534286 | Hs.20953 | ESTs | 2.7 |
| | 457791 | AW117431 | Hs.191906 | ESTs | 2.7 |
| | 417735 | AA188175 | Hs.82506 | KIAA1254 protein | 2.7 |
| | 411773 | NM_006799 | Hs.72026 | protease, serine, 21 (testisin) | 2.7 |
| 10 | 417076 | AW973454 | Hs.238442 | ESTs, Moderately similar to ALU7_HUMAN A | 2.7 |
| | 436476 | AA326108 | Hs.33829 | bHLH protein DEC2 | 2.7 |
| | 440945 | AW505345 | Hs.7540 | I-box and leucine-rich repeat protein 3A | 2.7 |
| | 425826 | U97698 | | mucin 6, gastric | 2.7 |
| | 422795 | AB033109 | Hs.120866 | KIAA1283 protein | 2.7 |
| 15 | 433921 | AA618174 | | gb:nq14f01.s1 NCI_CGAP_Thy1 Homo sapiens | 2.7 |
| | 414272 | AI651603 | Hs.46988 | ESTs | 2.7 |
| | 418047 | R37633 | Hs.4847 | ESTs | 2.7 |
| | 421089 | AB037771 | Hs.101799 | KIAA1350 protein | 2.7 |
| | 419763 | AI039691 | Hs.127486 | ESTs | 2.7 |
| 20 | 459265 | AJ003616 | | gb:AJ003616 Selected chromosome 21 cDNA | 2.7 |
| | 410970 | AW812151 | | gb:RC5-ST0178-081099-011-A06 ST0178 Homo | 2.7 |
| | 401925 | N98378 | | sialyltransferase 1 (beta-galactoside al | 2.7 |
| | 418504 | BE159718 | Hs.85335 | Homo sapiens mRNA; cDNA DKFZp564D1462 (I | 2.6 |
| | 433789 | AA220977 | | gb:zr01a08.r1 Stratagene NT2 neuronal pr | 2.6 |
| 25 | 418308 | AA215738 | Hs.182514 | ESTs, Weakly similar to A46010 X-linked | 2.6 |
| | 444618 | AV653785 | Hs.173334 | ELL-RELATED RNA POLYMERASE II, ELONGATIO | 2.6 |
| | 406299 | | | Target Exon | 2.6 |
| | 422963 | M79141 | Hs.13234 | ESTs | 2.6 |
| | 441244 | BE612935 | Hs.184052 | PP1201 protein | 2.6 |
| 30 | 439954 | AL046748 | Hs.6790 | DnaJ (Hsp40) homolog, subfamily B, membe | 2.6 |
| | 405088 | | | Target Exon | 2.6 |
| | 404741 | | | Target Exon | 2.6 |
| | 451927 | AL355687 | Hs.27261 | Homo sapiens mRNA full length insert cDN | 2.6 |
| | 439103 | AF085959 | Hs.38705 | ESTs | 2.6 |
| 35 | 437241 | AL137318 | Hs.306450 | Homo sapiens mRNA; cDNA DKFZp434L171 (fr | 2.6 |
| | 442379 | NM_004613 | Hs.8265 | transglutaminase 2 (C polypeptide, prote | 2.6 |
| | 457394 | M86528 | Hs.266902 | neurotrophin 5 (neurotrophin 4/5) | 2.6 |
| | 427229 | AI799751 | Hs.5635 | ESTs | 2.6 |
| | 414630 | BE410857 | Hs.16064 | gb:601301177F1 NIH_MGC_21 Homo sapiens c | 2.6 |
| 40 | 406744 | AA554082 | Hs.279860 | tumor protein, translationally-controlled | 2.6 |
| | 443984 | AI424415 | Hs.143719 | ESTs | 2.6 |
| | 421221 | AW276914 | Hs.326714 | Homo sapiens clone IMAGE:713177, mRNA se | 2.6 |
| | 421709 | AA159394 | Hs.107056 | CED-6 protein | 2.6 |
| | 426747 | AA535210 | Hs.171995 | kallikrein 3, (prostate specific antigen | 2.6 |
| 45 | 439480 | AL038511 | Hs.125316 | ESTs, Weakly similar to S33990 finger pr | 2.6 |
| | 419567 | AW339890 | Hs.128187 | ESTs | 2.6 |
| | 421922 | AW295043 | Hs.109590 | genethonin 1 | 2.6 |
| | 421859 | AA356620 | Hs.108947 | KIAA0050 gene product | 2.6 |
| | 431441 | U81961 | Hs.2794 | sodium channel, nonvoltage-gated 1 alpha | 2.6 |
| 50 | 444843 | AA400172 | | gb:zu69e01.r1 Soares_testis_NHT Homo sap | 2.6 |
| | 416729 | U46165 | Hs.1027 | Ras-related associated with diabetes | 2.6 |
| | 439238 | N47305 | Hs.302161 | ESTs | 2.6 |
| | 439183 | AW970600 | Hs.303261 | ESTs | 2.6 |
| | 408739 | W01556 | Hs.238797 | ESTs, Moderately similar to I38022 hypot | 2.6 |
| 55 | 412061 | AA833763 | Hs.330211 | ESTs | 2.6 |
| | 432114 | AL036021 | Hs.8934 | ESTs | 2.6 |
| | 425337 | AA355442 | Hs.169054 | ESTs | 2.6 |
| | 424299 | AK000377 | Hs.82294 | homolog of mouse C2PA | 2.6 |
| | 448871 | BE616709 | Hs.159265 | kruppel-related zinc finger protein hckr | 2.6 |
| 60 | 414516 | AI307802 | Hs.135560 | ESTs, Weakly similar to T43458 hypotheti | 2.6 |
| | 456235 | AA203637 | | gb:zx58b12.r1 Soares_fetal_liver_spleen_ | 2.6 |
| | 410429 | AA310600 | Hs.63657 | peptide:N-glycanase similar to yeast PNG | 2.6 |
| | 449251 | AW151660 | Hs.31444 | ESTs | 2.6 |
| | 436546 | AW023329 | Hs.132743 | ESTs | 2.6 |
| 65 | 450546 | AA010200 | Hs.175551 | ESTs | 2.6 |
| | 437255 | R58970 | Hs.9887 | ESTs | 2.6 |
| | 409041 | AB033025 | Hs.50081 | Hypothetical protein, XP_051860 (KIAA119 | 2.6 |
| | 427983 | M17706 | Hs.2233 | colony stimulating factor 3 (granulocyte | 2.5 |
| | 413341 | H78472 | Hs.191325 | ESTs, Weakly similar to T18967 hypotheti | 2.5 |
| 70 | 423763 | R98203 | Hs.132724 | nuclear transcription factor Y, alpha | 2.5 |
| | 413282 | BE078159 | | gb:CM0-BT0615-140200-175-e06 BT0615 Homo | 2.5 |
| | 415590 | T74068 | Hs.170081 | gb:yc81f07.r1 Soares infant brain 1N1B H | 2.5 |
| | 406215 | | | Target Exon | 2.5 |
| | 453938 | AF082569 | Hs.36794 | D-type cyclin-interacting protein 1 | 2.5 |
| 75 | 424310 | AA338648 | Hs.50334 | testes development-related NYD-SP22 | 2.5 |
| | 442097 | AW015799 | Hs.128474 | ESTs | 2.5 |
| | 456650 | AA620501 | Hs.106773 | ESTs, Weakly similar to T42689 hypotheti | 2.5 |
| | 413231 | D87461 | Hs.75244 | BCL2-like 2 | 2.5 |
| | 457297 | AW968188 | | gb:EST380383 MAGE resequences, MAGJ Homo | 2.5 |
| 80 | 444942 | AW293458 | Hs.283807 | chromosome 11 open reading frame 16 | 2.5 |
| | 425764 | AW996009 | Hs.112572 | Homo sapiens cDNA FLJ14130 fis, clone MA | 2.5 |
| | 435712 | AA694607 | Hs.176956 | ESTs | 2.5 |
| | 436624 | T64297 | | fatty acid binding protein 1, liver | 2.5 |
| | 443155 | R54485 | Hs.23772 | ESTs | 2.5 |

| | | | | | |
|------------|-------------|---------------------------------------|---|--|-----|
| 5 | 425907 | AA365752 | Hs.155965 | ESTs | |
| | 414759 | AW295157 | Hs.47587 | ESTs | 2.5 |
| | 414699 | AI815523 | Hs.76930 | synuclein, alpha (non A4 component of am | 2.5 |
| | 411426 | BE141714 | | gb:QVD-HT0101-061099-032-c04 HT0101 Homo | 2.5 |
| | 404492 | | | C80000677:gi10432400 embjCAC10290.1 (A | 2.5 |
| 10 | 425153 | AW023193 | Hs.27046 | ESTs | 2.5 |
| | 426372 | BE304680 | Hs.169531 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypep | 2.5 |
| | 434803 | AW974640 | Hs.303413 | ESTs | 2.5 |
| | 425694 | U51333 | Hs.159237 | hexokinase 3 (white cell) | 2.5 |
| | 433069 | X76732 | Hs.3164 | nucleobindin 2 | 2.5 |
| 15 | 428054 | AI948688 | Hs.266619 | ESTs | 2.5 |
| | 424823 | NM_006226 | Hs.153322 | phosphatase C, epsilon | 2.5 |
| | 456972 | AI054347 | Hs.2017 | ribosomal protein L38 | 2.5 |
| | 431405 | AI470895 | Hs.334895 | ribosomal protein L10a | 2.5 |
| | 427982 | NM_016156 | Hs.181326 | KIAA1073 protein | 2.5 |
| 20 | 412831 | AA121352 | Hs.143314 | ESTs | 2.5 |
| | 437114 | AA836641 | Hs.163085 | ESTs | 2.5 |
| | 426157 | AA370977 | Hs.345728 | STAT induced STAT inhibitor 3 | 2.5 |
| | 448786 | BE048842 | Hs.179075 | Homo sapiens cDNA FLJ11881 fs, clone HE | 2.5 |
| | 432251 | AW972983 | Hs.232165 | polycythemia rubra vera 1; cell surface | 2.5 |
| 25 | 449239 | T24653 | Hs.23360 | likely ortholog of yeast ARV1 | 2.5 |
| | 453572 | AA382590 | Hs.46366 | KIAA0948 protein | 2.5 |
| TABLE 23B: | | | | | |
| 30 | Pkey: | Unique Eos probeset identifier number | | | |
| | CAT number: | Gene cluster number | | | |
| | Accession: | Genbank accession numbers | | | |
| 35 | Pkey | CAT Number | Accession | | |
| | 408182 | 104479_1 | AA047854 AA057506 AA053841 | | |
| | 409856 | 1156268_1 | AW502082 AW502979 AW502807 AW501876 | | |
| | 410509 | 1206699_1 | AW840743 AW752404 HA3469 | | |
| | 410538 | 1207341_1 | AW753115 AW753113 R45779 | | |
| 40 | 410786 | 1221063_1 | AW803340 AW803280 AW803275 AW803415 AW803343 AW803422 | | |
| | 410970 | 1228131_1 | AW812151 AW812186 AW812166 | | |
| | 411426 | 1245515_1 | BE141714 AW845993 AW845989 | | |
| | 411906 | 1265204_1 | AW875765 HS0294 AW875444 | | |
| | 412636 | 13165_1 | NM_004415 AL031058 MT7830 BE149760 AW752599 AW848723 AW376697 AW376817 AW376699 AW848371 AW376782 AW848789 AW361413 | | |
| 45 | | | AW849074 AW997139 AW799304 AW799309 BE077020 BE077017 BE185187 AW997196 BE156621 BE179915 BE006561 BE143155 AW890985 | | |
| | | | BE002107 AW103521 AA857316 AW383133 BE011378 AW170253 BE185750 AW866475 BE160433 J05211 BE082576 BE082584 BE004047 | | |
| | | | AW607238 AW377700 AW377699 BE082526 BE082505 BE082507 BE082514 AW178000 AW177933 AJ905935 AW747877 AW748114 BE148516 | | |
| | | | AW265328 AW847678 AW847688 AW365151 AW365148 AW365153 AW365156 AW365175 AW365157 AW365154 AW068840 BE005272 AW365145 | | |
| | | | BE001925 BE182166 BE144243 BE001923 AJ951766 AJ434518 BE184920 BE184933 AJ284090 BE184941 AW804674 BE184924 CD4715 W39488 | | |
| 50 | | | AW995615 BE184948 BE159646 AW606653 AA099891 AA131128 AA337270 AA340777 AW384371 AA852212 RS8704 AW366566 AW364859 | | |
| | | | AA025851 AA025852 AA455100 AA719958 AW352220 AW996245 BE165351 BE073467 AA377127 AW890264 AW609750 AW391912 AW849690 | | |
| | | | T87267 AW853812 AA852213 W74149 BE009090 AA056401 H91011 AW368529 AW390272 C18467 AW674920 N57176 AA026480 AW576767 | | |
| | | | H93284 AA026863 AW177787 AA026654 AW177786 BE092134 BE092137 BE092136 AW177784 AJ022862 BE091653 AW376811 AW848592 | | |
| | | | AA040018 BE185331 BE182164 AA368564 AW951576 T29918 AA131077 W95048 W25458 AW205789 H0899 N29754 W32490 R20904 BE167181 | | |
| 55 | | | BE167165 N84767 H27408 H30146 AI190590 C03378 AI554403 AI205263 AA128470 AI392926 AF139065 AW370813 AW370827 AW798417 | | |
| | | | AW798780 AW798883 AW798569 R33557 AA149190 C03029 AW177783 AA088866 AW370829 AA247685 BE002273 AJ760816 AJ439101 AW879451 | | |
| | | | AI700963 AA451923 AJ340326 AI590975 T48793 AI568096 AI142882 AA039975 AI470146 AA946936 BE067737 BE067786 W19287 AA644381 | | |
| | | | AA702424 AI417612 AI306554 AI568869 AI568892 AW190555 AI571075 AI220573 AA056527 AI471874 AI304772 AW517828 AI915596 AI527383 | | |
| | | | AI270345 AW021347 AW166807 AW105614 AJ346078 AA552300 W95070 AI494069 AI911702 AA149191 AA026864 AI830049 AI887258 AW780435 | | |
| 60 | | | AI910434 AI819984 AI858282 AI078449 AJ025932 AI860584 AI635878 AA026047 AA703232 D12062 AW192085 AA658154 AW514597 AW591892 | | |
| | | | T87181 AA782066 AW243815 AW150038 AW268383 AW004633 AI927207 AA782109 AW473233 AI804485 AW169216 AI572669 AA602182 | | |
| | | | AW015480 AW771865 AI270027 AA961816 AA283207 AJ076962 AI498487 AI348053 AI783914 H44405 AW799918 AA128330 AA515500 AA918281 | | |
| | | | W02156 AI905927 AA022701 W38382 R20795 T77861 AW860878 | | |
| | | | BE071799 BE071804 BE071798 | | |
| 65 | 413208 | 1353610_1 | BE300352 BE299274 BE075351 BE297444 | | |
| | 413256 | 1356260_1 | BE078159 BE078276 BE078163 BE078277 BE078279 BE078158 | | |
| | 413282 | 1358147_1 | BE144444 BE144430 | | |
| | 413493 | 1373555_1 | W70022 R35201 F12763 T74725 H63485 Z45782 H61126 | | |
| | 415606 | 1540470_1 | H72693 R08673 H72694 F20990 R08580 | | |
| 70 | 415666 | 1543492_1 | AA176633 AW961842 AA309418 | | |
| | 416233 | 158010_1 | AA235838 BE180775 | | |
| | 419269 | 183444_1 | AA236867 AA237066 AA354236 AW957759 H08961 | | |
| | 419386 | 184356_1 | U97698 AW815264 AI791966 AJ732669 AA588236 AI521662 AI804760 AI955717 AW292169 AI468227 AI420483 AA603459 AI868225 AI919551 | | |
| | 425826 | 25682_1 | AA502346 BE159863 | | |
| 75 | 431300 | 331217_1 | AA220977 AF091029 AA701227 | | |
| | 433789 | 37421_1 | AA618174 AI114549 R36464 R36465 | | |
| | 433921 | 377350_1 | T64297 AA894931 NM_001443 M10050 AW843109 AI698516 T53219 T48785 T64166 AA706930 R29613 T55913 T56518 T64679 R29666 M10617 | | |
| | 436624 | 4237_5 | AI768596 AA101894 W90338 AI742193 AW752206 AA099433 T53220 AW082135 AW272775 T29562 T55862 AJ343047 AJ345671 T68235 T68121 | | |
| | | | AW842284 | | |
| 80 | 444843 | 62260_1 | AA400172 AA400146 AV651691 | | |
| | 445797 | 650943_1 | AI253414 AJ366014 R34822 | | |
| | 447135 | 70963_1 | T58148 AW516579 AW059603 | | |
| | 449901 | 818599_1 | AI674072 BE268487 | | |
| | 450928 | 851593_1 | AJ744417 R91614 H77365 | | |
| | 452351 | 91233_1 | AA025647 R45716 AW753786 | | |
| | 455040 | 1250028_1 | AW852286 AW851934 AW852096 AW852274 | | |
| | 456235 | 168686_1 | AA203637 AA832266 H67452 | | |
| | 457297 | 313764_1 | AW968188 AA468196 AA468269 AA468298 | | |
| | 459265 | 966590_1 | AJ003616 AJ003654 AJ003617 | | |

TABLE 23C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

| Pkey | Ref | Strand | NL_position |
|--------|---------|--------|---|
| 400965 | 7770576 | Minus | 173043-173564 |
| 401507 | 7534110 | Plus | 71055-71259 |
| 401600 | 4388746 | Minus | 27363-27518,28727-28891,29526-29731 |
| 401783 | 7249190 | Plus | 139369-139827,140509-140591,140834-140990,141496-141657,141757-141882,142063-142283 |
| 401925 | 3892083 | Minus | 138252-138469,140239-140364,140437-140598,141037-141193,141925-142007,142787-143230 |
| 402198 | 8576116 | Plus | 79041-79191 |
| 402364 | 9454515 | Minus | 54983-55240,56507-56785,56982-57365 |
| 402429 | 9796372 | Minus | 57622-57793,59282-59402,59624-59827 |
| 403442 | 7210003 | Plus | 174560-175270 |
| 403469 | 9929739 | Minus | 4831-7707 |
| 403488 | 9966615 | Minus | 12450-12753 |
| 403512 | 7656757 | Minus | 114487-114610 |
| 403890 | 7710561 | Plus | 83165-83350 |
| 404036 | 8567760 | Minus | 65247-67529,112537-114863 |
| 404091 | 7684554 | Minus | 82121-83229 |
| 404333 | 9802821 | Minus | 137948-138024,138111-138300 |
| 404492 | 8123400 | Minus | 138612-138803 |
| 404559 | 8748893 | Minus | 73499-73651,89575-89739 |
| 404606 | 9212936 | Minus | 22310-23269 |
| 404661 | 9797073 | Plus | 33374-33675,33769-34008 |
| 404741 | 8574139 | Plus | 143025-143467 |
| 404845 | 7958980 | Minus | 47174-47326,52928-53146,53312-53602 |
| 405088 | 8072518 | Minus | 115690-117621 |
| 405354 | 2642452 | Plus | 52213-53089 |
| 405403 | 6850244 | Minus | 37491-37670,40951-41031 |
| 405474 | 8439781 | Plus | 172005-172175 |
| 405586 | 5002511 | Plus | 38810-39017 |
| 405670 | 4662655 | Plus | 96543-96870 |
| 405674 | 4589984 | Plus | 68302-68429 |
| 406085 | 9123888 | Plus | 18665-18843 |
| 406215 | 7342161 | Plus | 310-432 |
| 406270 | 7534217 | Plus | 13136-13591 |
| 406299 | 5686278 | Minus | 35655-36119 |
| 406308 | 9211532 | Plus | 358408-358651 |

TABLE 24A: ABOUT 1260 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT TISSUES

Table 24A lists about 1260 genes up-regulated in glioblastoma compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" glioblastoma to "average" normal adult tissues was greater than or equal to 2.5. The "average" glioblastoma level was set to the 75th percentile amongst various glioblastoma tumors. The "average" normal adult tissue level was set to the 85th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of 75th percentile tumor to 85th percentile normal body tissue

| Pkey | ExAccn | UnigenelD | Unigene Title | R1 |
|--------|-----------|-----------|--|------|
| 431917 | D16181 | Hs.2868 | peripheral myelin protein 2 | 75.2 |
| 427343 | A1880044 | Hs.176977 | protein kinase C binding protein 2 | 74.6 |
| 455601 | A1368680 | Hs.816 | SRY (sex determining region Y)-box 2 | 74.2 |
| 428321 | A1699994 | Hs.2868 | peripheral myelin protein 2 | 71.6 |
| 412719 | AW016610 | Hs.129911 | ESTs | 70.7 |
| 449494 | AW237014 | Hs.315369 | Homo sapiens cDNA: FLJ23075 fis, clone L | 66.3 |
| 415817 | U88967 | Hs.78867 | protein tyrosine phosphatase, receptor-l | 64.3 |
| 413472 | BE242870 | Hs.75379 | solute carrier family 1 (glial high affi | 60.1 |
| 456759 | BE259150 | Hs.127792 | delta (Drosophila)-like 3 | 52.3 |
| 435147 | AL133731 | Hs.4774 | Homo sapiens mRNA; cDNA DKFp761C1712 (f | 46.7 |
| 425842 | A1587490 | Hs.159623 | NK-2 (Drosophila) homolog B | 40.1 |
| 412733 | AA984472 | Hs.74554 | KIAA0080 protein | 39.0 |
| 418375 | NM_003081 | Hs.84389 | synaptosomal-associated protein, 25kD | 38.7 |
| 453392 | U23752 | Hs.32964 | SRY (sex determining region Y)-box 11 | 37.2 |
| 423849 | AL157425 | Hs.133315 | Homo sapiens mRNA; cDNA DKFp761J1324 (f | 36.8 |
| 413333 | M74028 | Hs.75297 | fibroblast growth factor 1 (acidic) | 32.8 |
| 416829 | AB013805 | Hs.80220 | catenin (cadherin-associated protein), d | 31.8 |
| 431941 | AK000106 | Hs.272227 | Homo sapiens cDNA FLJ20099 fis, clone CO | 31.8 |
| 436878 | BE465204 | Hs.47448 | ESTs | 31.4 |
| 426325 | D28114 | Hs.169309 | myelin-associated oligodendrocyte basic | 30.9 |
| 425057 | AA826434 | Hs.1619 | achaete-scute complex (Drosophila) homol | 30.4 |
| 446711 | AF169692 | Hs.12450 | protocadherin 9 | 30.2 |
| 439415 | F05538 | Hs.12825 | ESTs | 28.3 |
| 430838 | N46664 | Hs.169395 | hypothetical protein FLJ12015 | 26.9 |
| 429466 | M85835 | Hs.12827 | ESTs | 25.9 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 447004 | AW296968 | Hs.157539 | ESTs | |
| | 424581 | M62062 | Hs.150917 | | 25.3 |
| | 452744 | AI267652 | Hs.30504 | catenin (cadherin-associated protein), a | 24.6 |
| 5 | 441285 | NM_002374 | Hs.167 | Homo sapiens mRNA; cDNA DKFZp434E082 (tr | 24.8 |
| | 453642 | AI370936 | Hs.34074 | microtubule-associated protein 2 | 24.3 |
| | 424140 | Z48051 | Hs.141308 | dipeptidylpeptidase VI | 24.3 |
| | 450133 | AW969769 | Hs.105201 | myelin oligodendrocyte glycoprotein | 24.2 |
| | 408562 | AI436323 | Hs.311141 | ESTs | 24.2 |
| 10 | 448672 | AI955511 | Hs.225106 | Homo sapiens mRNA for KIAA1568 protein, | 23.3 |
| | 435708 | AI362949 | Hs.75169 | ESTs | 22.7 |
| | 407034 | U84540 | | ESTs | 22.0 |
| | 407168 | R45175 | Hs.117183 | gb:Human dystrobrevin isoform DTN-3 (DTN | 21.9 |
| | 431019 | NM_005249 | Hs.2714 | ESTs | 21.7 |
| 15 | 409049 | AI423132 | Hs.146343 | forkhead box G1B | 21.5 |
| | 433896 | AW294729 | Hs.274461 | ESTs | 21.4 |
| | 445041 | T64183 | Hs.282982 | ESTs | 21.1 |
| | 418738 | AW388633 | Hs.6682 | solute carrier | 21.0 |
| | 444378 | R41339 | Hs.12569 | solute carrier family 7, (cationic amino | 20.4 |
| 20 | 411305 | BE241596 | Hs.69547 | ESTs | 20.0 |
| | 437414 | AW894071 | Hs.48448 | myelin basic protein | 19.9 |
| | 441016 | AW138653 | Hs.25845 | hypothetical protein DKFZp547C176 | 19.8 |
| | 440435 | AL042201 | Hs.21273 | ESTs | 19.6 |
| 25 | 438209 | AL120659 | Hs.6111 | transcription factor NYD-sp10 | 18.5 |
| | 452461 | N78223 | Hs.108106 | aryl-hydrocarbon receptor nuclear transl | 18.4 |
| | 409395 | U46745 | Hs.54435 | transcription factor | 18.1 |
| | 417183 | R52089 | Hs.172717 | dystrobrevin, alpha | 18.1 |
| | 409638 | AW450420 | Hs.21335 | ESTs | 18.0 |
| | 428392 | H10233 | Hs.2265 | ESTs | 18.0 |
| 30 | 449611 | AI970394 | Hs.197075 | secretory granule, neuroendocrine protei | 17.0 |
| | 446692 | Z44514 | Hs.156829 | ESTs | 16.9 |
| | 425088 | AA663372 | Hs.169395 | Homo sapiens mRNA for KIAA1763 protein, | 16.9 |
| | 444471 | AB020684 | Hs.11217 | hypothetical protein FLJ12015 | 16.9 |
| | 421659 | NM_014459 | Hs.106511 | KIAA0877 protein | 16.8 |
| 35 | 431725 | X65724 | Hs.2839 | protocadherin 17 | 16.7 |
| | 429276 | AF056085 | Hs.198612 | Norrie disease (pseudoglioma) | 16.6 |
| | 416892 | L24498 | Hs.80409 | G protein-coupled receptor 51 | 16.6 |
| | 441440 | AI807981 | Hs.30495 | growth arrest and DNA-damage-inducible, | 16.5 |
| | 449433 | AI672096 | Hs.9012 | ESTs | 15.7 |
| 40 | 421264 | AL039123 | Hs.103042 | ESTs, Weakly similar to S26650 DNA-bindi | 15.7 |
| | 415910 | U20350 | Hs.78913 | microtubule-associated protein 1B | 15.5 |
| | 413597 | AW302885 | Hs.117183 | chemokine (C-X3-C) receptor 1 | 15.3 |
| | 424945 | AI221919 | Hs.173438 | ESTs | 15.1 |
| | 447414 | D82343 | Hs.18551 | hypothetical protein FLJ10582 | 14.9 |
| 45 | 426269 | H15302 | Hs.168950 | neuroblastoma (nerve tissue) protein | 14.9 |
| | 416857 | AA188775 | Hs.292453 | Homo sapiens mRNA; cDNA DKFZp566A1046 (f | 14.8 |
| | 419721 | NM_001650 | Hs.288650 | ESTs | 14.7 |
| | 411078 | AI222020 | Hs.182364 | aquaporin 4 | 14.6 |
| | 453924 | R49295 | Hs.24886 | CocoaCrisp | 14.4 |
| 50 | 409389 | AB007979 | Hs.301281 | ESTs | 14.4 |
| | 430130 | AL137311 | Hs.234074 | Homo sapiens mRNA, chromosome 1 specific | 14.3 |
| | 410909 | AW898161 | Hs.53112 | Homo sapiens mRNA; cDNA DKFZp761G02121 (| 14.1 |
| | 412266 | N59006 | Hs.26133 | ESTs, Moderately similar to ALU8_HUMAN A | 14.0 |
| | 412986 | X81120 | Hs.75110 | ESTs | 14.0 |
| 55 | 424790 | AL119344 | Hs.13326 | cannabinoid receptor 1 (brain) | 14.0 |
| | 439239 | AI031540 | Hs.235331 | ESTs, Weakly similar to 2004399A chromos | 14.0 |
| | 441497 | R51064 | Hs.23172 | ESTs | 14.0 |
| | 445495 | BE622641 | Hs.38489 | ESTs | 14.0 |
| | 414245 | BE148072 | Hs.75850 | ESTs, Weakly similar to I38022 hypothesi | 14.0 |
| 60 | 429900 | AA460421 | Hs.30875 | WAS protein family, member 1 | 13.7 |
| | 448595 | AB014544 | Hs.21572 | ESTs | 13.6 |
| | 449605 | AW138581 | Hs.198416 | KIAA0644 gene product | 13.6 |
| | 452526 | W38537 | Hs.280740 | ESTs | 13.6 |
| | 420547 | AF155140 | Hs.98738 | hypothetical protein MGC3040 | 13.6 |
| 65 | 441350 | AB020690 | Hs.7782 | gonadotropin-regulated testicular RNA he | 13.3 |
| | 420077 | AW512260 | Hs.87767 | paraneoplastic antigen MA2 | 13.3 |
| | 424120 | T80579 | Hs.290270 | ESTs | 13.2 |
| | 459965 | AW131888 | Hs.172792 | ESTs | 13.2 |
| | 423361 | AW170055 | Hs.47628 | ESTs, Weakly similar to hypothetical pro | 13.2 |
| 70 | 428409 | AW117207 | Hs.98523 | ESTs | 13.1 |
| | 417160 | N76497 | Hs.1787 | ESTs | 12.9 |
| | 451621 | AI879148 | Hs.26770 | proteolipid protein 1 (Pelizaeus-Merzbac | 12.6 |
| | 411379 | AI816344 | Hs.12554 | fatty acid binding protein 7, brain | 12.5 |
| | 436954 | AA740151 | Hs.130425 | ESTs, Weakly similar to NPL4_HUMAN NUCLE | 12.5 |
| 75 | 430691 | C14187 | Hs.103538 | ESTs | 12.4 |
| | 433551 | AI985544 | Hs.12450 | ESTs | 12.4 |
| | 422544 | AB018259 | Hs.118140 | protocadherin 9 | 12.4 |
| | 427540 | R12014 | Hs.20976 | KIAA0716 gene product | 12.2 |
| | 435624 | AF218942 | Hs.24889 | ESTs | 12.2 |
| 80 | 415849 | R20529 | Hs.6806 | formin 2 | 12.1 |
| | 428845 | AL157579 | Hs.153610 | ESTs | 12.1 |
| | 442671 | AI005668 | Hs.134779 | KIAA0751 gene product | 11.9 |
| | 444396 | T65213 | Hs.4257 | EST | 11.9 |
| | 452752 | AW044058 | Hs.33578 | ESTs | 11.8 |
| | | | | KIAA0820 protein | 11.8 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 425523 | AB007948 | Hs.158244 | KIAA0479 protein | 11.8 |
| | 416072 | AL110370 | Hs.79000 | growth associated protein 43 | 11.7 |
| | 440184 | AB002297 | Hs.7022 | dedicator of cyto-kinesis 3 | 11.7 |
| 5 | 428976 | AL037824 | Hs.194695 | ras homolog gene family, member 1 | 11.6 |
| | 444783 | AK001468 | Hs.62180 | anillin (Drosophila Scraps homolog), act | 11.6 |
| | 448299 | AA497044 | Hs.20887 | hypothetical protein FLJ10392 | 11.6 |
| | 414214 | D49958 | Hs.75819 | glycoprotein MGA | 11.5 |
| | 428982 | NM_005097 | Hs.194704 | leucine-rich, glioma inactivated 1 | 11.5 |
| | 405238 | | | | 11.4 |
| 10 | 420362 | U79734 | Hs.97206 | huntingtin interacting protein 1 | 11.4 |
| | 422980 | N46569 | Hs.76722 | CCAAT/enhancer binding protein (C/EBP), | 11.4 |
| | 424918 | R13982 | Hs.169309 | myelin-associated oligodendrocyte basic | 11.4 |
| | 434277 | X77748 | Hs.3786 | glutamate receptor, metabotropic 3 | 11.4 |
| | 451952 | AL120173 | Hs.301663 | ESTs | 11.3 |
| 15 | 408829 | NM_006042 | Hs.48384 | heparan sulfate (glucosamine) 3-O-sulfot | 11.3 |
| | 424278 | AK000723 | Hs.144517 | hypothetical protein FLJ20716 | 11.3 |
| | 429418 | AJ381028 | Hs.118769 | ESTs | 11.3 |
| | 429918 | AW873986 | Hs.119383 | ESTs | 11.3 |
| | 443912 | R37257 | Hs.184780 | ESTs | 11.3 |
| 20 | 448743 | AB032962 | Hs.21896 | KIAA1136 protein | 11.3 |
| | 420092 | AA814043 | Hs.88045 | ESTs | 11.2 |
| | 408081 | AW451597 | Hs.167409 | ESTs | 11.2 |
| | 411642 | NM_014932 | Hs.71132 | neurotigin 1 | 10.9 |
| | 415170 | R44386 | Hs.164578 | ESTs | 10.9 |
| 25 | 426320 | W47595 | Hs.169300 | transforming growth factor, beta 2 | 10.8 |
| | 450568 | AL050078 | Hs.25159 | Homo sapiens cDNA FLJ10784 fis, clone NT | 10.8 |
| | 425799 | T08133 | Hs.182906 | Homo sapiens mRNA for KIAA1872 protein, | 10.8 |
| | 423853 | AB011537 | Hs.133466 | slit (Drosophila) homolog 1 | 10.7 |
| | 400293 | N51002 | Hs.306480 | Homo sapiens mRNA; cDNA DKFZp761E2112 (f | 10.7 |
| 30 | 447773 | AJ423930 | Hs.36790 | ESTs, Weakly similar to putative p150 [H | 10.7 |
| | 448321 | NM_005883 | Hs.20912 | adenomatous polyposis coli like | 10.5 |
| | 448533 | AL119710 | Hs.21365 | nucleosome assembly protein 1-like 3 | 10.5 |
| | 440684 | AJ253123 | Hs.127356 | ESTs, Highly similar to S21424 nestin [H | 10.3 |
| | 444017 | U04840 | Hs.214 | neuro-oncological ventral antigen 1 | 10.3 |
| 35 | 438380 | T06430 | Hs.6194 | chondroitin sulfate proteoglycan BEHAB/b | 10.3 |
| | 440471 | AA886146 | Hs.307944 | ESTs | 10.2 |
| | 413063 | AL035737 | Hs.75184 | chitinase 3-like 1 (cartilage glycoprote | 10.1 |
| | 439978 | BE139460 | Hs.124673 | Homo sapiens cDNA FLJ11477 fis, clone HE | 10.1 |
| | 448902 | Z45988 | Hs.22543 | Homo sapiens mRNA; cDNA DKFZp761I1912 (f | 10.1 |
| 40 | 424932 | R14070 | Hs.315369 | Homo sapiens cDNA: FLJ23075 fis, clone L | 9.9 |
| | 431721 | AB032996 | Hs.268044 | KIAA1170 protein | 9.9 |
| | 419088 | AJ538323 | Hs.52620 | integrin, beta 8 | 9.8 |
| | 420602 | AF060877 | Hs.99236 | regulator of G-protein signalling 20 | 9.8 |
| | 436511 | AA721252 | Hs.291502 | ESTs | 9.8 |
| 45 | 414696 | AF002020 | Hs.76918 | Niemann-Pick disease, type C1 | 9.7 |
| | 449539 | W80363 | Hs.58446 | ESTs | 9.7 |
| | 412959 | D87458 | Hs.75090 | KIAA0282 protein | 9.6 |
| | 412811 | H06382 | Hs.21400 | ESTs | 9.6 |
| | 449300 | AJ656959 | Hs.222165 | ESTs | 9.6 |
| 50 | 426344 | H41821 | Hs.322469 | transcriptional activator of the c-fos p | 9.5 |
| | 419271 | N34901 | Hs.238532 | ESTs | 9.5 |
| | 419078 | M93119 | Hs.89584 | insulinoma-associated 1 | 9.4 |
| | 451516 | AJ800515 | Hs.12024 | ESTs | 9.4 |
| 55 | 422656 | AJ870435 | Hs.1569 | UIM homeobox protein 2 | 9.3 |
| | 449318 | AW236021 | Hs.78531 | Homo sapiens, Similar to RIKEN cDNA 5730 | 9.3 |
| | 414175 | AJ308876 | Hs.103849 | hypothetical protein DKFZp761D112 | 9.3 |
| | 415279 | F04237 | Hs.1447 | glial fibrillary acidic protein | 9.2 |
| | 428784 | Y12851 | Hs.193470 | purinergic receptor P2X, ligand-gated io | 9.2 |
| | 429903 | AL134197 | Hs.93597 | cyclin-dependent kinase 5, regulatory su | 9.2 |
| 60 | 424641 | AB001106 | Hs.151413 | glia maturation factor, beta | 9.1 |
| | 417435 | NM_005181 | Hs.82129 | carbonic anhydrase III, muscle specific | 9.1 |
| | 449448 | D60730 | Hs.57471 | ESTs | 9.1 |
| | 408508 | AJ806109 | Hs.135736 | KIAA1580 protein | 9.0 |
| | 452785 | AL359942 | Hs.296434 | erythroid differentiation and denucleati | 9.0 |
| 65 | 448986 | H42169 | Hs.18653 | hypothetical protein FLJ14627 | 8.9 |
| | 447072 | D61594 | Hs.17279 | tyrosylprotein sulfotransferase 1 | 8.9 |
| | 433800 | AJ034361 | Hs.135150 | lung type-I cell membrane-associated gly | 8.9 |
| | 408926 | AF217525 | Hs.49002 | Down syndrome cell adhesion molecule | 8.8 |
| | 449625 | NM_014253 | Hs.23796 | odx (odd Oz/ten-m, Drosophila) homolog 1 | 8.8 |
| 70 | 400292 | AA250737 | Hs.72472 | ESTs | 8.7 |
| | 417404 | NM_007350 | Hs.82101 | pleckstrin homology-like domain, family | 8.7 |
| | 420345 | AW295230 | Hs.25231 | ESTs | 8.7 |
| | 429927 | NM_001115 | Hs.2522 | adenylate cyclase 8 (brain) | 8.7 |
| | 437528 | N59646 | Hs.169745 | crumbs (Drosophila) homolog 1 | 8.7 |
| 75 | 440152 | AB002376 | Hs.7006 | KIAA0378 protein | 8.7 |
| | 451099 | R52795 | Hs.25954 | interleukin 13 receptor, alpha 2 | 8.6 |
| | 400780 | | | | 8.6 |
| | 434891 | AA814309 | Hs.123583 | ESTs | 8.6 |
| | 449277 | AA001064 | Hs.172976 | ESTs | 8.6 |
| 80 | 415709 | AA649850 | Hs.278558 | ESTs | 8.5 |
| | 439947 | AB006627 | Hs.6788 | astrotactin | 8.5 |
| | 447197 | R36075 | | gb:yh88b01.s1 Soares placenta Nb2HP Homo | 8.5 |
| | 433042 | AW193534 | Hs.281895 | Homo sapiens cDNA FLJ11660 fis, clone HE | 8.4 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 416370 | N90470 | Hs.203697 | ESTs, Weakly similar to I38022 hypothe | 8.4 |
| | 452786 | R61362 | Hs.106642 | ESTs, Weakly similar to T09052 hypothe | 8.4 |
| | 415796 | R87548 | Hs.78854 | ATPase, Na ⁺ /K ⁺ transporting, beta 2 poly | 8.3 |
| 5 | 426271 | AF026547 | Hs.169047 | chondroitin sulfate proteoglycan 3 (neur | 8.3 |
| | 408947 | AL080093 | Hs.49117 | Homo sapiens mRNA; cDNA DKFZp564N1662 (I | 8.3 |
| | 419863 | AW952691 | Hs.93485 | Homo sapiens mRNA; cDNA DKFZp761D191 (fr | 8.3 |
| | 433447 | U29195 | Hs.3281 | neuronal pentraxin II | 8.3 |
| | 431467 | N71831 | Hs.256398 | Homo sapiens mRNA; cDNA DKFZp434E0528 (I | 8.3 |
| 10 | 409327 | L41162 | Hs.53563 | collagen, type IX, alpha 3 | 8.3 |
| | 414300 | AJ304870 | Hs.188680 | ESTs | 8.2 |
| | 407728 | AW071502 | Hs.175931 | ESTs | 8.2 |
| | 422798 | R92347 | Hs.34574 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 8.2 |
| | 419704 | AA429104 | Hs.45057 | ESTs | 8.2 |
| 15 | 429007 | D80642 | | gb:HUM092E098 Human fetal brain (TFujiwa | 8.1 |
| | 442710 | AJ015631 | Hs.23210 | ESTs | 8.1 |
| | 425048 | H05468 | Hs.164502 | ESTs | 8.1 |
| | 429149 | AW193360 | Hs.197962 | ESTs, Weakly similar to I38022 hypothe | 8.0 |
| | 445740 | T78281 | Hs.13226 | Homo sapiens clone 25181 mRNA sequence | 8.0 |
| 20 | 418771 | AA807881 | Hs.25329 | ESTs | 7.9 |
| | 422728 | AW937826 | Hs.103262 | ESTs, Weakly similar to ZN91_HUMAN ZINC | 7.9 |
| | 425984 | AW836277 | Hs.165636 | hypothetical protein DKFZp761C07121 | 7.9 |
| | 448408 | AA322866 | Hs.21107 | neurodigin | 7.9 |
| | 455364 | H72176 | Hs.4273 | hypothetical protein FLJ13159 | 7.9 |
| 25 | 446619 | AU076643 | Hs.313 | secreted phosphoprotein 1 (osteopontin, | 7.9 |
| | 435501 | AW051819 | Hs.129908 | KIAA0591 protein | 7.8 |
| | 423600 | AJ633559 | Hs.310359 | ESTs | 7.8 |
| | 450625 | AW970107 | | gb:EST382188 MAGE resequences, MAGK Homo | 7.8 |
| | 415314 | N88802 | Hs.5422 | glycoprotein M6B | 7.7 |
| 30 | 420036 | R60336 | Hs.52792 | Homo sapiens mRNA; cDNA DKFZp586I1823 (I | 7.7 |
| | 427687 | AW003867 | Hs.1570 | histamine receptor H1 | 7.7 |
| | 449328 | AJ962493 | Hs.197647 | ESTs | 7.7 |
| | 419249 | X14767 | Hs.89768 | gamma-aminobutyric acid (GABA) A recepto | 7.7 |
| | 407896 | D76435 | Hs.41154 | Zic family member 1 (odd-paired Drosophi | 7.7 |
| 35 | 419103 | Z40229 | Hs.96423 | hypothetical protein FLJ23033 | 7.6 |
| | 438779 | NM_003787 | Hs.6414 | nucleolar protein 4 | 7.6 |
| | 433532 | AW975367 | | gb:EST387475 MAGE resequences, MAGN Homo | 7.6 |
| | 448555 | AJ536697 | Hs.159863 | ESTs | 7.5 |
| | 439662 | H97552 | Hs.269060 | ESTs | 7.5 |
| 40 | 448543 | AW897741 | Hs.21380 | Homo sapiens mRNA; cDNA DKFZp586P1124 (I | 7.5 |
| | 410099 | AA081630 | Hs.169387 | KIAA0036 gene product | 7.5 |
| | 431592 | R69016 | Hs.213194 | hypothetical protein MGC10895 | 7.4 |
| | 409731 | AA125985 | Hs.56145 | thymosin, beta, identified in neuroblast | 7.4 |
| | 405819 | | | | 7.4 |
| 45 | 407886 | AW969688 | Hs.100826 | ESTs | 7.4 |
| | 437416 | AL359605 | Hs.283851 | Homo sapiens mRNA; cDNA DKFZp547G036 (fr | 7.4 |
| | 437698 | R61837 | Hs.7990 | ESTs, Moderately similar to I84505 calci | 7.4 |
| | 408604 | D51408 | Hs.21925 | ESTs | 7.4 |
| | 418506 | AA084248 | Hs.85339 | G protein-coupled receptor 39 | 7.3 |
| 50 | 447499 | AW262580 | Hs.147674 | protocadherin beta 16 | 7.3 |
| | 454036 | AA374756 | Hs.93560 | Homo sapiens mRNA for KIAA1771 protein, | 7.3 |
| | 409746 | NM_004794 | Hs.56294 | RA833A, member RAS oncogene family | 7.2 |
| | 410037 | AB020725 | Hs.58009 | KIAA0918 protein | 7.2 |
| | 419318 | AW969742 | Hs.291005 | ESTs | 7.2 |
| 55 | 424051 | AL110203 | Hs.138411 | Homo sapiens mRNA; cDNA DKFZp586J1922 (I | 7.2 |
| | 442026 | AJ243749 | Hs.8074 | brain-specific angiogenesis inhibitor 3 | 7.2 |
| | 448243 | AW369771 | Hs.52620 | integrin, beta 8 | 7.2 |
| | 436281 | AW411194 | Hs.85195 | myeloid leukemia factor 1 | 7.2 |
| | 426429 | X73114 | Hs.169849 | myosin-binding protein C, slow-type | 7.2 |
| 60 | 407182 | AA312551 | Hs.230157 | ESTs | 7.1 |
| | 415293 | R49462 | Hs.106541 | ESTs | 7.1 |
| | 422764 | AJ767727 | Hs.47522 | ESTs | 7.1 |
| | 451592 | AJ805416 | Hs.213897 | ESTs | 7.1 |
| | 429469 | M64590 | Hs.27 | glycine dehydrogenase (decarboxylating; | 7.0 |
| 65 | 415734 | NM_014747 | Hs.78748 | KIAA0237 gene product | 7.0 |
| | 434149 | Z43829 | Hs.19574 | hypothetical protein MGCS469 | 7.0 |
| | 436726 | AA324975 | Hs.128993 | ESTs, Weakly similar to T00079 hypothe | 7.0 |
| | 417632 | R20855 | Hs.5422 | glycoprotein M6B | 7.0 |
| | 422421 | AA325138 | Hs.235873 | hypothetical protein FLJ22672 | 6.9 |
| 70 | 435267 | N23797 | Hs.110114 | ESTs | 6.9 |
| | 437117 | AL049256 | Hs.122593 | ESTs | 6.9 |
| | 445523 | Z30118 | Hs.293788 | ESTs, Moderately similar to unnamed prot | 6.9 |
| | 445900 | AF070526 | Hs.13429 | Homo sapiens clone 24787 mRNA sequence | 6.9 |
| | 445745 | AB007924 | Hs.13245 | KIAA0455 gene product | 6.9 |
| 75 | 424085 | NM_002914 | Hs.139226 | replication factor C (activator 1) 2 (40 | 6.9 |
| | 428588 | F12101 | Hs.185701 | Homo sapiens mRNA full length insert cDN | 6.8 |
| | 421723 | AA620400 | Hs.300717 | sodium channel, voltage-gated, type III, | 6.8 |
| | 447342 | AJ199268 | Hs.19322 | Homo sapiens, Similar to RIKEN cDNA 2010 | 6.7 |
| | 443297 | AJ049864 | Hs.133029 | ESTs | 6.7 |
| 80 | 443992 | AW022228 | Hs.322922 | ESTs | 6.7 |
| | 453096 | AW294631 | Hs.11325 | ESTs | 6.7 |
| | 453857 | AL080235 | Hs.35861 | DKFZP586E1621 protein | 6.7 |
| | 443761 | AJ525743 | Hs.160603 | ESTs | 6.6 |
| | 429609 | AF002246 | Hs.210883 | cell adhesion molecule with homology to | 6.6 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 435056 | AW023337 | Hs.5422 | glycoprotein M6B | 6.5 |
| | 453431 | AF094754 | Hs.32973 | glycine receptor, beta | 6.5 |
| | 444190 | AJ878918 | Hs.10526 | cysteine and glycine-rich protein 2 | 6.5 |
| 5 | 418110 | R43523 | Hs.217754 | hypothetical protein FLJ22202 | 6.5 |
| | 413588 | M81883 | Hs.324784 | glutamate decarboxylase 1 (brain, 67kD) | 6.5 |
| | 420805 | L10333 | Hs.99947 | reticulin 1 | 6.4 |
| | 429125 | AA446854 | Hs.271004 | ESTs, Weakly similar to I38022 hypotheti | 6.4 |
| | 435256 | AF193766 | Hs.13872 | cytokine-like protein C17 | 6.4 |
| 10 | 407866 | AW088232 | Hs.89506 | paired box gene 6 (aniridia, keratitis) | 6.3 |
| | 440700 | AW952281 | Hs.296184 | guanine nucleotide binding protein (G pr | 6.3 |
| | 427701 | AA411101 | Hs.243886 | nuclear autoantigenic sperm protein (his | 6.3 |
| | 422949 | AA319435 | | gb:EST21657 Adrenal gland tumor Homo sap | 6.2 |
| | 445102 | AW204610 | Hs.22270 | ESTs | 6.2 |
| 15 | 452401 | NM_007115 | Hs.29352 | tumor necrosis factor, alpha-induced pro | 6.2 |
| | 435538 | AB011540 | Hs.4930 | low density lipoprotein receptor-related | 6.2 |
| | 410102 | AW248508 | Hs.279727 | Homo sapiens cDNA FLJ14035 fis, clone HE | 6.2 |
| | 416871 | H98716 | | gb:yr13d08.s1 Soares melanocyte 2NbHM Ho | 6.1 |
| | 416702 | AA186428 | Hs.85591 | ESTs | 6.1 |
| 20 | 419347 | C15944 | Hs.90005 | superiorocervical ganglia, neural specifi | 6.1 |
| | 424997 | AL138167 | Hs.96920 | ESTs | 6.1 |
| | 438660 | U95740 | Hs.6349 | Homo sapiens, clone IMAGE:3010666, mRNA, | 6.1 |
| | 453649 | Y07494 | Hs.34114 | ATPase, Na ⁺ /K ⁺ transporting, alpha 2 (-) | 6.1 |
| | 449444 | AW818436 | Hs.23590 | solute carrier family 16 (monocarboxylic | 6.1 |
| 25 | 414117 | W88559 | Hs.1787 | proteolipid protein 1 (Pelizaeus-Merzbac | 6.0 |
| | 425517 | AF121179 | | gb:AF121179 Homo sapiens liver (Chang L- | 6.0 |
| | 427457 | AW779105 | Hs.164682 | ESTs | 6.0 |
| | 437034 | AA742643 | | gb:my91c01.s1 NCI_CGAP_GCB1 Homo sapiens | 6.0 |
| | 444170 | AW613879 | Hs.102408 | ESTs | 6.0 |
| 30 | 457183 | H91882 | Hs.118569 | DNA-binding protein IDAX (inhibition of | 6.0 |
| | 448999 | AF179274 | Hs.22791 | transmembrane protein with EGF-like and | 6.0 |
| | 454048 | H05626 | Hs.6921 | ESTs | 6.0 |
| | 439772 | AL365406 | Hs.10268 | Homo sapiens mRNA full length insert cDN | 5.9 |
| | 448944 | AB014605 | Hs.22599 | atrophin-1 interacting protein 1; activi | 5.9 |
| 35 | 410011 | AB020641 | Hs.57856 | PFTAIRE protein kinase 1 | 5.9 |
| | 415486 | H12214 | Hs.13284 | ESTs, Weakly similar to 2109260A B cell | 5.9 |
| | 438993 | AA828995 | | gb:cd77b08.s1 NCI_CGAP_Ov2 Homo sapiens | 5.9 |
| | 447350 | AI375572 | Hs.172634 | ESTs | 5.9 |
| | 451783 | R42554 | Hs.210862 | T-box, brain, 1 | 5.9 |
| 40 | 447101 | N72185 | Hs.44189 | ESTs | 5.9 |
| | 440492 | R39127 | Hs.21433 | hypothetical protein DKFZp547J036 | 5.9 |
| | 440274 | R24595 | Hs.7122 | scrapie responsive protein 1 | 5.9 |
| | 438461 | AW075485 | Hs.286049 | phosphoserine aminotransferase | 5.9 |
| | 418064 | BE387287 | Hs.83384 | S100 calcium-binding protein, beta (neur | 5.8 |
| 45 | 437036 | AI571514 | Hs.133022 | ESTs | 5.7 |
| | 412225 | AW902042 | | gb:QVD-NN1022-170400-193-c02 NN1022 Homo | 5.7 |
| | 426342 | AF093419 | Hs.169378 | multiple PDZ domain protein | 5.7 |
| | 444218 | AF070641 | Hs.10684 | Homo sapiens clone 24421 mRNA sequence | 5.7 |
| | 445828 | F05802 | Hs.81907 | ESTs | 5.7 |
| 50 | 447198 | D61523 | Hs.283435 | ESTs | 5.7 |
| | 427897 | NM_017413 | Hs.303084 | apelin; peptide ligand for APJ receptor | 5.7 |
| | 448499 | BE613280 | Hs.77550 | hypothetical protein MGC1780 | 5.7 |
| | 443672 | AA323362 | Hs.9667 | butyrobetaine (gamma), 2-oxoglutarate di | 5.6 |
| | 412155 | R38167 | Hs.12449 | Homo sapiens transmembrane protein HTMP1 | 5.6 |
| 55 | 435718 | R06569 | Hs.269534 | ESTs | 5.6 |
| | 449340 | AW235786 | Hs.195359 | hypothetical protein MGC10954 | 5.6 |
| | 424481 | R19453 | Hs.1787 | proteolipid protein 1 (Pelizaeus-Merzbac | 5.6 |
| | 451996 | AW514021 | Hs.245510 | ESTs | 5.6 |
| | 422411 | AW749443 | Hs.22511 | ESTs | 5.6 |
| 60 | 438328 | AI492261 | Hs.32450 | ESTs | 5.6 |
| | 433244 | AB040943 | Hs.271285 | KIAA1510 protein | 5.6 |
| | 435191 | R15912 | Hs.4817 | Homo sapiens clone 24461 mRNA sequence | 5.5 |
| | 418677 | S83308 | Hs.87224 | SRY (sex determining region Y)-box 5 | 5.5 |
| | 400859 | | | | 5.5 |
| 65 | 413625 | AW451103 | Hs.71371 | ESTs | 5.5 |
| | 421863 | AI952677 | Hs.108972 | Homo sapiens mRNA; cDNA DKFZp434P228 (fr | 5.5 |
| | 434933 | R91095 | Hs.4276 | KIAA1701 protein | 5.5 |
| | 438702 | AI879064 | Hs.54618 | ESTs | 5.5 |
| | 452055 | AI377431 | Hs.141693 | hypothetical protein MGC10858 | 5.5 |
| 70 | 430979 | AI479755 | Hs.129010 | ESTs | 5.5 |
| | 412709 | AL022327 | Hs.74518 | KIAA0027 protein | 5.5 |
| | 439920 | H05430 | Hs.288433 | neurotrophin | 5.5 |
| | 424343 | AW956360 | Hs.4748 | adenylate cyclase activating polypeptide | 5.4 |
| | 407846 | AA426202 | Hs.40403 | Cbp/p300-interacting transactivator, wit | 5.4 |
| 75 | 419235 | AW470411 | Hs.288433 | neurotrophin | 5.4 |
| | 418030 | BE207573 | Hs.83321 | neuromedin B | 5.4 |
| | 410330 | AW023630 | Hs.46786 | ESTs | 5.4 |
| | 410781 | AI375672 | Hs.165028 | ESTs | 5.4 |
| | 420658 | AW965215 | Hs.336656 | ESTs | 5.4 |
| 80 | 421308 | AA687322 | Hs.192843 | leucine zipper protein FKSG14 | 5.4 |
| | 443740 | R56434 | Hs.21082 | ESTs | 5.4 |
| | 426457 | AW894667 | Hs.169965 | chimerin (chimaerin) 1 | 5.4 |
| | 450375 | AA009647 | Hs.8850 | a disintegrin and metalloproteinase doma | 5.4 |
| | 412494 | AL133900 | Hs.792 | ADP-ribosylation factor domain protein 1 | 5.4 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| 5 | 426600 | NM_003378 | Hs.171014 | VGF nerve growth factor inducible | 5.4 |
| | 424432 | AB037821 | Hs.146858 | protocadherin 10 | 5.4 |
| | 429250 | H56585 | Hs.198308 | tryptophan rich basic protein | 5.4 |
| | 443785 | AW449952 | Hs.190125 | basic-helix-loop-helix-PAS protein | 5.4 |
| | 436282 | R91913 | Hs.272104 | ESTs, Moderately similar to ALU1_HUMAN A | 5.4 |
| 10 | 404584 | | | | 5.3 |
| | 430091 | AB032958 | Hs.233023 | KIAA1132 protein | 5.3 |
| | 439845 | AL355743 | Hs.56663 | Homo sapiens EST from clone 41214, full | 5.3 |
| | 424001 | W67883 | Hs.137476 | paternally expressed 10 | 5.3 |
| | 425073 | W39609 | Hs.22003 | solute carrier family 6 (neurotransmitter) | 5.3 |
| 15 | 426625 | T78300 | Hs.300642 | serologically defined colon cancer antigen | 5.3 |
| | 428137 | AA421792 | Hs.170999 | ESTs | 5.3 |
| | 428679 | AA431765 | | gb:zw80c03.s1 Soares_testis_NHT Homo sap | 5.3 |
| | 438176 | AW138970 | Hs.122113 | ESTs | 5.3 |
| | 440138 | AB033023 | Hs.318127 | hypothetical protein FLJ10201 | 5.3 |
| 20 | 451018 | AW965599 | Hs.247324 | mitochondrial ribosomal protein S14 | 5.3 |
| | 416340 | N31772 | Hs.79226 | fasciculation and elongation protein zeta | 5.3 |
| | 435244 | N77221 | Hs.187824 | ESTs | 5.3 |
| | 446035 | NM_006558 | Hs.13565 | Sam68-like phosphotyrosine protein, T-ST | 5.3 |
| | 424624 | AB032947 | Hs.151301 | Ca2+-dependent activator protein for sec | 5.3 |
| 25 | 407748 | AL079409 | Hs.38176 | KIAA0606 protein; SCN Circadian Oscillator | 5.3 |
| | 430437 | A1768801 | Hs.169943 | Homo sapiens cDNA FLJ13569 fs, clone PL | 5.2 |
| | 414825 | X06370 | Hs.77432 | epidermal growth factor receptor (avian) | 5.2 |
| | 453941 | U39817 | Hs.36820 | Bloom syndrome | 5.2 |
| | 424998 | U58515 | Hs.154138 | chitinase 3-like 2 | 5.2 |
| 30 | 423419 | R55336 | Hs.23539 | ESTs | 5.2 |
| | 424922 | BE386547 | Hs.217112 | hypothetical protein MGC10825 | 5.2 |
| | 447359 | NM_012093 | Hs.18268 | adenylate kinase 5 | 5.2 |
| | 408206 | AF041853 | Hs.43670 | kinesin family member 3A | 5.2 |
| | 421013 | M52397 | Hs.1345 | mutated in colorectal cancers | 5.2 |
| 35 | 429443 | AB028967 | Hs.202687 | potassium voltage-gated channel, Shal-re | 5.2 |
| | 434367 | AB020700 | Hs.3830 | KIAA0893 protein | 5.2 |
| | 444861 | R46789 | Hs.76118 | ubiquitin carboxyl-terminal esterase L1 | 5.2 |
| | 446142 | A1754693 | Hs.145968 | ESTs | 5.2 |
| | 448816 | AB033052 | Hs.22151 | KIAA1226 protein | 5.2 |
| 40 | 451050 | AW937420 | Hs.69662 | ESTs | 5.2 |
| | 451106 | BE382701 | Hs.25960 | v-myc avian myelocytomatosis viral related | 5.2 |
| | 439285 | AL133916 | Hs.172572 | hypothetical protein FLJ20093 | 5.2 |
| | 416737 | AF154335 | Hs.79691 | LIM domain protein | 5.2 |
| | 424800 | AL035588 | Hs.153203 | MyoD family inhibitor | 5.2 |
| 45 | 443695 | AW204099 | Hs.337720 | ESTs, Weakly similar to AF126780 1 retin | 5.2 |
| | 415257 | F03016 | Hs.27513 | ESTs | 5.2 |
| | 433929 | A1375499 | Hs.27379 | ESTs | 5.1 |
| | 415651 | A1207162 | Hs.3815 | stathmin-like-protein RB3 | 5.1 |
| | 451027 | AW519204 | Hs.40808 | ESTs | 5.1 |
| 50 | 409172 | Z99399 | Hs.118145 | ESTs | 5.1 |
| | 423343 | AA324643 | Hs.246106 | ESTs | 5.1 |
| | 429172 | AA447417 | Hs.285491 | ESTs | 5.1 |
| | 437268 | A1754847 | Hs.227571 | regulator of G-protein signalling 4 | 5.1 |
| | 451270 | AW341392 | Hs.235795 | ESTs | 5.1 |
| 55 | 452904 | AL157581 | Hs.30957 | Homo sapiens mRNA; cDNA DKFZp434E0626 f1 | 5.1 |
| | 420560 | AW207748 | Hs.59115 | ESTs | 5.1 |
| | 418097 | R45137 | Hs.21868 | ESTs | 5.1 |
| | 442910 | A1365130 | Hs.11307 | ESTs, Weakly similar to T19326 hypotheti | 5.1 |
| | 434849 | AW292765 | Hs.8053 | ESTs | 5.1 |
| 60 | 413554 | AA319146 | Hs.75426 | secretogranin II (chromogranin C) | 5.1 |
| | 414217 | AL309298 | Hs.279898 | Homo sapiens cDNA: FLJ23165 fs, clone L | 5.1 |
| | 412068 | S72043 | Hs.73133 | metallothionein 3 (growth inhibitory fac | 5.0 |
| | 413627 | BE182082 | Hs.246973 | ESTs | 5.0 |
| | 418661 | NM_001949 | Hs.1189 | E2F transcription factor 3 | 5.0 |
| 65 | 422438 | AA445925 | Hs.270896 | ESTs, Moderately similar to Z195_HUMAN Z | 5.0 |
| | 423728 | AW891294 | Hs.132136 | solute carrier family 4, sodium bicarbon | 5.0 |
| | 431431 | AL096711 | Hs.252953 | Human DNA sequence from clone RP3-403A15 | 5.0 |
| | 435087 | AW975241 | Hs.23567 | ESTs | 5.0 |
| | 452097 | AB002364 | Hs.27916 | a disintegrin-like and metalloprotease (| 5.0 |
| 70 | 410434 | AF051152 | Hs.63668 | tol-like receptor 2 | 4.9 |
| | 408692 | AL040127 | Hs.34074 | dipeptidylpeptidase VI | 4.9 |
| | 407808 | AA663559 | Hs.279789 | histone deacetylase 3 | 4.9 |
| | 418940 | H17739 | Hs.288513 | Human DNA sequence from clone RPS-899C14 | 4.9 |
| | 425977 | R15138 | Hs.165570 | Homo sapiens clone 25052 mRNA sequence | 4.9 |
| 75 | 426814 | AF036943 | Hs.172619 | myelin transcription factor 1-like | 4.9 |
| | 447112 | H17800 | Hs.7154 | ESTs | 4.9 |
| | 449574 | F05048 | Hs.175373 | ESTs | 4.9 |
| | 453652 | AW009640 | Hs.28368 | ESTs, Moderately similar to S65657 alpha | 4.9 |
| | 423869 | BE409301 | Hs.134012 | C1q-related factor | 4.9 |
| 80 | 413248 | T64858 | Hs.21433 | hypothetical protein DKFZp547J036 | 4.9 |
| | 449176 | A1633545 | Hs.198072 | ESTs | 4.9 |
| | 448451 | AW015994 | | gb:UH-BI0p-abh-g-09-0-UI.s1 NCI_CGAP_S | 4.8 |
| | 402604 | | | | 4.8 |
| | 436039 | AW023323 | Hs.121070 | ESTs | 4.8 |
| | 448769 | N66037 | Hs.38173 | ESTs | 4.8 |
| | 423678 | AW963357 | Hs.7847 | ESTs | 4.8 |
| | 439451 | AF086270 | Hs.278554 | heterochromatin-like protein 1 | 4.8 |

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|----|--------|-----------|-----------|---|-----|
| | 425870 | R13406 | Hs.56782 | ESTs | 4.8 |
| | 408777 | U71204 | Hs.47626 | Ric (Drosophila)-like, expressed in neur | 4.8 |
| | 413409 | AJ638418 | Hs.78580 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypep | 4.8 |
| 5 | 413623 | AA825721 | Hs.246973 | ESTs | 4.8 |
| | 417246 | AI760098 | Hs.21411 | ESTs | 4.8 |
| | 420900 | AL045633 | Hs.44269 | ESTs | 4.8 |
| | 424153 | AA451737 | Hs.141496 | MAGE-like 2 | 4.8 |
| | 443539 | AI076182 | Hs.134074 | ESTs, Moderately similar to ALLU6_HUMAN A | 4.8 |
| | 448750 | U95020 | Hs.21903 | calcium channel, voltage-dependent, beta | 4.8 |
| 10 | 454030 | AW021429 | Hs.231980 | ESTs | 4.8 |
| | 424458 | M29273 | Hs.1780 | myelin associated glycoprotein | 4.8 |
| | 444119 | R41231 | Hs.184261 | ESTs, Weakly similar to T26686 hypotheti | 4.8 |
| | 407792 | AI077715 | Hs.39384 | putative secreted ligand homologous to f | 4.8 |
| 15 | 431462 | AW583672 | Hs.256311 | granin-like neuroendocrine peptide precu | 4.7 |
| | 431103 | M57399 | Hs.44 | pleiotrophin (heparin binding growth fac | 4.7 |
| | 429956 | AI374651 | Hs.22542 | ESTs | 4.7 |
| | 435060 | AI422719 | Hs.233349 | ESTs, Weakly similar to fork head like p | 4.7 |
| | 436203 | BE384982 | Hs.5076 | Homo sapiens cDNA: FLJ22128 fis, clone H | 4.7 |
| 20 | 448475 | BE613134 | Hs.247474 | hypothetical protein FLJ21032 | 4.7 |
| | 422222 | AI699372 | Hs.193247 | hypothetical protein DKFZp434A171 | 4.7 |
| | 431733 | AW298410 | Hs.21475 | ESTs | 4.7 |
| | 449353 | AA001220 | Hs.271369 | ESTs | 4.7 |
| | 452022 | AW072330 | Hs.293875 | ESTs | 4.7 |
| 25 | 454269 | AI961060 | Hs.129908 | KIAA0591 protein | 4.7 |
| | 404541 | | | | 4.7 |
| | 428189 | AA424030 | Hs.46627 | ESTs | 4.7 |
| | 409125 | R17268 | Hs.259873 | axonal transport of synaptic vesicles | 4.7 |
| | 458435 | AI418718 | Hs.144121 | ESTs, Weakly similar to T46916 hypotheti | 4.6 |
| 30 | 425745 | U44060 | Hs.14427 | Homo sapiens cDNA: FLJ21800 fis, clone H | 4.6 |
| | 413492 | D87470 | Hs.75400 | KIAA0280 protein | 4.6 |
| | 419629 | AB020695 | Hs.91662 | KIAA0888 protein | 4.6 |
| | 407638 | AJ404672 | Hs.334483 | hypothetical protein FLJ23571 | 4.6 |
| | 436140 | W87355 | Hs.269587 | ESTs | 4.6 |
| 35 | 439169 | AI912122 | Hs.41095 | ESTs | 4.6 |
| | 443150 | AI034467 | Hs.34650 | ESTs | 4.6 |
| | 451073 | AI758905 | Hs.206063 | ESTs | 4.6 |
| | 451659 | BE379761 | Hs.14248 | ESTs | 4.6 |
| | 452106 | AI141031 | Hs.21342 | ESTs | 4.6 |
| 40 | 451407 | AA131376 | Hs.326401 | fibroblast growth factor 12B | 4.6 |
| | 448765 | R15337 | Hs.21958 | Homo sapiens mRNA; cDNA DKFZp547D086 (fr | 4.6 |
| | 430147 | R60704 | Hs.234434 | hair/enhancer-of-split related with YRP | 4.6 |
| | 437204 | AL110216 | Hs.12285 | ESTs, Weakly similar to I55214 salivary | 4.6 |
| | 431117 | AF003522 | Hs.250500 | delta (Drosophila)-like 1 | 4.5 |
| 45 | 422175 | N79885 | Hs.6382 | ESTs, Highly similar to T00391 hypotheti | 4.5 |
| | 407889 | R34556 | Hs.30800 | ESTs, Weakly similar to S65657 alpha-1C- | 4.5 |
| | 419343 | AA456245 | Hs.85603 | down-regulated by Ctnnb1, a | 4.5 |
| | 421790 | AW896201 | Hs.22654 | sodium channel, voltage-gated, type I, a | 4.5 |
| | 429399 | AA452244 | Hs.16727 | ESTs | 4.5 |
| 50 | 450149 | AW969781 | Hs.132863 | Zic family member 2 (odd-paired Drosophi | 4.5 |
| | 453118 | AI195849 | Hs.252757 | ESTs | 4.5 |
| | 443455 | AB001025 | Hs.9349 | ryanodine receptor 3 | 4.4 |
| | 442613 | AI004002 | Hs.130522 | Kv channel-interacting protein 1 | 4.4 |
| | 429643 | AA455889 | Hs.167279 | FYVE-finger-containing Rab5 effector pro | 4.4 |
| 55 | 416209 | AA236776 | Hs.79078 | MAD2 (mitotic arrest deficient, yeast, h | 4.4 |
| | 418845 | AA852985 | Hs.89232 | chromobox homolog 5 (Drosophila HP1 alph | 4.4 |
| | 435202 | AI971313 | Hs.170204 | KIAA0551 protein | 4.4 |
| | 437496 | AA452378 | Hs.170144 | Homo sapiens mRNA; cDNA DKFZp547J125 (fr | 4.4 |
| | 451254 | AI571016 | Hs.172967 | ESTs | 4.4 |
| 60 | 439039 | AI656707 | Hs.48713 | ESTs | 4.4 |
| | 439979 | AW600291 | Hs.6823 | hypothetical protein FLJ10430 | 4.4 |
| | 441607 | NM_005010 | Hs.7912 | neuronal cell adhesion molecule | 4.4 |
| | 424983 | AI742434 | Hs.169911 | ESTs | 4.4 |
| | 410611 | AW954134 | Hs.20924 | KIAA1628 protein | 4.4 |
| 65 | 402605 | | | | 4.4 |
| | 409248 | AB033035 | Hs.51965 | KIAA1209 protein | 4.4 |
| | 442222 | AI061301 | Hs.164773 | ESTs | 4.4 |
| | 454027 | R40192 | Hs.21527 | Human DNA sequence from clone GS1-115M3 | 4.4 |
| | 454293 | H49739 | Hs.134013 | ESTs, Moderately similar to HK61_HUMAN H | 4.4 |
| 70 | 442832 | AW206560 | Hs.253569 | ESTs | 4.4 |
| | 407304 | AA565832 | | gb:nj32b03.s1 NCI_CGAP_AA1 Homo sapiens | 4.4 |
| | 423279 | AW959861 | Hs.290943 | ESTs | 4.3 |
| | 427194 | AA399018 | Hs.250835 | ESTs | 4.3 |
| | 419723 | AL120193 | Hs.92614 | longevity assurance (LAG1, S. cerevisiae | 4.3 |
| 75 | 445810 | AW265700 | Hs.155660 | ESTs | 4.3 |
| | 409734 | BE161664 | Hs.56155 | hypothetical protein | 4.3 |
| | 410389 | AW954049 | Hs.8177 | ESTs, Weakly similar to PIHUB6 salivary | 4.3 |
| | 411571 | AA122393 | Hs.70811 | hypothetical protein FLJ20516 | 4.3 |
| | 433024 | AA573847 | Hs.26549 | KIAA1708 protein | 4.3 |
| 80 | 453202 | AW085781 | Hs.26270 | hypothetical protein FLJ11588 | 4.3 |
| | 425264 | AA353953 | Hs.20369 | ESTs, Weakly similar to gonadotropin ind | 4.3 |
| | 416427 | BE244050 | Hs.79307 | Rac/Cdc42 guanine exchange factor (GEF) | 4.3 |
| | 431789 | H19500 | Hs.269222 | mitogen-activated protein kinase 4 | 4.3 |
| | 444600 | R41398 | Hs.6996 | ESTs | 4.3 |

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|----|--------|-----------|-----------|---|-----|
| | 454042 | H22570 | Hs.172572 | hypothetical protein FLJ20093 | 4.3 |
| | 441899 | AI372588 | Hs.8022 | TU3A protein | 4.3 |
| | 425256 | BE297611 | Hs.155392 | collapsin response mediator protein 1 | 4.3 |
| 5 | 410358 | AW975168 | Hs.13337 | ESTs, Weakly similar to unnamed protein | 4.2 |
| | 430291 | AV660345 | Hs.238126 | CGI-49 protein | 4.2 |
| | 433597 | AA708205 | Hs.100343 | ESTs | 4.2 |
| | 444127 | N63620 | Hs.13281 | ESTs | 4.2 |
| | 448507 | AL133109 | Hs.21333 | Homo sapiens mRNA; cDNA DKFZp566N1047 (f | 4.2 |
| 10 | 413589 | AW452631 | Hs.313803 | ESTs, Highly similar to AF157833.1 noncl | 4.2 |
| | 408577 | H50572 | Hs.19515 | ESTs, Highly similar to NRG3_HUMAN PRO-N | 4.2 |
| | 409719 | AJ769160 | Hs.108681 | Homo sapiens brain tumor associated prot | 4.2 |
| | 428536 | AI143139 | Hs.2288 | visinin-like 1 | 4.2 |
| | 429118 | H20669 | Hs.35406 | ESTs, Highly similar to unnamed protein | 4.2 |
| 15 | 432865 | AI753709 | Hs.152484 | ESTs, Weakly similar to I38022 hypotheti | 4.2 |
| | 447138 | AI439112 | Hs.93828 | ESTs, Weakly similar to 2109260A B cell | 4.2 |
| | 450648 | AI703366 | Hs.26766 | ESTs | 4.2 |
| | 451459 | AI797515 | Hs.270560 | ESTs, Moderately similar to ALU7_HUMAN A | 4.2 |
| | 421686 | AB011156 | Hs.106794 | KIAA0584 protein | 4.2 |
| 20 | 452776 | AA194540 | Hs.13522 | ESTs, Weakly similar to I38022 hypotheti | 4.2 |
| | 436421 | AI678031 | Hs.122813 | ESTs, Weakly similar to ZN22_HUMAN ZINC | 4.2 |
| | 423858 | AL137326 | Hs.133483 | Homo sapiens mRNA; cDNA DKFZp43480650 (f | 4.2 |
| | 434001 | AW950905 | Hs.3697 | serine (or cysteine) proteinase inhibito | 4.2 |
| | 437380 | AL359577 | Hs.112198 | Homo sapiens mRNA; cDNA DKFZp547M073 (fr | 4.2 |
| 25 | 432328 | AI572739 | Hs.195471 | 6-phosphofructo-2-kinase/fructose-2,6-bi | 4.1 |
| | 439607 | BES40565 | Hs.159460 | ESTs | 4.1 |
| | 424028 | AF055084 | Hs.153692 | Homo sapiens cDNA FLJ14354 fs, clone Y7 | 4.1 |
| | 446936 | H10207 | Hs.47314 | ESTs | 4.1 |
| | 424240 | AB023185 | Hs.143535 | calcium/calmodulin-dependent protein kin | 4.1 |
| 30 | 412446 | AI768015 | Hs.92127 | ESTs | 4.1 |
| | 409953 | AA332277 | Hs.57691 | cadherin 18, type 2 | 4.1 |
| | 416220 | N49776 | Hs.170994 | hypothetical protein MGC10946 | 4.1 |
| | 419683 | AA248897 | Hs.48784 | ESTs | 4.1 |
| | 426071 | AW138057 | Hs.163835 | ESTs | 4.1 |
| 35 | 428743 | AL080060 | Hs.301549 | Homo sapiens mRNA; cDNA DKFZp564H172 (fr | 4.1 |
| | 432809 | AA565509 | Hs.131703 | ESTs | 4.1 |
| | 440105 | AA694010 | Hs.6932 | Homo sapiens clone 23809 mRNA sequence | 4.1 |
| | 452039 | AI922988 | Hs.172510 | ESTs | 4.1 |
| 40 | 425905 | AB032959 | Hs.318584 | novel C3HC4 type Zinc finger (ring finger | 4.1 |
| | 457561 | AA331517 | Hs.286055 | chimerin (chimaerin) 2 | 4.1 |
| | 429038 | AL023513 | Hs.194766 | seizure related gene 6 (mouse)-like | 4.1 |
| | 433932 | AW954599 | Hs.169330 | neuronal protein | 4.1 |
| | 436537 | AI783629 | Hs.26766 | ESTs | 4.1 |
| | 439231 | AW581935 | Hs.141480 | Homo sapiens mRNA; cDNA DKFZp434N079 (fr | 4.1 |
| 45 | 450530 | NM_006668 | Hs.25121 | cytochrome P450, subfamily 46 (cholester | 4.1 |
| | 407721 | Y12735 | Hs.38018 | dual-specificity tyrosine-(Y)-phosphoryl | 4.1 |
| | 407881 | AW072003 | Hs.40968 | heparan sulfate (glucosamine) 3-O-sulfot | 4.1 |
| | 410486 | AW235094 | Hs.69233 | zinc finger protein | 4.0 |
| | 413916 | N49813 | Hs.75615 | apolipoprotein C-II | 4.0 |
| 50 | 438703 | AI803373 | Hs.31599 | ESTs | 4.0 |
| | 424726 | AK001007 | Hs.138760 | Homo sapiens cDNA FLJ10145 fs, clone HE | 4.0 |
| | 405771 | | | | 4.0 |
| | 418841 | NM_002332 | Hs.89137 | low density lipoprotein-related protein | 4.0 |
| | 421764 | AI681535 | Hs.148135 | serine/threonine kinase 33 | 4.0 |
| 55 | 424176 | AL137273 | Hs.142307 | hypothetical protein | 4.0 |
| | 425773 | N21279 | Hs.237749 | ESTs | 4.0 |
| | 427304 | AA761526 | Hs.163853 | ESTs | 4.0 |
| | 428882 | AA436915 | Hs.131748 | ESTs, Moderately similar to ALU7_HUMAN A | 4.0 |
| | 452834 | AI638627 | Hs.105685 | KIAA1688 protein | 4.0 |
| 60 | 453745 | AA952989 | Hs.63908 | hypothetical protein MGC14726 | 4.0 |
| | 405239 | U89281 | Hs.11958 | oxidative 3 alpha hydroxysteroid dehydro | 4.0 |
| | 413801 | M62246 | Hs.35406 | ESTs, Highly similar to unnamed protein | 4.0 |
| | 429698 | AI685086 | Hs.26339 | ESTs, Weakly similar to S21348 probable | 4.0 |
| | 435854 | AJ278120 | Hs.4996 | putative ankyrin-repeat containing prote | 4.0 |
| 65 | 439199 | R40373 | Hs.26299 | ESTs | 4.0 |
| | 439450 | R51613 | Hs.125304 | ESTs | 4.0 |
| | 446782 | AI653048 | Hs.144006 | ESTs | 4.0 |
| | 419687 | AI638859 | Hs.227699 | ESTs, Weakly similar to T2D3_HUMAN TRANS | 4.0 |
| | 402408 | | | | 3.9 |
| 70 | 453362 | H14988 | Hs.107375 | ESTs | 3.9 |
| | 414219 | V20010 | Hs.75823 | ALL1-fused gene from chromosome 1q | 3.9 |
| | 420578 | AA813546 | Hs.99034 | GTP-binding protein Rho7 | 3.9 |
| | 425010 | T16837 | Hs.4241 | ESTs | 3.9 |
| | 444230 | H95537 | Hs.146067 | ESTs | 3.9 |
| 75 | 441736 | AW292779 | Hs.169799 | ESTs | 3.9 |
| | 418951 | F07809 | Hs.89506 | paired box gene 6 (aniridia, keratitis) | 3.9 |
| | 406311 | | | | 3.9 |
| | 408460 | AA054726 | Hs.285574 | ESTs | 3.9 |
| | 410658 | AW105231 | Hs.192035 | ESTs | 3.9 |
| 80 | 414699 | AI815523 | Hs.76930 | synuclein, alpha (non A4 component of am | 3.9 |
| | 418849 | AW474547 | Hs.53565 | Homo sapiens PTG-M mRNA for mannosyltran | 3.9 |
| | 429477 | AI275514 | Hs.6658 | ESTs | 3.9 |
| | 433766 | AA609234 | Hs.112669 | ESTs | 3.9 |
| | 436190 | AK001059 | | gb:Homo sapiens cDNA FLJ10197 fs, clone | 3.9 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 447891 | R41754 | Hs.6496 | ESTs | 3.9 |
| | 450221 | AA328102 | Hs.24641 | cytoskeleton associated protein 2 | 3.9 |
| | 404283 | | | | 3.9 |
| 5 | 453919 | AW959912 | Hs.7076 | KIAA1705 protein | 3.9 |
| | 429656 | X05608 | Hs.211584 | neurofilament, light polypeptide (68kD) | 3.9 |
| | 412754 | AW160375 | Hs.74565 | amyloid beta (A4) precursor-like protein | 3.9 |
| | 445314 | AI689948 | Hs.65489 | Homo sapiens cDNA: FLJ21517 fis, clone C | 3.9 |
| | 435652 | N32388 | Hs.334370 | uncharacterized hypothalamus protein HBE | 3.9 |
| 10 | 407378 | AA299264 | Hs.57776 | ESTs, Moderately similar to I38022 hypot | 3.9 |
| | 438054 | AA776626 | Hs.62183 | ESTs | 3.9 |
| | 436420 | AA443966 | Hs.31595 | ESTs | 3.9 |
| | 445133 | AW157646 | Hs.153506 | ESTs | 3.9 |
| | 432590 | AI609273 | Hs.110783 | ESTs | 3.9 |
| 15 | 453331 | AI240565 | Hs.8895 | ESTs | 3.9 |
| | 410227 | AB009284 | Hs.61152 | exostoses (multiple)-like 2 | 3.8 |
| | 424635 | AA420687 | Hs.115455 | Homo sapiens cDNA FLJ14259 fis, clone PL | 3.8 |
| | 451489 | NM_005503 | Hs.26468 | amyloid beta (A4) precursor protein-bind | 3.8 |
| | 447247 | AW369351 | Hs.287955 | Homo sapiens cDNA FLJ13090 fis, clone NT | 3.8 |
| 20 | 448302 | AI480208 | Hs.182906 | Homo sapiens mRNA for KIAA1872 protein, | 3.8 |
| | 415669 | NM_005025 | Hs.78589 | serine (or cysteine) proteinase inhibitor | 3.8 |
| | 417355 | D13168 | Hs.82002 | endothelin receptor type B | 3.8 |
| | 446727 | AB011095 | Hs.16032 | KIAA0523 protein | 3.8 |
| | 424340 | AA339036 | Hs.7033 | ESTs | 3.8 |
| 25 | 423346 | AI267677 | Hs.127416 | synaptotagmin 1 | 3.8 |
| | 412788 | AA120960 | Hs.198416 | ESTs | 3.8 |
| | 404593 | | | | 3.8 |
| | 416856 | N27833 | Hs.269028 | ESTs, Weakly similar to I38022 hypotheti | 3.8 |
| | 429896 | AA460367 | Hs.224223 | ESTs, Moderately similar to I38022 hypot | 3.8 |
| 30 | 439619 | AW975998 | Hs.58595 | ESTs, Weakly similar to I38022 hypotheti | 3.8 |
| | 439634 | W79377 | Hs.167 | microtubule-associated protein 2 | 3.8 |
| | 440322 | AA879430 | | gb:q91d08.s1 Soares_NFL_T_GBC_S1 Homo s | 3.8 |
| | 447761 | AF061573 | Hs.19492 | protocadherin 8 | 3.8 |
| | 452453 | AI902519 | | gb:QV-BT009-101198-051 BT009 Homo sapien | 3.8 |
| 35 | 439671 | AW162840 | Hs.6641 | kinesin family member 5C | 3.8 |
| | 447937 | AL109716 | Hs.20034 | Homo sapiens mRNA full length insert cDN | 3.8 |
| | 459278 | AW294659 | Hs.34054 | Homo sapiens cDNA: FLJ22488 fis, clone H | 3.8 |
| | 447028 | AI973128 | Hs.167257 | brain link protein-1 | 3.8 |
| | 449458 | AI805078 | Hs.208261 | ESTs | 3.8 |
| 40 | 445888 | AF070564 | Hs.13415 | Homo sapiens clone 24571 mRNA sequence | 3.8 |
| | 407385 | AA610150 | Hs.272072 | ESTs, Weakly similar to I38022 hypotheti | 3.8 |
| | 428841 | AI418430 | Hs.104935 | ESTs | 3.8 |
| | 430643 | AW970065 | Hs.287425 | MEGF10 protein | 3.8 |
| | 422263 | AA307639 | Hs.129908 | KIAA0591 protein | 3.8 |
| 45 | 451625 | R56793 | Hs.106576 | alanine-glyoxylate aminotransferase 2-li | 3.8 |
| | 439236 | BE160952 | Hs.247117 | ESTs, Moderately similar to ALUF_HUMAN ! | 3.8 |
| | 441928 | AI370188 | Hs.211454 | ESTs | 3.8 |
| | 441797 | AI936933 | Hs.214635 | ESTs | 3.7 |
| | 414922 | D00723 | Hs.77631 | glycine cleavage system protein H (amino | 3.7 |
| | 425588 | F07396 | Hs.46751 | ESTs | 3.7 |
| 50 | 437007 | AA741300 | Hs.202599 | ESTs, Weakly similar to I38022 hypotheti | 3.7 |
| | 435793 | AB037734 | Hs.4993 | KIAA1313 protein | 3.7 |
| | 443682 | AI383061 | Hs.47248 | ESTs, Highly similar to similar to Cdc14 | 3.7 |
| | 425741 | AF052152 | Hs.159412 | Homo sapiens clone 24528 mRNA sequence | 3.7 |
| 55 | 418211 | BE244746 | Hs.247474 | hypothetical protein FLJ21032 | 3.7 |
| | 440080 | AW051597 | Hs.143707 | ESTs | 3.7 |
| | 452898 | AA814497 | Hs.78792 | ESTs | 3.7 |
| | 435575 | AF213457 | Hs.44234 | triggering receptor expressed on myeloid | 3.7 |
| | 409234 | AI879419 | Hs.27206 | ESTs | 3.7 |
| 60 | 420489 | AA815089 | Hs.193513 | ESTs | 3.7 |
| | 426890 | AA393167 | Hs.41294 | ESTs | 3.7 |
| | 438849 | W28948 | Hs.10762 | ESTs | 3.7 |
| | 441869 | NM_003947 | Hs.8004 | huntingtin-associated protein interactin | 3.7 |
| | 448796 | AA147829 | Hs.301431 | endothelial zinc finger protein induced | 3.7 |
| 65 | 459318 | NM_000038 | | gb:Homo sapiens adenomatosis polyposis c | 3.7 |
| | 459518 | AI937419 | Hs.294069 | Homo sapiens cDNA FLJ13384 fis, clone PL | 3.7 |
| | 434444 | AI765276 | Hs.101257 | hypothetical protein MGC3295 | 3.7 |
| | 421183 | AL135740 | Hs.102447 | TSC-22-like | 3.7 |
| | 410555 | U92649 | Hs.64311 | a disintegrin and metalloproteinase doma | 3.7 |
| 70 | 421637 | AF035290 | Hs.106300 | Homo sapiens clone 23556 mRNA sequence | 3.7 |
| | 418522 | AA605038 | Hs.7149 | Homo sapiens cDNA: FLJ21950 fis, clone H | 3.7 |
| | 420807 | AA280627 | Hs.57846 | ESTs | 3.7 |
| | 449961 | AW265634 | Hs.133100 | ESTs | 3.7 |
| | 422634 | NM_016010 | Hs.118821 | CGI-62 protein | 3.7 |
| 75 | 421030 | AW161357 | Hs.101174 | microtubule-associated protein tau | 3.7 |
| | 427099 | AB032953 | Hs.173560 | odd Oz/ten-m homolog 2 (Drosophila, mous | 3.7 |
| | 452355 | N54926 | Hs.29202 | G protein-coupled receptor 34 | 3.7 |
| | 440483 | AI200836 | Hs.150386 | ESTs | 3.7 |
| | 429597 | NM_003816 | Hs.2442 | a disintegrin and metalloproteinase doma | 3.7 |
| 80 | 423756 | AA828125 | | gb:od71a09.s1 NCI_CGAP_Ov2 Homo sapiens | 3.6 |
| | 425187 | AW014486 | Hs.22509 | ESTs | 3.6 |
| | 434859 | BE255080 | Hs.299315 | collapsin response mediator protein-5; C | 3.6 |
| | 413199 | M62843 | Hs.75236 | ELAV (embryonic lethal, abnormal vision, | 3.6 |
| | 445729 | H21066 | Hs.13223 | Homo sapiens mRNA full length insert cDN | 3.6 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 416120 | H46739 | | gb:yo14h02.s1 Soares adult brain N2b5HB5 | 3.6 |
| | 429239 | AA448419 | Hs.45209 | ESTs | 3.6 |
| | 419086 | NM_000216 | Hs.89591 | Kallmann syndrome 1 sequence | 3.6 |
| 5 | 446659 | AJ335361 | Hs.226376 | ESTs | 3.6 |
| | 426757 | AW205640 | Hs.158206 | ESTs | 3.6 |
| | 418819 | AA228776 | Hs.191721 | ESTs | 3.6 |
| | 458332 | AJ000341 | Hs.220491 | ESTs | 3.6 |
| | 408826 | AF216077 | Hs.48376 | Homo sapiens clone HB-2 mRNA sequence | 3.6 |
| 10 | 410343 | AA084273 | Hs.76561 | ESTs, Weakly similar to S47072 finger pr | 3.6 |
| | 410507 | AA355288 | Hs.40834 | transitional epithelia response protein | 3.6 |
| | 422977 | AA631498 | | gb:np83h04.s1 NCL_CGAP_Thy1 Homo sapiens | 3.6 |
| | 425305 | AA363025 | Hs.155572 | Human clone Z3801 mRNA sequence | 3.6 |
| | 426002 | AA418703 | | gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi | 3.6 |
| 15 | 428505 | AL035461 | Hs.2281 | chromogranin B (secretogranin 1) | 3.6 |
| | 430530 | AA480870 | Hs.47660 | ESTs | 3.6 |
| | 436425 | AB913146 | Hs.318725 | CGI-72 protein | 3.6 |
| | 438078 | AJ016377 | Hs.131693 | ESTs | 3.6 |
| | 442927 | AJ024347 | Hs.131519 | ESTs | 3.6 |
| 20 | 446242 | N66336 | Hs.7360 | ESTs | 3.6 |
| | 448831 | AL080123 | Hs.22182 | zinc finger protein 23 (KOX 16) | 3.6 |
| | 450474 | AW872844 | Hs.201919 | ESTs | 3.6 |
| | 452198 | AJ097560 | Hs.61210 | ESTs, Weakly similar to I38022 hypothe | 3.6 |
| | 455800 | R22479 | Hs.167073 | Homo sapiens cDNA FLJ13047 fis, clone NT | 3.6 |
| 25 | 436443 | AW138211 | Hs.128746 | ESTs | 3.6 |
| | 426514 | BE616633 | Hs.170195 | bone morphogenetic protein 7 (osteogenic | 3.6 |
| | 456038 | AA203285 | Hs.294141 | ESTs, Weakly similar to alternatively sp | 3.6 |
| | 408902 | AW014869 | Hs.5510 | ESTs | 3.6 |
| | 442950 | AJ500417 | Hs.46764 | ESTs | 3.6 |
| 30 | 423905 | AW579960 | Hs.135150 | lung type-I cell membrane-associated gly | 3.6 |
| | 425478 | AB007953 | Hs.268840 | ESTs | 3.6 |
| | 453884 | AA355925 | Hs.36232 | KIAA0186 gene product | 3.6 |
| | 404721 | | | | 3.6 |
| | 408453 | AJ369838 | Hs.45127 | chondroitin sulfate proteoglycan 5 (neur | 3.6 |
| 35 | 440553 | AA889416 | Hs.295362 | Homo sapiens cDNA FLJ14459 fis, clone HE | 3.5 |
| | 446372 | AB020644 | Hs.14945 | long fatty acyl-CoA synthetase 2 gene | 3.5 |
| | 413999 | N46124 | Hs.34460 | ESTs | 3.5 |
| | 421458 | NM_003654 | Hs.104576 | carbohydrate (keratan sulfate Gal-6) sul | 3.5 |
| | 425017 | AL119305 | Hs.288405 | ESTs | 3.5 |
| 40 | 435958 | H98180 | Hs.117975 | ESTs | 3.5 |
| | 415101 | R45531 | Hs.144534 | ESTs | 3.5 |
| | 451320 | AW118072 | Hs.89981 | diacylglycerol kinase, zeta (104kD) | 3.5 |
| | 430290 | AJ734110 | Hs.136355 | ESTs | 3.5 |
| | 416836 | D54745 | Hs.80247 | cholecystokinin | 3.5 |
| 45 | 414821 | M63835 | Hs.77424 | Fc fragment of IgG, high affinity Ia, re | 3.5 |
| | 419412 | AW161058 | Hs.90297 | synuclein, beta | 3.5 |
| | 437860 | AA333063 | Hs.279898 | Homo sapiens cDNA: FLJ23165 fis, clone L | 3.5 |
| | 452689 | F33868 | Hs.284176 | transferrin | 3.5 |
| | 416661 | AA634543 | Hs.79440 | IGF-II mRNA-binding protein 3 | 3.5 |
| 50 | 427491 | R43279 | Hs.22574 | ESTs, Weakly similar to I38022 hypothe | 3.5 |
| | 428037 | N47474 | Hs.89230 | potassium intermediate/small conductance | 3.5 |
| | 444584 | AJ168422 | | gb:ok30e11.x1 Soares_NSF_F8_9W_OT_PA_P_S | 3.5 |
| | 408296 | AL117452 | Hs.44155 | DKFZP586G1517 protein | 3.5 |
| | 453775 | NM_002916 | Hs.35120 | replication factor C (activator 1) 4 (37 | 3.5 |
| 55 | 412659 | AW753865 | Hs.74376 | olfactomedin related ER localized protei | 3.5 |
| | 429077 | AB028983 | Hs.2352 | adenylate cyclase 2 (brain) | 3.5 |
| | 436887 | AW953157 | Hs.193235 | hypothetical protein DKFZp547D155 | 3.5 |
| | 450784 | AW246803 | Hs.47289 | ESTs | 3.5 |
| | 446827 | AW451243 | Hs.157069 | ESTs | 3.5 |
| 60 | 436434 | N50465 | Hs.92927 | putative 47 kDa protein | 3.5 |
| | 412777 | AJ335773 | Hs.270123 | ESTs | 3.5 |
| | 436476 | AA326108 | Hs.33829 | bHLH protein DEC2 | 3.5 |
| | 408601 | U47928 | Hs.86122 | protein A | 3.5 |
| | 429401 | AW296102 | Hs.99272 | ESTs, Weakly similar to S32567 A4 protei | 3.4 |
| 65 | 448425 | AJ500359 | Hs.233401 | ESTs | 3.4 |
| | 418727 | AA227609 | Hs.94834 | ESTs | 3.4 |
| | 451729 | AW160725 | Hs.312469 | ESTs | 3.4 |
| | 435910 | AJ084152 | Hs.21782 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 3.4 |
| | 434577 | R37316 | Hs.179769 | Homo sapiens cDNA: FLJ22487 fis, clone H | 3.4 |
| 70 | 414598 | AJ094221 | Hs.135150 | lung type-I cell membrane-associated gly | 3.4 |
| | 439627 | BE621702 | Hs.29076 | hypothetical protein FLJ21841 | 3.4 |
| | 413293 | AL047483 | Hs.302498 | GTP-binding protein homologous to Saccha | 3.4 |
| | 423992 | AW898292 | Hs.137206 | Homo sapiens mRNA; cDNA DKFZp564H1663 (f | 3.4 |
| | 426249 | F05422 | Hs.168352 | nucleoporin-like protein 1 | 3.4 |
| 75 | 426958 | U07616 | Hs.173034 | amphiphysin (Sliff-Mann syndrome with br | 3.4 |
| | 430388 | AA356923 | Hs.240770 | nuclear cap binding protein subunit 2, 2 | 3.4 |
| | 435061 | AJ651474 | Hs.163944 | ESTs | 3.4 |
| | 452291 | AF015592 | Hs.28853 | CDC7 (cell division cycle 7, S. cerevisi | 3.4 |
| | 449714 | AB033015 | Hs.23941 | KIAA1189 protein | 3.4 |
| 80 | 443392 | AJ055821 | Hs.293420 | ESTs | 3.4 |
| | 410082 | AA081594 | Hs.158311 | Musashi (Drosophila) homolog 1 | 3.4 |
| | 445337 | NM_013280 | Hs.12523 | fibronectin leucine rich transmembrane p | 3.4 |
| | 408493 | BE206854 | Hs.46039 | phosphoglycerate mutase 2 (muscle) | 3.4 |
| | 432731 | R31178 | Hs.287820 | fibronectin 1 | 3.4 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 448758 | AB018311 | Hs.21917 | KIAA0768 protein | 3.4 |
| | 432613 | AW081698 | Hs.80712 | KIAA0202 protein | 3.4 |
| | 434164 | AW207019 | Hs.148135 | serine/threonine kinase 33 | 3.4 |
| | 425294 | AF033827 | Hs.155553 | HNK-1 sulfotransferase | 3.4 |
| 5 | 410108 | AA081659 | Hs.318775 | OSBP-related protein 6 | 3.4 |
| | 406815 | AA833930 | Hs.288036 | tRNA isopentenylpyrophosphate transferase | 3.4 |
| | 402855 | | | | 3.3 |
| | 422170 | AJ791949 | Hs.112432 | anti-Mullerian hormone | 3.3 |
| | 445034 | AW293376 | Hs.143659 | ESTs | 3.3 |
| 10 | 424378 | W28020 | Hs.167988 | neural cell adhesion molecule 1 | 3.3 |
| | 423611 | AB011163 | Hs.129908 | KIAA0591 protein | 3.3 |
| | 435593 | R88872 | Hs.4964 | DKFZP586J1624 protein | 3.3 |
| | 404819 | | | | 3.3 |
| | 436607 | AW661783 | Hs.211061 | ESTs | 3.3 |
| 15 | 427315 | AA179949 | Hs.175563 | Homo sapiens mRNA; cDNA DKFZp564N0763 (f | 3.3 |
| | 452693 | T79153 | Hs.48589 | zinc finger protein 228 | 3.3 |
| | 454996 | AW850180 | | gb:IL3-CT0219-271099-022-C09 CT0219 Homo | 3.3 |
| | 406927 | M26460 | | gb:Homo sapiens (clone 104) retinoblasto | 3.3 |
| | 409045 | AA635062 | Hs.50094 | Homo sapiens mRNA; cDNA DKFZp434O0515 (f | 3.3 |
| 20 | 415238 | R37780 | Hs.21422 | ESTs | 3.3 |
| | 417845 | AL117461 | Hs.82719 | Homo sapiens mRNA; cDNA DKFZp586F1822 (f | 3.3 |
| | 421192 | AA833718 | Hs.204529 | KIAA1806 protein | 3.3 |
| | 426695 | AW118191 | Hs.112729 | ESTs | 3.3 |
| | 438885 | AJ886558 | Hs.184987 | ESTs | 3.3 |
| 25 | 451762 | AF222980 | Hs.26985 | disrupted in schizophrenia 1 | 3.3 |
| | 452103 | R42764 | Hs.339654 | ESTs, Weakly similar to I38022 hypothe | 3.3 |
| | 453590 | AF150278 | Hs.33578 | KIAA0820 protein | 3.3 |
| | 453616 | NM_003462 | Hs.33846 | dynein, axonemal, light intermediate pol | 3.3 |
| 30 | 457285 | AJ038858 | Hs.130522 | Kv channel-interacting protein 1 | 3.3 |
| | 436045 | AB037723 | Hs.5028 | DKFZP564O0423 protein | 3.3 |
| | 437470 | AL390147 | Hs.134742 | hypothetical protein DKFZp547D065 | 3.3 |
| | 448520 | AB002367 | Hs.21355 | doublecortin and Cam kinase-like 1 | 3.3 |
| | 436480 | AJ271643 | Hs.87469 | putative acid-sensing ion channel | 3.3 |
| | 432656 | NM_000246 | Hs.3076 | MHC class II transactivator | 3.3 |
| 35 | 443898 | AW804296 | Hs.9950 | Sec61 gamma | 3.3 |
| | 423582 | BE000831 | Hs.23837 | Homo sapiens cDNA FLJ11812 fis, clone HE | 3.3 |
| | 445953 | AJ612775 | Hs.145710 | ESTs | 3.3 |
| | 427940 | AA417812 | Hs.38775 | ESTs | 3.3 |
| | 414683 | S78296 | Hs.76888 | hypothetical protein MGC12702 | 3.3 |
| 40 | 428484 | AF104032 | Hs.184601 | solute carrier family 7 (cationic amino | 3.3 |
| | 420549 | AJ866964 | Hs.124704 | ESTs, Moderately similar to S65657 alpha | 3.3 |
| | 419498 | AL036591 | Hs.20887 | hypothetical protein FLJ10392 | 3.3 |
| | 457579 | AB030816 | Hs.36761 | HRAS-like suppressor | 3.3 |
| | 436556 | AJ364997 | Hs.7572 | ESTs | 3.2 |
| 45 | 424369 | R87622 | Hs.26714 | KIAA1831 protein | 3.2 |
| | 457065 | AJ476318 | Hs.192480 | ESTs | 3.2 |
| | 440210 | AW674562 | Hs.125296 | ESTs | 3.2 |
| | 444513 | AL120214 | Hs.7117 | glutamate receptor, ionotropic, AMPA 1 | 3.2 |
| 50 | 434353 | AA630863 | Hs.131375 | ESTs, Moderately similar to ALUB_HUMAN I | 3.2 |
| | 414430 | AJ346201 | Hs.76118 | ubiquitin carboxyl-terminal esterase L1 | 3.2 |
| | 439924 | AJ985897 | Hs.125293 | ESTs | 3.2 |
| | 411505 | AF155659 | Hs.70565 | molybdenum cofactor synthesis 2 | 3.2 |
| | 423175 | W27595 | Hs.18653 | hypothetical protein FLJ14627 | 3.2 |
| 55 | 415115 | AA214228 | Hs.127751 | hypothetical protein | 3.2 |
| | 407878 | D87468 | Hs.40888 | activity-regulated cytoskeleton-associat | 3.2 |
| | 410274 | AA381807 | Hs.61762 | hypoxia-inducible protein 2 | 3.2 |
| | 437762 | T78028 | Hs.154679 | synaptotagmin I | 3.2 |
| | 438944 | AA302517 | Hs.92732 | KIAA1444 protein | 3.2 |
| 60 | 450313 | AJ038989 | Hs.332633 | Bardet-Biedl syndrome 2 | 3.2 |
| | 409459 | D86407 | Hs.54481 | low density lipoprotein receptor-related | 3.2 |
| | 410953 | AW811766 | Hs.334858 | hypothetical protein MGC12250 | 3.2 |
| | 418527 | AA450386 | Hs.7149 | Homo sapiens cDNA: FLJ21950 fis, clone H | 3.2 |
| | 420081 | AW510776 | Hs.94958 | tubulin tyrosine ligase-like 1 | 3.2 |
| 65 | 429496 | AA453800 | Hs.192793 | ESTs | 3.2 |
| | 430099 | AW194988 | Hs.20537 | hypothetical protein FLJ13942 | 3.2 |
| | 434928 | AW015595 | Hs.4267 | Homo sapiens clones 24714 and 24715 mRNA | 3.2 |
| | 435532 | AW291488 | Hs.117305 | Homo sapiens, clone IMAGE:3682908, mRNA | 3.2 |
| | 438306 | AW188266 | Hs.163645 | ESTs | 3.2 |
| | 439274 | AF086092 | Hs.48372 | ESTs | 3.2 |
| 70 | 440847 | AA907511 | Hs.130178 | ESTs | 3.2 |
| | 447750 | AJ422234 | Hs.143434 | contactin 1 | 3.2 |
| | 455350 | AW901809 | | gb:QV0-NN1020-170400-195-b02 NN1020 Homo | 3.2 |
| | 430890 | X54232 | Hs.2699 | glypican 1 | 3.2 |
| | 420568 | F09247 | Hs.247735 | protocadherin alpha 10 | 3.2 |
| 75 | 410768 | AF038185 | Hs.66187 | Homo sapiens clone 23700 mRNA sequence | 3.2 |
| | 427450 | AB014526 | Hs.178121 | KIAA0626 gene product | 3.2 |
| | 430456 | AA314998 | Hs.241503 | hypothetical protein | 3.2 |
| | 430181 | AF065314 | Hs.234785 | cyclic nucleotide gated channel alpha 3 | 3.2 |
| | 418512 | AW498974 | Hs.89981 | diacylglycerol kinase, zeta (104kD) | 3.2 |
| 80 | 419912 | AF249745 | Hs.6066 | Rho guanine nucleotide exchange factor (| 3.2 |
| | 450689 | AJ389275 | Hs.243010 | Homo sapiens cDNA FLJ14445 fis, clone HE | 3.2 |
| | 424899 | AL119387 | Hs.119062 | ESTs | 3.2 |
| | 436277 | R88520 | Hs.120917 | ESTs | 3.2 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 451455 | AI937227 | Hs.8821 | hepoid antimicrobial peptide | 3.2 |
| | 445078 | AI869975 | Hs.4775 | junctophilin 3 | 3.2 |
| | 447746 | AW015920 | Hs.161359 | ESTs | 3.2 |
| 5 | 435458 | F11872 | Hs.4892 | Homo sapiens clone 24841 mRNA sequence | 3.2 |
| | 427729 | AB033100 | Hs.300646 | KIAA protein (similar to mouse paladin) | 3.2 |
| | 417417 | F05745 | Hs.89512 | ATPase, Ca ⁺⁺ transporting, plasma membra | 3.1 |
| | 438810 | AW897846 | Hs.6421 | hypothetical protein DKFZp761N09121 | 3.1 |
| | 439570 | T79925 | Hs.269165 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.1 |
| 10 | 432527 | AW975028 | Hs.102754 | ESTs | 3.1 |
| | 416801 | X98834 | Hs.79971 | sal (Drosophila)-like 2 | 3.1 |
| | 421988 | AW450481 | Hs.161333 | ESTs | 3.1 |
| | 426509 | M31166 | Hs.2050 | pentaxin-related gene, rapidly induced b | 3.1 |
| | 408786 | AA773187 | Hs.294027 | ESTs | 3.1 |
| 15 | 433494 | AB029396 | Hs.3353 | beta-1,3-glucuronyltransferase 1 (glucur | 3.1 |
| | 412723 | AA648459 | Hs.335951 | hypothetical protein AF301222 | 3.1 |
| | 418329 | AW247430 | Hs.84152 | cystathionine-beta-synthase | 3.1 |
| | 439456 | AI752409 | Hs.109314 | hypothetical protein FLJ20980 | 3.1 |
| | 428832 | AA578229 | Hs.324239 | ESTs, Moderately similar to ZN91_HUMAN Z | 3.1 |
| 20 | 452780 | BE171598 | Hs.13522 | ESTs, Weakly similar to I38022 hypothe | 3.1 |
| | 438192 | AI859065 | Hs.337620 | Homo sapiens AFG3L1 isoform 1 mRNA, part | 3.1 |
| | 424939 | AK000059 | Hs.153881 | Homo sapiens NY-REN-62 antigen mRNA, par | 3.1 |
| | 403053 | R58624 | Hs.2186 | eukaryotic translation elongation factor | 3.1 |
| | 404299 | | | | 3.1 |
| 25 | 407864 | AF069291 | Hs.40539 | chromosome 8 open reading frame 1 | 3.1 |
| | 410181 | AI468210 | Hs.261285 | pleiotropic regulator 1 (PRL1, Arabidops | 3.1 |
| | 418852 | BE537037 | Hs.273294 | hypothetical protein FLJ20069 | 3.1 |
| | 449101 | AA205847 | Hs.23016 | G protein-coupled receptor | 3.1 |
| | 453240 | AI969564 | Hs.166254 | hypothetical protein DKFZp566I133 | 3.1 |
| 30 | 440486 | BE243513 | Hs.7212 | hypothetical protein PP1044 | 3.1 |
| | 408096 | BE250162 | Hs.83765 | dihydrofolate reductase | 3.1 |
| | 439864 | AI720078 | Hs.291997 | ESTs, Weakly similar to A47582 B-cell gr | 3.1 |
| | 414706 | AW340125 | Hs.76989 | KIAA0097 gene product | 3.1 |
| | 436315 | BE390513 | Hs.27935 | hypothetical protein MGC4837 | 3.1 |
| 35 | 426855 | AL117427 | Hs.172778 | Homo sapiens mRNA; cDNA DKFZp566P013 (fr | 3.1 |
| | 425683 | AB037813 | Hs.159200 | hypothetical protein DKFZp762K222 | 3.1 |
| | 410126 | BE169274 | Hs.169387 | KIAA0036 gene product | 3.1 |
| | 435312 | AJ243396 | Hs.4865 | voltage-gated sodium channel beta-3 subu | 3.1 |
| | 425491 | AA883316 | Hs.255221 | ESTs | 3.1 |
| 40 | 456273 | AF154846 | Hs.1148 | zinc finger protein | 3.1 |
| | 412140 | AA219691 | Hs.73625 | RAB6 interacting, kinesin-like (rakbines | 3.1 |
| | 445255 | NM_014841 | Hs.12477 | synaposomal-associated protein, 91 kDa | 3.1 |
| | 432154 | AI701523 | Hs.112577 | ESTs | 3.1 |
| | 453128 | AW026516 | Hs.31791 | acylphosphatase 2, muscle type | 3.1 |
| 45 | 438458 | AW975186 | | gb:EST387294 MAGE resequences, MAGN Homo | 3.1 |
| | 448616 | AF035621 | Hs.21611 | kinesin family member 3C | 3.0 |
| | 429281 | AA830856 | Hs.29808 | Homo sapiens cDNA: FLJ21122 fis, clone C | 3.0 |
| | 443906 | AA348031 | Hs.7913 | ESTs | 3.0 |
| | 417318 | AW953937 | Hs.12891 | ESTs | 3.0 |
| 50 | 452619 | AW298597 | Hs.61884 | Homo sapiens, clone IMAGE:4298026, mRNA, | 3.0 |
| | 444153 | AK001610 | Hs.10414 | hypothetical protein FLJ10748 | 3.0 |
| | 408790 | AW580227 | Hs.47860 | neurotrophic tyrosine kinase, receptor, | 3.0 |
| | 426327 | W03242 | Hs.44898 | Homo sapiens clone TCCCTA00151 mRNA sequ | 3.0 |
| 55 | 451468 | AW503398 | Hs.293663 | ESTs, Moderately similar to I38022 hypot | 3.0 |
| | 422758 | AF152329 | Hs.284180 | protocadherin gamma subfamily C, 3 | 3.0 |
| | 421633 | AF121860 | Hs.106260 | sorting nexin 10 | 3.0 |
| | 428361 | NM_015905 | Hs.183858 | transcriptional intermediary factor 1 | 3.0 |
| | 418932 | L34059 | Hs.89484 | cadherin 4, type 1, R-cadherin (retinal) | 3.0 |
| | 416805 | F13271 | Hs.79981 | Human clone Z3560 mRNA sequence | 3.0 |
| 60 | 419518 | U79289 | Hs.90798 | Human clone Z3695 mRNA sequence | 3.0 |
| | 422709 | AA315331 | Hs.153485 | ESTs | 3.0 |
| | 423135 | N67655 | Hs.26411 | ESTs | 3.0 |
| | 424901 | Z11933 | Hs.182505 | POU domain, class 3, transcription facto | 3.0 |
| | 426617 | WS8006 | Hs.266258 | endonuclease G-like 1 | 3.0 |
| 65 | 427386 | AW836261 | Hs.337717 | ESTs | 3.0 |
| | 429859 | NM_007050 | Hs.225952 | protein tyrosine phosphatase, receptor 1 | 3.0 |
| | 435071 | D60683 | Hs.35495 | ESTs | 3.0 |
| | 435092 | AL137310 | Hs.4749 | Homo sapiens mRNA; cDNA DKFZp761E13121 (| 3.0 |
| | 436211 | AK001581 | Hs.334828 | hypothetical protein FLJ10719; KIAA1794 | 3.0 |
| 70 | 436936 | AL134451 | Hs.197478 | ESTs | 3.0 |
| | 445855 | BE247129 | Hs.145569 | ESTs | 3.0 |
| | 452294 | AI871925 | Hs.117895 | ESTs, Moderately similar to A47582 B-cel | 3.0 |
| | 433980 | AA137152 | Hs.286049 | phosphoserine aminotransferase | 3.0 |
| | 430228 | AW950939 | Hs.6382 | ESTs, Highly similar to T00391 hypothe | 3.0 |
| 75 | 451026 | AA013218 | Hs.157492 | cer-d4 (mouse) homolog | 3.0 |
| | 435232 | NM_001262 | Hs.4854 | cyclin-dependent kinase inhibitor 2C (p1 | 3.0 |
| | 439566 | AF086387 | | gb:Homo sapiens full length insert cDNA | 3.0 |
| | 425782 | U66468 | Hs.159525 | cell growth regulatory with EF-hand doma | 3.0 |
| | 416586 | D44643 | Hs.14144 | secreted modular calcium-binding protein | 3.0 |
| 80 | 416874 | H98752 | Hs.42568 | ESTs | 3.0 |
| | 410386 | W26187 | Hs.3327 | Homo sapiens cDNA: FLJ22219 fis, clone H | 3.0 |
| | 411411 | AA345241 | Hs.55950 | ESTs, Weakly similar to KIAA1330 protein | 3.0 |
| | 424066 | Z99348 | Hs.112461 | ESTs, Weakly similar to I38022 hypothe | 3.0 |
| | 404048 | | | | 3.0 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 429163 | AA884766 | | gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s | 3.0 |
| | 454117 | BE410100 | Hs.40368 | adaptor-related protein complex 1, sigma | 3.0 |
| | 418196 | A1745649 | Hs.26549 | KIAA1708 protein | 3.0 |
| | 434131 | A1858275 | Hs.143659 | ESTs | 3.0 |
| 5 | 441255 | R06350 | Hs.171535 | ESTs | 2.9 |
| | 453900 | AW003582 | Hs.226414 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 2.9 |
| | 453905 | NM_002314 | Hs.36566 | UIM domain kinase 1 | 2.9 |
| | 416602 | NM_006159 | Hs.79389 | nel (chicken)-like 2 | 2.9 |
| 10 | 431173 | AW971198 | Hs.294068 | ESTs | 2.9 |
| | 425599 | AW366745 | Hs.214140 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.9 |
| | 436401 | A1087958 | Hs.29088 | ESTs | 2.9 |
| | 422960 | AW890487 | Hs.63984 | cadherin 13, H-cadherin (heart) | 2.9 |
| | 451558 | NM_001089 | Hs.26630 | ATP-binding cassette, sub-family A (ABC1 | 2.9 |
| 15 | 412490 | AW803564 | Hs.288850 | Homo sapiens cDNA: FLJ22528 fis, clone H | 2.9 |
| | 433149 | BE257672 | Hs.42949 | hypothetical protein HES6 | 2.9 |
| | 434811 | AW971205 | Hs.114280 | ESTs | 2.9 |
| | 425897 | AA935315 | Hs.48965 | Homo sapiens cDNA: FLJ21693 fis, clone C | 2.9 |
| | 452092 | BE245374 | Hs.27842 | hypothetical protein FLJ11210 | 2.9 |
| 20 | 453496 | AA442103 | Hs.33084 | solute carrier family 2 (facilitated glu | 2.9 |
| | 411124 | AW196937 | Hs.53929 | ESTs, Weakly similar to ALUB_HUMAN !!! | 2.9 |
| | 419227 | BE537383 | Hs.89739 | cholinergic receptor, nicotinic, beta po | 2.9 |
| | 427651 | AW405731 | Hs.18498 | Homo sapiens cDNA FLJ12277 fis, clone MA | 2.9 |
| | 441707 | R42637 | Hs.21963 | hypothetical protein DKFZp76180514 | 2.9 |
| 25 | 435741 | A1240668 | Hs.113099 | ESTs | 2.9 |
| | 437273 | AL137451 | Hs.120873 | ESTs, Highly similar to T46266 hypothe | 2.9 |
| | 422939 | AW394055 | Hs.98427 | ESTs, Weakly similar to I38022 hypothe | 2.9 |
| | 439376 | AA883521 | Hs.222064 | ESTs | 2.9 |
| | 439935 | S75105 | Hs.301676 | glutamate receptor, ionotropic, kainate | 2.9 |
| 30 | 437267 | AW511443 | Hs.258110 | ESTs | 2.9 |
| | 453740 | AL120295 | Hs.311809 | ESTs, Moderately similar to PC4259 ferri | 2.9 |
| | 400250 | | | | 2.9 |
| | 400992 | | | | 2.9 |
| | 408814 | N62499 | Hs.176227 | hypothetical protein FLJ11155 | 2.9 |
| 35 | 411849 | AW964970 | Hs.18861 | ESTs, Moderately similar to KIAA1276 pro | 2.9 |
| | 414853 | U31116 | Hs.77501 | sarcoglycan, beta (43kD dystrophin-assoc | 2.9 |
| | 423751 | AW235633 | Hs.46525 | ESTs | 2.9 |
| | 426910 | AA470023 | Hs.190089 | ESTs, Moderately similar to ALU1_HUMAN A | 2.9 |
| | 450203 | AF097994 | Hs.301528 | L-tryptophan/alpha-aminoadipate aminotra | 2.9 |
| 40 | 459311 | R40192 | Hs.21527 | Human DNA sequence from clone GS1-115M3 | 2.9 |
| | 425304 | AA463844 | Hs.31339 | fibroblast growth factor 11 | 2.9 |
| | 428500 | A1815395 | Hs.184641 | fatty acid desaturase 2 | 2.9 |
| | 421641 | A1638184 | Hs.106334 | Homo sapiens clone 23836 mRNA sequence | 2.9 |
| | 421141 | AW117261 | Hs.125914 | ESTs | 2.9 |
| 45 | 407870 | AB032990 | Hs.40719 | hypothetical protein KIAA1164 | 2.9 |
| | 456723 | Z43902 | Hs.4748 | adenylate cyclase activating polypeptide | 2.9 |
| | 436456 | AW292677 | Hs.248122 | G protein-coupled receptor 24 | 2.9 |
| | 421483 | NM_003388 | Hs.104717 | hypothetical protein MGC11333 | 2.9 |
| | 412190 | R16180 | Hs.274461 | ESTs | 2.9 |
| 50 | 446131 | NM_000929 | Hs.290 | phospholipase A2, group V | 2.9 |
| | 441668 | A1611973 | Hs.127525 | ESTs | 2.9 |
| | 437387 | A1198874 | Hs.28847 | AD026 protein | 2.9 |
| | 423420 | A1571364 | Hs.128382 | Homo sapiens mRNA; cDNA DKFZp76111224 (f | 2.9 |
| | 427958 | AA418000 | Hs.98280 | potassium intermediate/small conductance | 2.9 |
| 55 | 429084 | AJ001443 | Hs.195614 | splicing factor 3b, subunit 3, 130kD | 2.9 |
| | 447067 | R42098 | Hs.21964 | ESTs | 2.9 |
| | 430887 | N66801 | Hs.260287 | KIAA1841 protein | 2.9 |
| | 441824 | AB007871 | Hs.7977 | KIAA0411 gene product | 2.9 |
| | 424126 | AA335635 | Hs.96917 | ESTs | 2.9 |
| 60 | 408739 | W01556 | Hs.238797 | ESTs, Moderately similar to I38022 hypot | 2.9 |
| | 447422 | BE618703 | Hs.98258 | orthopedia (Drosophila) homolog | 2.9 |
| | 435615 | Y15065 | Hs.4975 | potassium voltage-gated channel, KQT-lik | 2.9 |
| | 446997 | AA383439 | Hs.16758 | Spir-1 protein | 2.9 |
| | 433573 | AF234887 | Hs.57652 | cadherin, EGF LAG seven-pass G-type reco | 2.9 |
| 65 | 408447 | AK002089 | Hs.45080 | Homo sapiens cDNA FLJ11227 fis, clone PL | 2.9 |
| | 419586 | A1088485 | Hs.144759 | ESTs, Weakly similar to I38022 hypothe | 2.8 |
| | 417022 | NM_014737 | Hs.80905 | Ras association (RalGDS/AF-6) domain fam | 2.8 |
| | 408432 | AW195262 | | gb:am67b05.x1 NCI_CGAP_CML1 Homo sapiens | 2.8 |
| | 420320 | AB002361 | Hs.96633 | KIAA0363 protein | 2.8 |
| 70 | 425241 | AA324624 | Hs.155247 | aldolase C, fructose-bisphosphate | 2.8 |
| | 428670 | AA431682 | Hs.134832 | ESTs | 2.8 |
| | 424415 | NM_001975 | Hs.146580 | enolase 2, (gamma, neuronal) | 2.8 |
| | 409185 | AW961601 | Hs.252406 | hypothetical protein FLJ12296 similar to | 2.8 |
| | 411555 | AF113537 | Hs.70669 | HMP19 protein | 2.8 |
| 75 | 426847 | S78723 | Hs.298623 | 5-hydroxytryptamine (serotonin) receptor | 2.8 |
| | 458809 | AW972512 | Hs.20985 | sin3-associated polypeptide, 30kD | 2.8 |
| | 420071 | AB028985 | Hs.94806 | ATP-binding cassette, sub-family A (ABC1 | 2.8 |
| | 424572 | M19650 | Hs.150741 | 2',3'-cyclic nucleotide 3' phosphodiester | 2.8 |
| | 444670 | H58373 | Hs.332938 | hypothetical protein MGC5370 | 2.8 |
| | 411089 | AA456454 | Hs.183418 | cell division cycle 2-like 1 (PITSLRE pr | 2.8 |
| 80 | 416111 | AA033813 | Hs.79018 | chromatin assembly factor 1, subunit A (| 2.8 |
| | 440637 | AW900115 | Hs.7309 | Homo sapiens clone 23741 mRNA sequence | 2.8 |
| | 408554 | AA836381 | Hs.315111 | nuclear receptor co-repressor/HDAC3 comp | 2.8 |
| | 403056 | R58624 | Hs.2186 | eukaryotic translation elongation factor | 2.8 |

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|----|--------|-----------|-----------|--|-----|
| | 423449 | AA97900 | Hs.33067 | ESTs | |
| | 424188 | AW954552 | Hs.142634 | zinc finger protein | 2.8 |
| | 429006 | AA443143 | Hs.50929 | hypothetical protein FLJ13842 | 2.8 |
| 5 | 434981 | AW182577 | Hs.293077 | ESTs | 2.8 |
| | 437435 | AA249439 | Hs.27027 | hypothetical protein DKFZp762H1311 | 2.8 |
| | 442748 | AI016713 | Hs.135787 | ESTs | 2.8 |
| | 443312 | NS2025 | Hs.46616 | ESTs | 2.8 |
| | 450940 | AI744943 | Hs.143209 | ESTs, Weakly similar to I38022 hypotheti | 2.8 |
| 10 | 452738 | AL133800 | Hs.7086 | hypothetical protein MGC12435 | 2.8 |
| | 409182 | AA064970 | Hs.118145 | ESTs | 2.8 |
| | 439793 | AA018825 | Hs.7934 | Kruppel-like factor 4 (gut) | 2.8 |
| | 432683 | AW995441 | Hs.10475 | ESTs | 2.8 |
| | 434269 | AK001991 | Hs.3781 | similar to murine leucine-rich repeat pr | 2.8 |
| | 429500 | X78565 | Hs.289114 | hexabrachion (tenascin C, cytactin) | 2.8 |
| 15 | 433290 | R20077 | Hs.302185 | Homo sapiens clone Z3518 mRNA sequence | 2.8 |
| | 434276 | AF123659 | Hs.53605 | leucine zipper, putative tumor suppresso | 2.8 |
| | 435977 | AL138079 | Hs.5012 | brain-specific membrane-anchored protein | 2.8 |
| | 430294 | AI538226 | Hs.32976 | guanine nucleotide binding protein 4 | 2.8 |
| 20 | 425168 | R96366 | | gb:q37d04.s1 Soares fetal liver spleen | 2.8 |
| | 428180 | AI129767 | Hs.182874 | guanine nucleotide binding protein (G pr | 2.8 |
| | 409348 | AI401535 | Hs.146090 | ESTs | 2.8 |
| | 409887 | AL137534 | Hs.56876 | Homo sapiens mRNA: cDNA DKFZp434H1419 (f | 2.8 |
| | 457211 | AW972565 | Hs.32399 | ESTs, Weakly similar to S51797 vasodilat | 2.8 |
| 25 | 430039 | BE253012 | Hs.153400 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.8 |
| | 417642 | BE302665 | Hs.105461 | hypothetical protein FLJ20357 | 2.8 |
| | 419169 | AW851980 | Hs.262346 | ESTs, Weakly similar to S72482 hypotheti | 2.8 |
| | 434008 | AA740878 | Hs.112982 | ESTs | 2.8 |
| | 446776 | AW293417 | Hs.156455 | ESTs | 2.8 |
| 30 | 408838 | AI669535 | Hs.40369 | ESTs | 2.8 |
| | 422565 | BE259035 | Hs.118400 | singed (Drosophila)-like (sea urchin fas | 2.8 |
| | 447397 | BE247676 | Hs.18442 | E-1 enzyme | 2.8 |
| | 412530 | AA766268 | Hs.266273 | hypothetical protein FLJ13346 | 2.8 |
| | 424330 | AW073953 | Hs.333396 | Homo sapiens cDNA FLJ13596 fis, clone PL | 2.8 |
| 35 | 446377 | AW014022 | Hs.170953 | ESTs | 2.8 |
| | 458924 | BE242158 | Hs.24427 | DKFZP566O1646 protein | 2.8 |
| | 447710 | AI420523 | Hs.328241 | ESTs | 2.8 |
| | 404049 | | | | 2.8 |
| | 416913 | AW934714 | | gb:RC1-DT0001-031299-011-a11 DT0001 Homo | 2.8 |
| 40 | 426400 | M78361 | Hs.169743 | Homo sapiens clone 25121 neuronal octact | 2.8 |
| | 413264 | W26456 | Hs.134757 | hypothetical protein FLJ20033 | 2.8 |
| | 458997 | AW937420 | Hs.69662 | ESTs | 2.7 |
| | 422864 | AA318323 | | gb:EST20390 Retina II Homo sapiens cDNA | 2.7 |
| 45 | 430526 | AF181862 | Hs.242407 | G protein-coupled receptor, family C, gr | 2.7 |
| | 452023 | AB032999 | Hs.27566 | KIAA1173 protein | 2.7 |
| | 432022 | AL162042 | Hs.272348 | Homo sapiens mRNA: cDNA DKFZp761L1212 (f | 2.7 |
| | 452438 | BE514230 | Hs.29595 | JM4 protein | 2.7 |
| | 435408 | H07897 | Hs.4302 | ESTs, Weakly similar to T29299 hypotheti | 2.7 |
| | 418791 | AA935633 | Hs.194628 | ESTs | 2.7 |
| 50 | 438821 | AA826425 | Hs.291829 | ESTs | 2.7 |
| | 423464 | NM_016240 | Hs.128856 | CSR1 protein | 2.7 |
| | 442091 | AW770493 | Hs.182874 | guanine nucleotide binding protein (G pr | 2.7 |
| | 442242 | AV647908 | Hs.90424 | Homo sapiens cDNA: FLJ23285 fis, clone H | 2.7 |
| 55 | 412436 | AA665089 | | gb:nu76d01.s1 NCI_CGAP_Alv1 Homo sapiens | 2.7 |
| | 432821 | BE170702 | Hs.279005 | solute carrier family 21 (organic anion | 2.7 |
| | 416404 | AA180138 | Hs.107924 | ESTs | 2.7 |
| | 441364 | AW450466 | Hs.126830 | ESTs, Weakly similar to YD38_YEAST HYPOT | 2.7 |
| | 450202 | AW969756 | Hs.34145 | ESTs, Weakly similar to B49647 GTP-bindi | 2.7 |
| 60 | 426304 | AA374532 | Hs.124673 | Homo sapiens cDNA FLJ11477 fis, clone HE | 2.7 |
| | 428722 | U76456 | Hs.190787 | tissue inhibitor of metalloproteinase 4 | 2.7 |
| | 449701 | AW952323 | Hs.129908 | KIAA0591 protein | 2.7 |
| | 420372 | AW950049 | Hs.293660 | Homo sapiens, clone IMAGE:3535476, mRNA, | 2.7 |
| | 410318 | AA084050 | Hs.269259 | ESTs, Weakly similar to S23650 retroviru | 2.7 |
| | 414603 | R58394 | Hs.25119 | ESTs, Weakly similar to YEX0_YEAST HYPOT | 2.7 |
| 65 | 416096 | H18577 | Hs.88974 | cytochrome b-245, beta polypeptide (chro | 2.7 |
| | 420896 | AW149342 | Hs.24444 | Homo sapiens cDNA: FLJ22165 fis, clone H | 2.7 |
| | 424856 | AA347746 | Hs.9521 | ESTs, Weakly similar to ZN43_HUMAN ZINC | 2.7 |
| | 436304 | AA339622 | Hs.108887 | ESTs | 2.7 |
| | 441027 | AI911412 | Hs.126444 | ESTs | 2.7 |
| 70 | 452545 | N31940 | Hs.14434 | ESTs, Weakly similar to I38022 hypotheti | 2.7 |
| | 454201 | AB023191 | Hs.44131 | KIAA0974 protein | 2.7 |
| | 448560 | BE613183 | Hs.23213 | ESTs | 2.7 |
| | 426807 | AA385315 | Hs.156682 | ESTs | 2.7 |
| | 425825 | AI929508 | Hs.159590 | lymphocyte antigen 6 complex, locus H | 2.7 |
| 75 | 440351 | AF030933 | Hs.7179 | RAD1 (S. pombe) homolog | 2.7 |
| | 425390 | AI092634 | Hs.156114 | protein tyrosine phosphatase, non-recept | 2.7 |
| | 427624 | AA406245 | Hs.24895 | ESTs | 2.7 |
| | 426413 | AA377823 | | gb:EST90805 Synovial sarcoma Homo sapien | 2.7 |
| 80 | 422491 | AA338548 | Hs.117546 | neuronatin | 2.7 |
| | 424560 | AA158727 | Hs.150555 | protein predicted by clone 23733 | 2.7 |
| | 432415 | T16971 | Hs.289014 | ESTs, Weakly similar to A43932 mucin 2 p | 2.7 |
| | 414865 | AA157155 | Hs.274414 | hypothetical protein FLJ14457 | 2.7 |
| | 415827 | H17462 | Hs.23079 | ESTs | 2.7 |
| | 445568 | H00918 | Hs.268744 | KIAA1796 protein | 2.7 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 433315 | R96754 | Hs.239706 | GRB2-associated binding protein 1 | 2.7 |
| | 428862 | NM_000346 | Hs.2316 | SRY (sex determining region Y)-box 9 (ca | 2.7 |
| | 447959 | AI452784 | Hs.270270 | ESTs, Weakly similar to 2109260A B cell | 2.7 |
| 5 | 426420 | BE383808 | Hs.322430 | NDRG family, member 4 | 2.7 |
| | 436899 | AA764852 | Hs.291567 | ESTs | 2.7 |
| | 444100 | AA383343 | Hs.22116 | CDC14 (cell division cycle 14, S. cerevi | 2.7 |
| | 426501 | AW043782 | Hs.293616 | ESTs | 2.7 |
| | 449092 | U91641 | Hs.22985 | alpha2,8-sialyltransferase | 2.7 |
| 10 | 427311 | AB020672 | Hs.175411 | KIAA0865 protein | 2.7 |
| | 453313 | BE005771 | Hs.153746 | hypothetical protein FLJ22490 | 2.7 |
| | 404029 | | | | 2.7 |
| | 416289 | W26333 | Hs.337438 | ESTs | 2.7 |
| | 439108 | AW163034 | Hs.6467 | synaptogyrin 3 | 2.6 |
| 15 | 418746 | AI955289 | Hs.300759 | ribosomal protein L36 | 2.6 |
| | 412046 | Y07847 | Hs.73088 | RAS-related on chromosome 22 | 2.6 |
| | 435040 | AI932350 | Hs.152825 | ESTs | 2.6 |
| | 453083 | U87223 | Hs.31622 | contactin associated protein 1 | 2.6 |
| | 428167 | AA770021 | Hs.16332 | ESTs | 2.6 |
| 20 | 420028 | AB014680 | Hs.8786 | carbohydrate (N-acetylglucosamine-6-O) s | 2.6 |
| | 443715 | AI583187 | Hs.9700 | cyclin E1 | 2.6 |
| | 421247 | BE391727 | Hs.102910 | general transcription factor IIH, polype | 2.6 |
| | 424687 | J05070 | Hs.151738 | matrix metalloproteinase 9 (gelatinase B | 2.6 |
| | 415056 | AB004662 | Hs.77867 | adenosine A1 receptor | 2.6 |
| 25 | 451697 | AW449774 | Hs.296380 | POM (POM121 rat homolog) and ZP3 fusion | 2.6 |
| | 433701 | AW445023 | Hs.15155 | ESTs | 2.6 |
| | 457358 | AI479755 | Hs.129010 | ESTs | 2.6 |
| | 430347 | NM_002039 | Hs.239706 | GRB2-associated binding protein 1 | 2.6 |
| | 418027 | AB037807 | Hs.83293 | hypothetical protein | 2.6 |
| 30 | 440491 | R35252 | Hs.24944 | ESTs, Weakly similar to 2109260A B cell | 2.6 |
| | 425171 | AW732240 | Hs.16365 | ESTs | 2.6 |
| | 459335 | AW298545 | Hs.250726 | EST | 2.6 |
| | 425402 | AI215881 | Hs.24970 | ESTs, Weakly similar to B34323 GTP-bind | 2.6 |
| | 453169 | AB037815 | Hs.32156 | KIAA1394 protein | 2.6 |
| 35 | 433647 | AA603367 | Hs.222294 | ESTs | 2.6 |
| | 450414 | AI907735 | Hs.21446 | KIAA1716 protein | 2.6 |
| | 446233 | AI282028 | Hs.25205 | ESTs | 2.6 |
| | 415446 | F08898 | Hs.66075 | ESTs | 2.6 |
| | 445873 | AA250970 | Hs.251946 | poly(A)-binding protein, cytoplasmic 1-4 | 2.6 |
| 40 | 413012 | D83777 | Hs.75137 | KIAA0193 gene product | 2.6 |
| | 428671 | BE297851 | Hs.189482 | zinc finger protein 179 | 2.6 |
| | 427158 | AA935603 | Hs.166231 | ESTs | 2.6 |
| | 408988 | AL119844 | Hs.49476 | Homo sapiens clone TUA8 Cri-du-chat regi | 2.6 |
| | 459516 | AI049662 | Hs.246858 | EST | 2.6 |
| | 402693 | | | | 2.6 |
| 45 | 408039 | AA131424 | Hs.50340 | ESTs | 2.6 |
| | 422896 | AW961489 | Hs.154116 | ESTs | 2.6 |
| | 423130 | AW897586 | Hs.21213 | ESTs | 2.6 |
| | 438796 | W67821 | Hs.109590 | genethonin 1 | 2.6 |
| 50 | 439871 | R88518 | Hs.46736 | hypothetical protein FLJ23476 | 2.6 |
| | 440192 | AA872282 | Hs.190596 | ESTs | 2.6 |
| | 419708 | AK000753 | Hs.92374 | hypothetical protein | 2.6 |
| | 449436 | AA860329 | Hs.279307 | hypothetical protein DKFZp434i2117 | 2.6 |
| | 436870 | AW204219 | Hs.155560 | calnexin | 2.6 |
| 55 | 448424 | AW009892 | Hs.31924 | ESTs | 2.6 |
| | 401324 | | | | 2.6 |
| | 414136 | AA812434 | Hs.119023 | SMC2 (structural maintenance of chromoso | 2.6 |
| | 433943 | AA992805 | Hs.44865 | lymphoid enhancer-binding factor 1 | 2.6 |
| 60 | 428001 | H97428 | Hs.219907 | ESTs, Moderately similar to Transforming | 2.6 |
| | 429139 | F09092 | Hs.66087 | ESTs | 2.6 |
| | 423073 | BE252922 | Hs.123119 | MAD (mothers against decapentaplegic, Dr | 2.6 |
| | 448966 | AW372914 | Hs.86149 | phosphoinositol 3-phosphate-binding prot | 2.6 |
| | 444001 | AI095087 | Hs.152299 | ESTs, Moderately similar to S65657 alpha | 2.6 |
| | 412049 | NS3437 | Hs.18268 | adenylate kinase 5 | 2.6 |
| 65 | 441783 | BE313412 | Hs.7961 | Homo sapiens clone 25012 mRNA sequence | 2.6 |
| | 425287 | R88249 | Hs.155524 | peanut (Drosophila)-like 2 | 2.6 |
| | 432149 | AW614326 | Hs.157022 | ESTs, Weakly similar to T34549 probable | 2.6 |
| | 452234 | AW084176 | Hs.223296 | ESTs, Weakly similar to I38022 hypotheti | 2.6 |
| | 453478 | AF083898 | Hs.33021 | neuro-oncological ventral antigen 2 | 2.6 |
| 70 | 418962 | AA714835 | Hs.271863 | ESTs | 2.6 |
| | 418858 | AW961605 | Hs.21145 | hypothetical protein RG083M05.2 | 2.6 |
| | 443257 | AI334040 | Hs.11614 | HSPC065 protein | 2.6 |
| | 428748 | AW593206 | Hs.98785 | Ksp37 protein | 2.6 |
| | 444984 | HI5474 | Hs.132898 | fatty acid desaturase 1 | 2.6 |
| 75 | 433404 | T32982 | Hs.102720 | ESTs | 2.6 |
| | 434779 | AF153815 | Hs.50151 | potassium inwardly-rectifying channel, s | 2.6 |
| | 420582 | BE047878 | Hs.99093 | Homo sapiens chromosome 19, cosmid R2837 | 2.6 |
| | 452856 | AF034799 | Hs.30881 | protein tyrosine phosphatase, receptor t | 2.6 |
| | 436440 | AI471862 | Hs.196008 | Homo sapiens cDNA FLJ11723 fts, clone HE | 2.6 |
| 80 | 438527 | AI969251 | Hs.115325 | RAB7, member RAS oncogene family-like 1 | 2.6 |
| | 433216 | AF217412 | Hs.47320 | neuroigin 3 | 2.6 |
| | 435380 | AA679001 | Hs.192221 | ESTs | 2.6 |
| | 428966 | AF059214 | Hs.194687 | cholesterol 25-hydroxylase | 2.6 |
| | 439653 | AW021103 | Hs.6631 | hypothetical protein FLJ20373 | 2.6 |

| | | | | | |
|----|-------------|---------------------------------------|--|--|-----|
| 5 | 419304 | AI271326 | Hs.146101 | ESTs, Weakly similar to T45070 protein k | 2.6 |
| | 422991 | H10940 | Hs.48965 | Homo sapiens cDNA: FLJ21693 fs, clone C | 2.6 |
| | 448548 | R13209 | Hs.21413 | solute carrier family 12, (potassium-chl | 2.6 |
| | 435370 | AI964074 | Hs.225838 | ESTs | 2.6 |
| | 408875 | NM_015434 | Hs.48604 | DKFZP434B168 protein | 2.6 |
| | 457005 | AJ007421 | Hs.172597 | sal (Drosophila)-like 3 | 2.5 |
| | 430154 | AW583058 | Hs.234726 | serine (or cysteine) proteinase inhibito | 2.5 |
| | 438549 | BE386801 | Hs.21858 | trinucleotide repeat containing 3 | 2.5 |
| 10 | 427951 | AI826125 | Hs.43546 | ESTs | 2.5 |
| | 411800 | N39342 | Hs.103042 | microtubule-associated protein 1B | 2.5 |
| | 457683 | AI821877 | Hs.140002 | ESTs, Moderately similar to ALU7_HUMAN A | 2.5 |
| | 451422 | AB002336 | Hs.26395 | erythrocyte membrane protein band 4.1-f | 2.5 |
| | 430713 | AA351647 | Hs.2642 | eukaryotic translation elongation factor | 2.5 |
| | 428826 | AL048842 | Hs.194019 | atractin | 2.5 |
| 15 | 428963 | AW382682 | Hs.258208 | Homo sapiens, clone MGC:15606, mRNA, com | 2.5 |
| | 428141 | D50402 | Hs.182611 | solute carrier family 11 (proton-coupled | 2.5 |
| | 429560 | AW293055 | Hs.119357 | ESTs | 2.5 |
| | 438662 | AA223599 | Hs.6351 | cleavage and polyadenylation specific fa | 2.5 |
| 20 | 435760 | AF231922 | Hs.213004 | chromosome 21 open reading frame 62 | 2.5 |
| | 427513 | AI476318 | Hs.192480 | ESTs | 2.5 |
| | 430061 | AB037817 | Hs.230188 | KIAA1396 protein | 2.5 |
| | 435923 | BE301830 | Hs.5010 | Homo sapiens clone 24672 mRNA sequence | 2.5 |
| | 417123 | BE326521 | Hs.159450 | ESTs | 2.5 |
| 25 | 439699 | AF086534 | Hs.187561 | ESTs, Moderately similar to ALU1_HUMAN A | 2.5 |
| | 412980 | AI815750 | Hs.20977 | hypothetical protein MGC3129 similar to | 2.5 |
| | 427209 | H06509 | Hs.92423 | KIAA1566 protein | 2.5 |
| | 424327 | AA431707 | Hs.31209 | ESTs | 2.5 |
| | 436340 | R42246 | Hs.21606 | ESTs | 2.5 |
| 30 | 450650 | T65617 | Hs.101257 | hypothetical protein MGC3295 | 2.5 |
| | 439444 | AI277652 | Hs.54578 | ESTs, Weakly similar to I38022 hypotheti | 2.5 |
| | 400777 | | | | 2.5 |
| | 439478 | AF049460 | Hs.6574 | deformed epidermal autoregulatory factor | 2.5 |
| 35 | 450407 | NM_000810 | Hs.24969 | gamma-aminobutyric acid (GABA) A recepto | 2.5 |
| | 450385 | AI631024 | Hs.24948 | synuclein, alpha interacting protein (sy | 2.5 |
| | 432558 | R97268 | Hs.177269 | ESTs | 2.5 |
| | 400860 | | | | 2.5 |
| | 410361 | BE391804 | Hs.62661 | guanylate binding protein 1, interferon- | 2.5 |
| 40 | 416063 | BE047699 | Hs.93454 | ESTs | 2.5 |
| | 414998 | NM_002543 | Hs.77729 | oxidised low density lipoprotein (lectin | 2.5 |
| | 452823 | AB012124 | Hs.30696 | transcription factor-like 5 (basic helix | 2.5 |
| | 417791 | AW965339 | Hs.111471 | ESTs | 2.5 |
| | 418079 | R40058 | Hs.6911 | ESTs | 2.5 |
| | 408495 | W68796 | Hs.237731 | ESTs | 2.5 |
| 45 | 442104 | L20971 | Hs.188 | phosphodiesterase 4B, cAMP-specific (dun | 2.5 |
| | 437370 | AL359567 | Hs.161962 | Homo sapiens mRNA; cDNA DKFZp547D023 (fr | 2.5 |
| | 429803 | W81489 | Hs.223025 | RAB31, member RAS oncogene family | 2.5 |
| | 424959 | NM_005781 | Hs.153937 | activated p21cdc42Hs kinase | 2.5 |
| | 427413 | BE547647 | Hs.177781 | hypothetical protein MGC5618 | 2.5 |
| 50 | 408955 | BE315170 | Hs.8087 | NAG-5 protein | 2.5 |
| | 415261 | T40928 | Hs.8346 | ESTs | 2.5 |
| | 415716 | N59294 | Hs.179662 | nucleosome assembly protein 1-like 1 | 2.5 |
| | 417873 | BE266659 | Hs.293659 | Homo sapiens, Similar to RIKEN cDNA A430 | 2.5 |
| 55 | 418388 | R72332 | Hs.29258 | Homo sapiens cDNA FLJ111364 fs, clone HE | 2.5 |
| | 421002 | AF116030 | Hs.100932 | transcription factor 17 | 2.5 |
| | 423244 | AL039379 | Hs.209602 | ESTs, Weakly similar to ubiquitous TPR m | 2.5 |
| | 423553 | AA405635 | Hs.96854 | ESTs, Weakly similar to DYLL_HUMAN CYTOP | 2.5 |
| | 427961 | AW293165 | Hs.143134 | ESTs | 2.5 |
| 60 | 428301 | AW628666 | Hs.98440 | ESTs, Weakly similar to I38022 hypotheti | 2.5 |
| | 428508 | BE252363 | Hs.184668 | SBB131 protein | 2.5 |
| | 428858 | AA436760 | | gb:zv67d11.r1 Soares_total_fetus_Nb2HF8_ | 2.5 |
| | 428943 | AW086180 | Hs.37636 | ESTs, Weakly similar to KIAA1392 protein | 2.5 |
| | 432427 | AL037630 | Hs.6638 | Homo sapiens cDNA FLJ11602 fs, clone HE | 2.5 |
| | 435347 | AW014873 | Hs.116963 | ESTs | 2.5 |
| 65 | 437949 | U78519 | Hs.41654 | ESTs, Weakly similar to A46010 X-linked | 2.5 |
| | 438208 | AL041224 | Hs.65379 | ESTs | 2.5 |
| | 440286 | U29589 | Hs.7138 | cholinergic receptor, muscarinic 3 | 2.5 |
| | 441523 | AW514263 | Hs.301771 | ESTs, Weakly similar to ALUF_HUMAN !!!! | 2.5 |
| | 441805 | AA285136 | Hs.301914 | neuronal specific transcription factor D | 2.5 |
| 70 | 442337 | AI371029 | Hs.129257 | ESTs, Weakly similar to TC17_HUMAN TRANS | 2.5 |
| | 442789 | AW904361 | Hs.131191 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 2.5 |
| | 445556 | AI910241 | Hs.12887 | actin-related protein 3-beta | 2.5 |
| | 449086 | AI628357 | Hs.208037 | ESTs | 2.5 |
| | 459583 | AI907673 | | gb:IL-BT152-080399-004 BT152 Homo sapien | 2.5 |
| 75 | TABLE 24B: | | | | |
| | Pkey: | Unique Eos probeset identifier number | | | |
| | CAT number: | Gene cluster number | | | |
| | Accession: | Genbank accession numbers | | | |
| 80 | Pkey | CAT Number | Accession | | |
| | 408432 | 1058667_1 | AW195262 R27868 AW811262 | | |
| | 412225 | 1284108_1 | AW902042 N77591 | | |
| | 412436 | 129439_1 | AA665089 AA135130 AA484059 AA102419 AW877765 | | |

| | | | |
|----|--------|-----------|---|
| 5 | 416120 | 1571266_1 | H46739 H51513 H19779 |
| | 416871 | 1626761_1 | H98716 N90792 N24283 |
| | 416913 | 163001_1 | AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AWS13465 BE161006 BE162499 |
| | 422864 | 222336_1 | AA318323 H11145 R15289 AA451945 AA476690 AA436954 Z43802 F11753 T65491 D81821 |
| | 422949 | 223184_1 | AA319435 N56456 AA319377 AW961532 T48452 AA894424 |
| | 422977 | 223410_1 | AA631498 AJ017191 AA491211 AA761823 AA714555 AA768099 AA808286 AI934069 AA570223 AA574389 AA582438 AI745346 AW964510 AA319642 |
| | | | AW853758 H56414 |
| 10 | 423756 | 231725_1 | AA828125 AA834883 AA330555 |
| | 425168 | 247552_1 | R96366 AL133929 AA351636 H78818 AA477084 Z28957 H80194 |
| | 425517 | 252729_1 | AF121179 BE162736 AA358827 |
| | 426413 | 266650_1 | AA377823 AW954494 AI022688 |
| | 428002 | 285602_1 | AA418703 AA418711 BE071915 BE071920 BE071912 |
| | 428679 | 294049_1 | AA431765 AA432015 |
| 15 | 428858 | 296453_1 | AA436760 AW237453 BE327496 N47347 N56967 |
| | 429007 | 298301_1 | D80642 AA443145 AL119015 AW904500 |
| | 429163 | 300543_1 | AA884766 AW974271 AA592975 AA447312 |
| | 433532 | 368950_1 | AW975367 AA598607 AA742735 |
| | 436190 | 41555_1 | AK001059 AA633055 |
| 20 | 437034 | 431713_1 | AA742643 AA808575 AW976668 |
| | 438458 | 457837_1 | AW975186 AA807807 D29548 |
| | 438993 | 467651_1 | AA828995 AA834879 AI926361 |
| | 439566 | 47387_1 | AF086387 W77884 W72711 |
| | 440322 | 491966_1 | AA879430 BE070262 BE070493 BE070272 BE070484 BE070397 BE070395 BE070201 BE070198 BE070404 BE070270 BE070400 |
| 25 | 444584 | 611496_1 | AI168422 D80113 T59074 |
| | 447197 | 711623_1 | R36075 AI366546 R36167 |
| | 448451 | 764066_1 | AW015994 R39898 AW000978 AI598202 AI521706 |
| | 450625 | 84032_1 | AW970107 AA513951 AA010406 |
| | 452453 | 918300_1 | AI902519 AI902518 AI902516 |
| 30 | 454996 | 1248640_1 | AW850180 AW850326 |
| | 455350 | 1283853_1 | AW901809 AW901787 AW901795 AW901792 AW901744 AW901753 AW901807 AW901798 |

TABLE 24C:

| | |
|--------------|---|
| Pkey: | Unique number corresponding to an Eos probeset |
| Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <u>Nature</u> 402:489-495. |
| Strand: | Indicates DNA strand from which exons were predicted. |
| Nt_position: | Indicates nucleotide positions of predicted exons. |

| | | | | |
|----|--------|---------|--------|---|
| 40 | Pkey | Ref | Strand | Nt_position |
| | 400777 | 8131663 | Plus | 70745-71121 |
| | 400780 | 8131663 | Minus | 118372-118619 |
| | 400859 | 9757499 | Minus | 91888-92018,98131-98294,99474-99570 |
| | 400860 | 9757499 | Minus | 151830-152104,152649-152744 |
| 45 | 400992 | 8096828 | Plus | 140390-140822 |
| | 401324 | 9863791 | Plus | 234057-234174 |
| | 402408 | 9796239 | Minus | 110326-110491 |
| | 402604 | 9909420 | Plus | 20393-20767 |
| | 402605 | 9909420 | Minus | 47680-47973 |
| 50 | 402693 | 8569863 | Minus | 82366-82515 |
| | 402855 | 9662953 | Minus | 59763-59909 |
| | 404029 | 7671252 | Plus | 108716-111112 |
| | 404048 | 3688074 | Minus | 54421-56808 |
| | 404049 | 3688074 | Minus | 75765-78155 |
| 55 | 404283 | 2276311 | Minus | 99460-99564 |
| | 404299 | 5738652 | Minus | 3826-4025 |
| | 404541 | 8318559 | Plus | 103456-103664 |
| | 404584 | 9857511 | Plus | 138651-139153 |
| | 404593 | 9944086 | Minus | 74922-75788 |
| 60 | 404721 | 9856648 | Minus | 173763-174294 |
| | 404819 | 4678240 | Plus | 16223-16319,16427-16513,16736-16859,16941-17075,17170-17287,17389-17529,18261-18357,18443-18578 |
| | 405238 | 7249119 | Minus | 51728-51836 |
| | 405771 | 7018349 | Plus | 91191-91254,91510-91589 |
| | 405819 | 4007557 | Plus | 2830-2967 |
| 65 | 406311 | 9211559 | Minus | 137114-139033 |

TABLE 25A: ABOUT 1202 GENES UP-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CENTRAL NERVOUS SYSTEM (CNS)

Table 25A lists about 1202 genes up-regulated in glioblastoma compared to normal adult central nervous system (CNS). These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" glioblastoma to "average" normal adult CNS tissues was greater than or equal to 2.0. The "average" glioblastoma level was set to the 75th percentile amongst various glioblastoma tumors. The "average" normal adult CNS tissue level was set to the 95th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

| | |
|----------------|--|
| Pkey: | Unique Eos probeset identifier number |
| ExAccn: | Exemplar Accession number, Genbank accession number |
| UnigenelD: | Unigene number |
| Unigene Title: | Unigene gene title |
| R1: | Ratio of 75 th percentile tumor to 95 th percentile normal adult nervous system tissue |

| | | | | | |
|----|--------|----------|-----------|------------------------|------|
| 80 | Pkey | ExAccn | UnigenelD | Unigene Title | R1 |
| | 452461 | N78223 | Hs.108106 | transcription factor | 20.1 |
| | 436895 | AF037335 | Hs.5338 | carbonic anhydrase XII | 15.2 |
| | 453941 | U39817 | Hs.36820 | Bloom syndrome | 14.2 |
| | 443247 | BE614387 | Hs.333893 | c-Myc target JPO1 | 12.4 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 428330 | L22524 | Hs.2256 | matrix metalloproteinase 7 (matrilysin, | 12.0 |
| | 447342 | AI199268 | Hs.19322 | Homo sapiens, Similar to RIKEN cDNA 2010 | 11.7 |
| | 422163 | AF027208 | Hs.112350 | prominin (mouse)-like 1 | 11.4 |
| 5 | 439451 | AF086270 | Hs.278554 | heterochromatin-like protein 1 | 11.2 |
| | 424800 | AL035588 | Hs.153203 | MyoD family inhibitor | 10.2 |
| | 416111 | AA033813 | Hs.79018 | chromatin assembly factor 1, subunit A (| 10.0 |
| | 444190 | AB78918 | Hs.10526 | cysteine and glycine-rich protein 2 | 9.9 |
| | 412140 | AA219691 | Hs.73625 | RAB6 interacting, kinesin-like (rabkines | 9.9 |
| 10 | 449340 | AW235786 | Hs.195359 | hypothetical protein MGC10954 | 9.8 |
| | 409731 | AA125985 | Hs.56145 | thymosin, beta, identified in neuroblast | 9.4 |
| | 439978 | BE139460 | Hs.124673 | Homo sapiens cDNA FLJ11477 fis, clone HE | 8.9 |
| | 411411 | AA345241 | Hs.55950 | ESTs, Weakly similar to KIAA1330 protein | 8.9 |
| | 456516 | BE172704 | Hs.222746 | KIAA1610 protein | 8.2 |
| 15 | 420092 | AA814043 | Hs.88045 | ESTs | 7.9 |
| | 422631 | BE218919 | Hs.118793 | hypothetical protein FLJ10688 | 7.9 |
| | 453392 | U23752 | Hs.32964 | SRY (sex determining region Y)-box 11 | 7.9 |
| | 438527 | AI969251 | Hs.115325 | RAB7, member RAS oncogene family-like 1 | 7.9 |
| | 427581 | NM_014788 | Hs.179703 | KIAA0129 gene product | 7.8 |
| 20 | 418861 | NM_001949 | Hs.1189 | E2F transcription factor 3 | 7.8 |
| | 440684 | AI253123 | Hs.127356 | ESTs, Highly similar to S21424 nestin [H | 7.8 |
| | 429643 | AA455889 | Hs.167279 | FYVE-finger-containing Rab5 effector pro | 7.7 |
| | 409638 | AW450420 | Hs.21335 | ESTs | 7.5 |
| | 444665 | BE613126 | Hs.47783 | B aggressive lymphoma gene | 7.5 |
| 25 | 456759 | BE259150 | Hs.127792 | delta (Drosophila)-like 3 | 7.5 |
| | 412777 | AI335773 | Hs.270123 | ESTs | 7.4 |
| | 436607 | AW661783 | Hs.211061 | ESTs | 7.3 |
| | 432058 | AW665996 | Hs.130729 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 7.3 |
| | 417061 | AI675944 | Hs.188691 | Homo sapiens cDNA FLJ12033 fis, clone HE | 7.3 |
| 30 | 428976 | AL037824 | Hs.194695 | ras homolog gene family, member 1 | 7.2 |
| | 433244 | AB040943 | Hs.271285 | KIAA1510 protein | 7.1 |
| | 436726 | AA324975 | Hs.128993 | ESTs, Weakly similar to T00079 hypotheti | 7.1 |
| | 408432 | AW195262 | | gb:cn67b05.x1 NCI_CGAP_CML1 Homo sapiens | 7.1 |
| | 434164 | AW207019 | Hs.148135 | serine/threonine kinase 33 | 7.0 |
| 35 | 445873 | AA250970 | Hs.251946 | poly(A)-binding protein, cytoplasmic 1-I | 7.0 |
| | 439726 | AW449893 | Hs.293707 | ESTs, Weakly similar to I38598 zinc fing | 7.0 |
| | 432656 | NM_000246 | Hs.3076 | MHC class II transactivator | 6.8 |
| | 431117 | AF003522 | Hs.250500 | delta (Drosophila)-like 1 | 6.8 |
| | 453387 | AI990741 | Hs.252809 | ESTs | 6.8 |
| 40 | 418821 | AA436002 | Hs.183161 | ESTs | 6.6 |
| | 437034 | AA742643 | | gb:ny91c01.s1 NCI_CGAP_GCB1 Homo sapiens | 6.6 |
| | 411252 | AB018549 | Hs.69328 | MD-2 protein | 6.5 |
| | 424687 | J05070 | Hs.151738 | matrix metalloproteinase 9 (gelatinase B | 6.4 |
| | 452953 | AI932884 | Hs.271741 | ESTs, Weakly similar to A46010 X-linked | 6.3 |
| 45 | 433532 | AW975367 | | gb:EST387475 MAGE resequences, MAGN Homo | 6.3 |
| | 420311 | AW445044 | Hs.38207 | Human DNA sequence from clone RP4-53015 | 6.3 |
| | 418097 | R45137 | Hs.21868 | ESTs | 6.2 |
| | 407304 | AA565832 | | gb:nj32b03.s1 NCI_CGAP_AA1 Homo sapiens | 6.2 |
| | 435256 | AF193766 | Hs.13872 | cytokine-like protein C17 | 6.1 |
| 50 | 449448 | D60730 | Hs.57471 | ESTs | 6.1 |
| | 403790 | | | | 6.0 |
| | 425517 | AF121179 | | gb:AF121179 Homo sapiens liver (Chang L- | 6.0 |
| | 420674 | NM_000055 | Hs.1327 | butyrylcholinesterase | 6.0 |
| | 435542 | AA687376 | Hs.269533 | ESTs | 5.9 |
| 55 | 418216 | AA662240 | Hs.283099 | AF15q14 protein | 5.8 |
| | 439086 | AF085947 | | gb:Homo sapiens full length insert cDNA | 5.8 |
| | 408037 | AW271720 | Hs.42233 | hypothetical protein FLJ10300 | 5.7 |
| | 412225 | AW902042 | | gb:QV0-NN1022-170400-193-c02 NN1022 Homo | 5.7 |
| | 436109 | AA922153 | Hs.132760 | hypothetical protein MGC15729 | 5.7 |
| 60 | 435005 | U80743 | Hs.306094 | trinucleotide repeat containing 12 | 5.7 |
| | 429149 | AW193360 | Hs.197962 | ESTs, Weakly similar to I38022 hypotheti | 5.7 |
| | 418113 | AI272141 | Hs.83484 | SRY (sex determining region Y)-box 4 | 5.6 |
| | 405558 | | | | 5.6 |
| | 442432 | BE093589 | Hs.38178 | hypothetical protein FLJ23468 | 5.6 |
| 65 | 442547 | AA306997 | Hs.217484 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 5.6 |
| | 413063 | AL035737 | Hs.75184 | chitinase 3-like 1 (cartilage glycoprote | 5.5 |
| | 420560 | AW207748 | Hs.59115 | ESTs | 5.5 |
| | 408096 | BE250162 | Hs.83765 | dihydrofolate reductase | 5.5 |
| | 443539 | AI076182 | Hs.134074 | ESTs, Moderately similar to ALU6_HUMAN A | 5.4 |
| 70 | 426318 | AA375125 | Hs.147112 | Homo sapiens cDNA: FLJ22322 fis, clone H | 5.4 |
| | 429115 | AA446728 | Hs.289020 | Homo sapiens cDNA FLJ14098 fis, clone MA | 5.3 |
| | 453900 | AW003582 | Hs.226414 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 5.3 |
| | 444168 | AW379879 | | gb:RC1-HT0256-081199-011-r01 HT0256 Homo | 5.3 |
| | 432789 | D26361 | Hs.3104 | KIAA0042 gene product | 5.3 |
| 75 | 437036 | AI571514 | Hs.133022 | ESTs | 5.2 |
| | 421247 | BE391727 | Hs.102910 | general transcription factor IIIH, polype | 5.2 |
| | 441523 | AW514263 | Hs.301771 | ESTs, Weakly similar to ALUF_HUMAN !!!! | 5.1 |
| | 451106 | BE382701 | Hs.25960 | v-myc avian myelocytomatosis viral relat | 5.1 |
| | 457211 | AW972565 | Hs.32399 | ESTs, Weakly similar to S51797 vasodilat | 5.1 |
| 80 | 454157 | AW162906 | Hs.312481 | ESTs, Weakly similar to S66668 hydrogen | 5.1 |
| | 423343 | AA324643 | Hs.246106 | ESTs | 5.1 |
| | 425292 | NM_005824 | Hs.155545 | 37 kDa leucine-rich repeat (LRR) protein | 5.1 |
| | 406679 | AA070786 | | gb:zm66b07.r1 Stratagene neuroepithelium | 5.1 |
| | 442671 | AI005668 | Hs.134779 | EST | 5.1 |

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|----|--------|-----------|-----------|--|-----|
| | 433001 | AF217513 | Hs.279905 | clone HQ0310 PRO0310p1 | 5.0 |
| | 418819 | AA228776 | Hs.191721 | ESTs | 5.0 |
| | 432946 | U60899 | Hs.279854 | mannosidase, alpha, class 2B, member 1 | 4.9 |
| 5 | 420730 | NM_002691 | Hs.99890 | polymerase (DNA directed), delta 1, cata | 4.9 |
| | 441217 | AI922183 | Hs.213246 | ESTs | 4.9 |
| | 453385 | AW296101 | Hs.252806 | ESTs | 4.8 |
| | 418203 | X54942 | Hs.83758 | CDC28 protein kinase 2 | 4.7 |
| | 450813 | AI739525 | Hs.203376 | ESTs | 4.7 |
| 10 | 444006 | BE395085 | Hs.10086 | type I transmembrane protein Fn14 | 4.7 |
| | 412530 | AA766268 | Hs.266273 | hypothetical protein FLJ13346 | 4.7 |
| | 431070 | AW408164 | Hs.249184 | transcription factor 19 (SC1) | 4.7 |
| | 429786 | AL080232 | Hs.220696 | Homo sapiens mRNA; cDNA DKFZp586A061 (fr | 4.7 |
| | 405771 | | | | 4.6 |
| 15 | 457065 | AM76318 | Hs.192480 | ESTs | 4.6 |
| | 436190 | AK001059 | | gb:Homo sapiens cDNA FLJ10197 fis, clone | 4.6 |
| | 400859 | | | | 4.6 |
| | 435267 | N23797 | Hs.110114 | ESTs | 4.6 |
| | 443454 | AI057494 | Hs.133421 | ESTs | 4.5 |
| 20 | 452811 | AA937079 | Hs.118983 | hypothetical protein FLJ12150 | 4.5 |
| | 437267 | AW511443 | Hs.258110 | ESTs | 4.5 |
| | 435020 | AW505076 | Hs.301855 | DiGeorge syndrome critical region gene 8 | 4.5 |
| | 454269 | AI961060 | Hs.129908 | KIAA0591 protein | 4.5 |
| | 422106 | D84239 | Hs.111732 | Fc fragment of IgG binding protein | 4.5 |
| 25 | 422765 | AW409701 | Hs.1578 | baculoviral IAP repeat-containing 5 (sur | 4.5 |
| | 456534 | X91195 | Hs.100623 | phospholipase C, beta 3, neighbor pseudo | 4.5 |
| | 423756 | AA828125 | | gb:od71a09.s1 NCI_CGAP_Ov2 Homo sapiens | 4.5 |
| | 417308 | H60720 | Hs.81892 | KIAA0101 gene product | 4.5 |
| | 422170 | AI791949 | Hs.112432 | anti-Mullerian hormone | 4.4 |
| 30 | 429500 | X78565 | Hs.289114 | hexabrachion (tenascin C, cytotoxic) | 4.4 |
| | 406568 | AF088886 | Hs.11590 | cathepsin F | 4.4 |
| | 426812 | AF105365 | Hs.172613 | solute carrier family 12 (potassium/chloro | 4.4 |
| | 402516 | | | | 4.4 |
| | 432865 | AI753709 | Hs.152484 | ESTs, Weakly similar to I38022 hypothe | 4.4 |
| 35 | 413625 | AW451103 | Hs.71371 | ESTs | 4.4 |
| | 436098 | R20597 | Hs.9739 | glycerol-3-phosphate dehydrogenase 1 (so | 4.4 |
| | 418333 | W92113 | | gb:zh48e01.r1 Soares_fetal_liver_spleen_ | 4.4 |
| | 416933 | BE561850 | Hs.80506 | small nuclear ribonucleoprotein polypept | 4.4 |
| | 438192 | AI859065 | Hs.337620 | Homo sapiens AFG3L1 isoform 1 mRNA, part | 4.3 |
| 40 | 457374 | AA493662 | | gb:nh05d12.s1 NCI_CGAP_Thy1 Homo sapiens | 4.3 |
| | 433159 | AB035898 | Hs.150587 | kinesin-like protein 2 | 4.3 |
| | 444386 | BE065183 | | gb:RC1-BT0314-020200-012-c04 BT0314 Homo | 4.3 |
| | 453202 | AW085781 | Hs.26270 | hypothetical protein FLJ11588 | 4.3 |
| | 441020 | W79283 | Hs.35962 | ESTs | 4.3 |
| 45 | 414733 | BE514535 | Hs.77171 | minichromosome maintenance deficient (S. | 4.3 |
| | 407902 | AL117474 | Hs.41181 | Homo sapiens mRNA; cDNA DKFZp727C191 (fr | 4.3 |
| | 405701 | | | | 4.3 |
| | 451659 | BE379761 | Hs.14248 | ESTs | 4.3 |
| | 418845 | AA852985 | Hs.89232 | chromobox homolog 5 (Drosophila HP1 alph | 4.2 |
| 50 | 433323 | AA805132 | Hs.30701 | ESTs | 4.2 |
| | 439811 | AA135332 | Hs.71608 | ESTs | 4.2 |
| | 415406 | T26510 | | gb:AB282FBR Infant brain, LLNL array of | 4.2 |
| | 436282 | R91913 | Hs.272104 | ESTs, Moderately similar to ALU1_HUMAN A | 4.1 |
| | 441269 | AW015206 | Hs.178784 | ESTs | 4.1 |
| 55 | 418727 | AA227609 | Hs.94834 | ESTs | 4.1 |
| | 433006 | BE242758 | Hs.190223 | ESTs, Moderately similar to T29285 hypot | 4.1 |
| | 436480 | AJ271643 | Hs.87469 | putative acid-sensing ion channel | 4.1 |
| | 430786 | AA486144 | Hs.31293 | ESTs | 4.1 |
| | 445372 | N36417 | Hs.144928 | ESTs | 4.1 |
| 60 | 410555 | U92649 | Hs.64311 | a disintegrin and metalloproteinase doma | 4.0 |
| | 457465 | AW301344 | Hs.122908 | DNA replication factor | 4.0 |
| | 422094 | AF129535 | Hs.272027 | F-box only protein 5 | 4.0 |
| | 442029 | AW956698 | Hs.14456 | neural precursor cell expressed, develop | 4.0 |
| | 459321 | AW044477 | Hs.299538 | ESTs | 4.0 |
| 65 | 421308 | AA687322 | Hs.192843 | leucine zipper protein FKSG14 | 4.0 |
| | 420567 | AK000812 | Hs.98874 | similar to proline-rich protein 48 | 4.0 |
| | 447004 | AW296968 | Hs.157539 | ESTs | 4.0 |
| | 448295 | AI381911 | Hs.334859 | KIAA1814 protein | 3.9 |
| | 439699 | AF086534 | Hs.187561 | ESTs, Moderately similar to ALU1_HUMAN A | 3.9 |
| 70 | 440704 | M69241 | Hs.162 | insulin-like growth factor binding prote | 3.9 |
| | 453096 | AW294631 | Hs.11325 | ESTs | 3.9 |
| | 457026 | AA397620 | Hs.48692 | ESTs | 3.9 |
| | 404642 | | | | 3.9 |
| | 450375 | AA009647 | Hs.8850 | a disintegrin and metalloproteinase doma | 3.9 |
| 75 | 430132 | AA204686 | Hs.234149 | hypothetical protein FLJ20647 | 3.9 |
| | 437718 | AI927288 | Hs.196779 | ESTs | 3.9 |
| | 438490 | AW593272 | Hs.301299 | ESTs | 3.9 |
| | 429919 | AA460692 | Hs.278945 | hypothetical protein FLJ23024 | 3.9 |
| | 413604 | R51767 | | gb:yg73g11.r1 Soares infant brain 1N1B H | 3.9 |
| 80 | 425599 | AW366745 | Hs.214140 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.9 |
| | 448796 | AA147829 | Hs.301431 | endothelial zinc finger protein induced | 3.9 |
| | 449300 | AI656959 | Hs.222165 | ESTs | 3.8 |
| | 452203 | X57522 | Hs.158164 | transporter 1, ATP-binding cassette, sub | 3.8 |
| | 425769 | U72513 | Hs.159486 | Human RPL13-2 pseudogene mRNA, complete | 3.8 |

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|----|--------|-----------|-----------|--|-----|
| | 404295 | | | | |
| | 410361 | BE391804 | Hs.62661 | guanylate binding protein 1, interferon- | 3.8 |
| | 428728 | NM_016625 | Hs.191381 | hypothetical protein | 3.8 |
| 5 | 409142 | AL136877 | Hs.50758 | SMC4 (structural maintenance of chromoso | 3.8 |
| | 430172 | AA468591 | Hs.161889 | ESTs | 3.8 |
| | 447499 | AW262580 | Hs.147674 | protocadherin beta 16 | 3.8 |
| | 405884 | | | | 3.8 |
| | 437236 | AW137817 | Hs.244353 | ESTs | 3.8 |
| 10 | 418883 | BE387036 | Hs.1211 | acid phosphatase 5, tartrate resistant | 3.7 |
| | 444143 | AW747996 | Hs.160999 | ESTs, Moderately similar to A56194 throm | 3.7 |
| | 425529 | NM_014656 | Hs.158282 | KIAA0040 gene product | 3.7 |
| | 425502 | R98895 | Hs.125823 | ESTs | 3.7 |
| | 419741 | NM_007019 | Hs.93002 | ubiquitin carrier protein E2-C | 3.7 |
| | 402424 | | | | 3.7 |
| 15 | 429469 | M64590 | Hs.27 | glycine dehydrogenase (decarboxylating; | 3.7 |
| | 434072 | H70854 | Hs.283059 | Homo sapiens PRO1082 mRNA, complete cds | 3.7 |
| | 414872 | U82010 | Hs.77513 | COX10 (yeast) homolog, cytochrome c oxid | 3.7 |
| | 426071 | AW138057 | Hs.163835 | ESTs | 3.7 |
| 20 | 419078 | M93119 | Hs.89584 | insulinoma-associated 1 | 3.7 |
| | 428037 | N47474 | Hs.89230 | potassium intermediate/small conductance | 3.7 |
| | 416547 | H62914 | Hs.268946 | ESTs, Weakly similar to PC4259 ferritin | 3.7 |
| | 436899 | AA764852 | Hs.291567 | ESTs | 3.7 |
| | 436722 | AW975977 | | gb:EST388086 MAGE resequences, MAGN Homo | 3.6 |
| 25 | 440652 | AI216751 | Hs.143977 | ESTs | 3.6 |
| | 428450 | NM_014791 | Hs.184339 | KIAA0175 gene product | 3.6 |
| | 452103 | R42764 | Hs.339654 | ESTs, Weakly similar to I38022 hypothe | 3.6 |
| | 409048 | H59990 | Hs.37699 | ESTs | 3.6 |
| | 439546 | AF088056 | | gb:Homo sapiens full length insert cDNA | 3.6 |
| 30 | 443544 | AI076315 | Hs.16359 | ESTs | 3.6 |
| | 418478 | U38945 | Hs.1174 | cyclin-dependent kinase inhibitor 2A (me | 3.6 |
| | 435889 | AI249107 | Hs.269901 | ESTs | 3.6 |
| | 420301 | AA767526 | Hs.22030 | paired box gene 5 (B-cell lineage specif | 3.6 |
| | 438078 | AI016377 | Hs.131693 | ESTs | 3.6 |
| 35 | 408420 | NM_006915 | Hs.44766 | retinitis pigmentosa 2 (X-linked recessi | 3.6 |
| | 416871 | H98716 | | gb:yx13d08.s1 Soares melanocyte 2NbHM Ho | 3.6 |
| | 424085 | NM_002914 | Hs.139226 | replication factor C (activator 1) 2 (40 | 3.5 |
| | 446291 | BE397753 | Hs.14623 | interferon, gamma-inducible protein 30 | 3.5 |
| | 432281 | AK001239 | Hs.274263 | hypothetical protein FLJ10377 | 3.5 |
| 40 | 436123 | AA057484 | Hs.35406 | ESTs, Highly similar to unnamed protein | 3.5 |
| | 411256 | AW834039 | | gb:QV0-TT0010-091199-053-e09 TT0010 Homo | 3.5 |
| | 419239 | AA468183 | Hs.184598 | Homo sapiens cDNA: FLJ23241 fis, clone C | 3.5 |
| | 435065 | BE064391 | | gb:RC4-BT0310-110300-015-b08 BT0310 Homo | 3.5 |
| | 435532 | AW291488 | Hs.117305 | Homo sapiens, clone IMAGE:3682908, mRNA | 3.5 |
| 45 | 447101 | N72185 | Hs.44189 | ESTs | 3.5 |
| | 410530 | M25809 | Hs.64173 | ATPase, H+ transporting, lysosomal (vacu | 3.5 |
| | 422156 | N34524 | | gb:yy56d10.s1 Soares multiple sclerosis_ | 3.5 |
| | 453616 | NM_003462 | Hs.33846 | dynein, axonemal, light intermediate pol | 3.5 |
| 50 | 439743 | AL389956 | Hs.283858 | Homo sapiens mRNA full length insert cDN | 3.5 |
| | 453884 | AA355925 | Hs.36232 | KIAA0186 gene product | 3.5 |
| | 424954 | NM_000546 | Hs.1846 | tumor protein p53 (Li-Fraumeni syndrome) | 3.5 |
| | 420721 | AA927802 | Hs.159471 | ZAP3 protein | 3.5 |
| | 426764 | AA732524 | Hs.151464 | ESTs, Weakly similar to ALUC_HUMAN !!!! | 3.5 |
| | 420649 | AI866964 | Hs.124704 | ESTs, Moderately similar to S65657 alpha | 3.4 |
| 55 | 448831 | AL080123 | Hs.22182 | zinc finger protein 23 (KOX 16) | 3.4 |
| | 444371 | BE540274 | Hs.239 | forkhead box M1 | 3.4 |
| | 402604 | | | | 3.4 |
| | 442407 | AW469584 | Hs.32353 | mitogen-activated protein kinase kinase | 3.4 |
| 60 | 414300 | AI304870 | Hs.188680 | ESTs | 3.4 |
| | 444670 | H58373 | Hs.332938 | hypothetical protein MGC5370 | 3.4 |
| | 414550 | BE379808 | | gb:601159567T1 NIH_MGC_53 Homo sapiens c | 3.4 |
| | 452211 | AI985513 | Hs.233420 | ESTs | 3.4 |
| | 414416 | AW409985 | Hs.76084 | hypothetical protein MGC2721 | 3.4 |
| | 449961 | AW265634 | Hs.133100 | ESTs | 3.4 |
| 65 | 413257 | BE075035 | | gb:PM3-BT0584-260300-002-g05 BT0584 Homo | 3.4 |
| | 453857 | AL080235 | Hs.35861 | DKFZP586E1621 protein | 3.4 |
| | 417404 | NM_007350 | Hs.82101 | pleckstrin homology-like domain, family | 3.4 |
| | 422846 | BE513934 | Hs.1583 | neutrophil cytosolic factor 1 (47kD, chr | 3.4 |
| 70 | 446189 | H85224 | Hs.214013 | ESTs | 3.4 |
| | 437385 | AA757055 | Hs.164060 | ESTs | 3.4 |
| | 453652 | AW009640 | Hs.28368 | ESTs, Moderately similar to S65657 alpha | 3.4 |
| | 408298 | AI745325 | Hs.271923 | Homo sapiens cDNA: FLJ22785 fis, clone K | 3.4 |
| | 455778 | BE088746 | | gb:CM2-BT0693-210300-123-d09 BT0693 Homo | 3.3 |
| | 417546 | H65569 | Hs.18845 | ESTs | 3.3 |
| 75 | 412471 | M63193 | Hs.73946 | endothelial cell growth factor 1 (plate | 3.3 |
| | 454631 | AW811324 | | gb:IL3-ST0141-131099-017-A02 ST0141 Homo | 3.3 |
| | 454294 | AB000734 | Hs.50640 | JAK binding protein | 3.3 |
| | 457131 | AC002310 | Hs.301463 | Human Chromosome 16 BAC clone CIT987SK-A | 3.3 |
| | 410102 | AW248508 | Hs.279727 | Homo sapiens cDNA FLJ14035 fis, clone HE | 3.3 |
| 80 | 449676 | AW380579 | Hs.209657 | ESTs | 3.3 |
| | 436211 | AK001581 | Hs.334828 | hypothetical protein FLJ10719; KIAA1794 | 3.3 |
| | 453745 | AL120611 | | gb:DKFZp761H119_r1 761 (synonym: hamy2) | 3.3 |
| | 452799 | AI948829 | Hs.213786 | ESTs | 3.3 |
| | 435380 | AA679001 | Hs.192221 | ESTs | 3.3 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| 5 | 426746 | J03626 | Hs.2057 | uridine monophosphate synthetase (orotat | 3.3 |
| | 453362 | H14988 | Hs.107375 | ESTs | 3.3 |
| | 456473 | AJ202788 | Hs.25682 | Homo sapiens mRNA for KIAA1863 protein, | 3.3 |
| | 416426 | AA180256 | Hs.210473 | Homo sapiens cDNA FLJ14872 fis, clone PL | 3.3 |
| | 445777 | AI580371 | Hs.145384 | ESTs | 3.3 |
| 10 | 423757 | AL049337 | Hs.132571 | Homo sapiens mRNA; cDNA DKFZp564P016 (fr | 3.3 |
| | 431941 | AK000106 | Hs.272227 | Homo sapiens cDNA FLJ20099 fis, clone CO | 3.3 |
| | 404299 | | | | 3.3 |
| | 404108 | | | | 3.3 |
| | 425189 | H16622 | | gb:ym26c07.r1 Soares infant brain 1MIB H | 3.3 |
| 15 | 449318 | AW236021 | Hs.78531 | Homo sapiens, Similar to RIKEN cDNA 5730 | 3.3 |
| | 450193 | AJ916071 | Hs.15607 | Homo sapiens Fanconi anemia complementat | 3.2 |
| | 427725 | U66839 | Hs.180533 | mitogen-activated protein kinase kinase | 3.2 |
| | 424051 | AL110203 | Hs.138411 | Homo sapiens mRNA; cDNA DKFZp586J1922 (f | 3.2 |
| | 418968 | NM_000078 | Hs.89538 | cholesteryl ester transfer protein, plas | 3.2 |
| 20 | 449248 | M33782 | Hs.23391 | Homo sapiens, Similar to transcription f | 3.2 |
| | 439416 | W58294 | Hs.56254 | ESTs | 3.2 |
| | 401596 | AA172106 | Hs.110950 | Rag C protein | 3.2 |
| | 408380 | AF123050 | Hs.44532 | diubiquitin | 3.2 |
| | 450325 | AF935962 | Hs.26289 | ESTs | 3.2 |
| 25 | 428730 | AA625947 | Hs.25750 | ESTs | 3.2 |
| | 457536 | AA305233 | Hs.278712 | eukaryotic translation initiation factor | 3.2 |
| | 426836 | N41720 | Hs.172684 | vesicle-associated membrane protein 8 (e | 3.2 |
| | 442710 | AI015631 | Hs.23210 | ESTs | 3.2 |
| | 435232 | NM_001262 | Hs.4854 | cyclin-dependent kinase inhibitor 2C (p1 | 3.2 |
| 30 | 430970 | AI018210 | Hs.144083 | ESTs | 3.2 |
| | 416192 | NM_005036 | Hs.998 | peroxisome proliferative activated recep | 3.2 |
| | 446676 | H09380 | Hs.300965 | ESTs | 3.2 |
| | 451459 | AJ797515 | Hs.270560 | ESTs, Moderately similar to ALU7_HUMAN A | 3.2 |
| | 407603 | AW955705 | Hs.62604 | Homo sapiens, clone IMAGE:4295322, mRNA, | 3.2 |
| 35 | 413840 | AI301558 | Hs.146381 | RNA binding motif protein, X chromosome | 3.2 |
| | 448751 | BE551203 | Hs.201792 | ESTs | 3.2 |
| | 432593 | AW301003 | Hs.51483 | ESTs, Weakly similar to hypothetical pro | 3.2 |
| | 458786 | AI457098 | Hs.280848 | ESTs | 3.2 |
| | 455909 | BE156417 | Hs.278798 | ESTs | 3.2 |
| 40 | 419311 | AA689591 | | gb:nv66a12.s1 NCI_CGAP_GCB1 Homo sapiens | 3.2 |
| | 439710 | AF086543 | | gb:Homo sapiens full length insert cDNA | 3.2 |
| | 434559 | AF147315 | | gb:Homo sapiens full length insert cDNA | 3.1 |
| | 455800 | R22479 | Hs.167073 | Homo sapiens cDNA FLJ13047 fis, clone NT | 3.1 |
| | 436703 | AW880614 | Hs.146381 | RNA binding motif protein, X chromosome | 3.1 |
| 45 | 414799 | AJ752416 | Hs.77326 | insulin-like growth factor binding prote | 3.1 |
| | 437860 | AA333063 | Hs.279898 | Homo sapiens cDNA: FLJ23165 fis, clone L | 3.1 |
| | 434182 | W20309 | Hs.118520 | G-protein gamma-12 subunit | 3.1 |
| | 417900 | BE250127 | Hs.82906 | CDC20 (cell division cycle 20, S. cerevi | 3.1 |
| | 434769 | AA648884 | Hs.134278 | Homo sapiens cDNA FLJ12676 fis, clone NT | 3.1 |
| 50 | 414825 | X06370 | Hs.77432 | epidermal growth factor receptor (avian | 3.1 |
| | 426413 | AA377823 | | gb:EST90805 Synovial sarcoma Homo sapien | 3.1 |
| | 447959 | AI452784 | Hs.270270 | ESTs, Weakly similar to 2109260A B cell | 3.1 |
| | 404589 | | | | 3.1 |
| | 421764 | AI681535 | Hs.148135 | serine/threonine kinase 33 | 3.1 |
| 55 | 419986 | AI345455 | Hs.78915 | GA-binding protein transcription factor, | 3.1 |
| | 416941 | BE000150 | Hs.48778 | niban protein | 3.1 |
| | 414761 | AJ077228 | Hs.77256 | enhancer of zeste (Drosophila) homolog 2 | 3.1 |
| | 449611 | AJ970394 | Hs.197075 | ESTs | 3.1 |
| | 434746 | AA648368 | Hs.295368 | ESTs | 3.1 |
| 60 | 434274 | AA628539 | Hs.116252 | ESTs, Moderately similar to ALU1_HUMAN A | 3.1 |
| | 427899 | AA829286 | Hs.332053 | serum amyloid A1 | 3.1 |
| | 417642 | BE302665 | Hs.105461 | hypothetical protein FLJ20357 | 3.1 |
| | 452472 | AW957300 | Hs.294142 | ESTs, Weakly similar to C55663 oligodend | 3.1 |
| | 446131 | NM_000929 | Hs.290 | phospholipase A2, group V | 3.1 |
| 65 | 440052 | AI633744 | Hs.195648 | ESTs, Weakly similar to I38022 hypotheti | 3.1 |
| | 426531 | AA381071 | | gb:EST94100 Activated T-cells XII Homo s | 3.1 |
| | 422158 | L10343 | Hs.112341 | protease inhibitor 3, skin-derived (SKAL | 3.1 |
| | 406267 | | | | 3.1 |
| | 447039 | AV661798 | Hs.282915 | ESTs | 3.1 |
| 70 | 404802 | | | | 3.1 |
| | 406927 | M26460 | | gb:Homo sapiens (clone 104) retinoblasto | 3.1 |
| | 419314 | AW971924 | Hs.87280 | ESTs | 3.0 |
| | 435894 | AI076667 | Hs.188011 | ESTs | 3.0 |
| | 432140 | AK000404 | Hs.272688 | hypothetical protein FLJ20397 | 3.0 |
| 75 | 43426 | AF098158 | Hs.9329 | chromosome 20 open reading frame 1 | 3.0 |
| | 425202 | AW962282 | Hs.152049 | ESTs, Weakly similar to I38022 hypotheti | 3.0 |
| | 407047 | X65965 | | gb:H.sapiens SOD-2 gene for manganese su | 3.0 |
| | 418241 | M26682 | Hs.1149 | UIM domain only 1 (thrombosin 1) | 3.0 |
| | 446599 | Z97832 | Hs.15476 | differentially expressed in FDCP (mouse | 3.0 |
| 80 | 412950 | BE018581 | Hs.245342 | hypothetical protein FLJ14642 | 3.0 |
| | 428670 | AA431682 | Hs.134832 | ESTs | 3.0 |
| | 446975 | BE246446 | Hs.16695 | ubiquitin-activating enzyme E1-like | 3.0 |
| | 437756 | AA767537 | Hs.197096 | ESTs | 3.0 |
| | 416084 | L16991 | Hs.79006 | deoxythymidylate kinase (thymidylate kin | 3.0 |
| | 402374 | AL135225 | Hs.301865 | dopachrome tautomerase (dopachrome delta | 3.0 |
| | 443885 | H91806 | Hs.15284 | ESTs | 3.0 |
| | 434008 | AA740878 | Hs.112982 | ESTs | 3.0 |

| | | | | | |
|----|--------|----------|-----------|--|-----|
| 5 | 452568 | AA805634 | Hs.300870 | Homo sapiens mRNA; cDNA DKFZp547M072 (fr | 3.0 |
| | 414239 | AI288330 | Hs.182330 | ESTs | 3.0 |
| | 421013 | M52397 | Hs.1345 | mutated in colorectal cancers | 3.0 |
| | 424635 | AA420687 | Hs.115455 | Homo sapiens cDNA FLJ14259 fis, clone PL | 3.0 |
| | 410276 | AI554545 | Hs.68301 | ESTs | 3.0 |
| 10 | 433865 | N29862 | Hs.44104 | ESTs | 3.0 |
| | 406028 | | | | 3.0 |
| | 401626 | | | | 3.0 |
| | 415949 | H10562 | Hs.21691 | ESTs | 3.0 |
| | 418583 | AA604379 | Hs.86211 | hypothetical protein | 3.0 |
| 15 | 417933 | X02308 | Hs.82962 | thymidylate synthetase | 3.0 |
| | 434577 | R37316 | Hs.179769 | Homo sapiens cDNA: FLJ22487 fis, clone H | 3.0 |
| | 430437 | AJ768801 | Hs.169943 | Homo sapiens cDNA FLJ13569 fis, clone PL | 3.0 |
| | 427940 | AA417812 | Hs.38775 | ESTs | 3.0 |
| | 456060 | C14904 | Hs.45184 | Homo sapiens cDNA FLJ12284 fis, clone MA | 2.9 |
| 20 | 421988 | AW450481 | Hs.161333 | ESTs | 2.9 |
| | 448775 | AB025237 | Hs.388 | nucleic acid diphosphate linked moi | 2.9 |
| | 438598 | AI805943 | Hs.326067 | hypothetical protein MGC5178 | 2.9 |
| | 429612 | AF062649 | Hs.252587 | pituitary tumor-transforming 1 | 2.9 |
| | 451189 | AA016019 | Hs.40905 | ESTs | 2.9 |
| 25 | 401558 | | | | 2.9 |
| | 426207 | BE390657 | Hs.30026 | HSPC182 protein | 2.9 |
| | 404721 | | | | 2.9 |
| | 401384 | | | | 2.9 |
| | 417288 | AI984792 | Hs.108812 | hypothetical protein FLJ22004 | 2.9 |
| 30 | 427648 | AI376722 | Hs.180062 | proteasome (prosome, macropain) subunit, | 2.9 |
| | 435928 | H64345 | Hs.183961 | ESTs | 2.9 |
| | 431740 | N75450 | Hs.183412 | ESTs, Moderately similar to AF116721 67 | 2.9 |
| | 428242 | H55709 | Hs.2250 | leukemia inhibitory factor (cholinergic | 2.9 |
| | 439972 | AI348100 | Hs.124662 | ESTs | 2.9 |
| 35 | 433112 | AA973801 | Hs.144553 | ESTs, Weakly similar to unnamed protein | 2.9 |
| | 423751 | AW235633 | Hs.46525 | ESTs | 2.9 |
| | 406748 | AW339106 | Hs.217493 | annexin A2 | 2.9 |
| | 422154 | T79045 | Hs.126927 | ESTs | 2.9 |
| | 405588 | | | | 2.9 |
| 40 | 440911 | AA909536 | Hs.143562 | ESTs | 2.9 |
| | 412420 | AL035668 | Hs.73853 | bone morphogenetic protein 2 | 2.9 |
| | 445043 | AW014413 | Hs.196066 | ESTs | 2.9 |
| | 410114 | AW590540 | Hs.271280 | ESTs | 2.9 |
| | 419217 | AA504571 | | gb:aa60e12.r1 NCI_CGAP_GCB1 Homo sapiens | 2.9 |
| 45 | 415849 | R20529 | Hs.6806 | ESTs | 2.9 |
| | 448140 | AF146761 | Hs.20450 | BCM-like membrane protein precursor | 2.9 |
| | 453331 | AI240665 | Hs.8895 | ESTs | 2.9 |
| | 432065 | AA401039 | Hs.2903 | protein phosphatase 4 (formerly X), cata | 2.9 |
| | 438380 | T06430 | Hs.6194 | chondroitin sulfate proteoglycan BEHAB/b | 2.9 |
| 50 | 454377 | AA076811 | | gb:7B03C12 Chromosome 7 Fetal Brain cDNA | 2.9 |
| | 421491 | H99999 | Hs.42736 | ESTs | 2.9 |
| | 452291 | AF015592 | Hs.28853 | CDK7 (cell division cycle 7, S. cerevisi | 2.8 |
| | 415446 | F08898 | Hs.66075 | ESTs | 2.8 |
| | 439518 | W76326 | | gb:zd60d04.r1 Soares_fetal_heart_NbHH19W | 2.8 |
| 55 | 427221 | L15409 | Hs.174007 | von Hippel-Lindau syndrome | 2.8 |
| | 422493 | AW474183 | Hs.250173 | hypothetical protein FLJ13158 | 2.8 |
| | 419451 | AI907117 | Hs.90535 | synaptobrevin binding protein 2 | 2.8 |
| | 448789 | BE539108 | Hs.22051 | hypothetical protein MGC15548 | 2.8 |
| | 424126 | AA335635 | Hs.96917 | ESTs | 2.8 |
| 60 | 458695 | AV660159 | Hs.282284 | ESTs, Weakly similar to I38022 hypothe | 2.8 |
| | 418973 | AA233056 | Hs.191518 | ESTs | 2.8 |
| | 440471 | AA886146 | Hs.307944 | ESTs | 2.8 |
| | 421016 | AA504583 | Hs.101047 | transcription factor 3 (E2A immunoglobul | 2.8 |
| | 433647 | AA603367 | Hs.222294 | ESTs | 2.8 |
| 65 | 415817 | U88967 | Hs.78867 | protein tyrosine phosphatase, receptor-t | 2.8 |
| | 421723 | AA620400 | Hs.300717 | sodium channel, voltage-gated, type III, | 2.8 |
| | 434964 | AI638850 | Hs.130746 | ESTs | 2.8 |
| | 432022 | AL162042 | Hs.272348 | Homo sapiens mRNA; cDNA DKFZp761L1212 (f | 2.8 |
| | 400517 | AF242388 | Hs.149585 | lengsin | 2.8 |
| 70 | 433023 | AW864793 | Hs.87409 | thrombospondin 1 | 2.8 |
| | 448734 | BE614070 | Hs.326416 | Homo sapiens mRNA; cDNA DKFZp564H1916 (f | 2.8 |
| | 406736 | AI254733 | Hs.182426 | ribosomal protein S2 | 2.8 |
| | 409207 | AW373564 | Hs.194637 | BANP homolog, SMAR1 homolog | 2.8 |
| | 440196 | N72847 | Hs.125221 | ESTs | 2.8 |
| 75 | 403961 | | | | 2.8 |
| | 425193 | AW965689 | Hs.22509 | ESTs | 2.8 |
| | 425268 | AI807883 | Hs.180059 | Homo sapiens cDNA FLJ20653 fis, clone KA | 2.8 |
| | 440483 | AI200836 | Hs.150386 | ESTs | 2.8 |
| | 412391 | AW947710 | | gb:RC0-MT0004-130300-011-e07 MT0004 Homo | 2.8 |
| 80 | 448769 | N66037 | Hs.38173 | ESTs | 2.8 |
| | 411632 | AW854829 | | gb:QV2-CT0261-201099-011-01 CT0261 Homo | 2.8 |
| | 438221 | AI798853 | Hs.122224 | ESTs, Weakly similar to ALU5_HUMAN ALU S | 2.8 |
| | 457578 | AA578027 | | gb:nl20h01.s1 NCI_CGAP_HSC1 Homo sapiens | 2.8 |
| | 455510 | AA422029 | Hs.143640 | ESTs, Weakly similar to hyperpolarizatio | 2.8 |
| | 447769 | AW873704 | Hs.320831 | Homo sapiens cDNA FLJ14597 fis, clone NT | 2.8 |
| | 427701 | AA411101 | Hs.243886 | nuclear autoantigenic sperm protein (his | 2.8 |
| | 433800 | AI034361 | Hs.135150 | lung type-I cell membrane-associated gly | 2.8 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 439662 | H97552 | Hs.269060 | ESTs | 2.8 |
| | 425694 | U51333 | Hs.159237 | hexokinase 3 (white cell) | 2.8 |
| | 414747 | U30872 | Hs.77204 | centromere protein F (350/400kD, mitotin | 2.8 |
| 5 | 414598 | AI094221 | Hs.135150 | lung type-I cell membrane-associated gly | 2.8 |
| | 447752 | M73700 | Hs.105938 | lactotransferrin | 2.8 |
| | 408761 | AA057264 | Hs.238936 | ESTs, Weakly similar to (define not ava | 2.8 |
| | 453350 | AI917771 | Hs.61790 | hypothetical protein FLJ23338 | 2.7 |
| | 456629 | AW891965 | Hs.279789 | histone deacetylase 3 | 2.7 |
| 10 | 439538 | AA837323 | Hs.164047 | ESTs | 2.7 |
| | 458814 | AI498957 | Hs.170861 | ESTs, Weakly similar to Z195_HUMAN ZINC | 2.7 |
| | 456029 | BE255990 | Hs.218329 | hypothetical protein | 2.7 |
| | 451129 | BE072881 | | gb:RC2-BT0548-200300-012-e09 BT0548 Homo | 2.7 |
| | 456412 | AW749617 | Hs.280776 | tankyrase, TRF1-interacting ankyrin-rela | 2.7 |
| 15 | 453536 | AA137000 | Hs.62578 | ESTs | 2.7 |
| | 438378 | AW970529 | Hs.86434 | hypothetical protein FLJ21816 | 2.7 |
| | 425745 | U44060 | Hs.14427 | Homo sapiens cDNA: FLJ21800 fis, clone H | 2.7 |
| | 446322 | N23033 | Hs.155814 | ESTs | 2.7 |
| | 451592 | AI805416 | Hs.213897 | ESTs | 2.7 |
| 20 | 429466 | M85835 | Hs.12627 | ESTs | 2.7 |
| | 429747 | M87507 | Hs.2490 | caspase 1, apoptosis-related cysteine pr | 2.7 |
| | 455514 | AW983871 | | gb:RC1-HN0003-220300-021-h07 HN0003 Homo | 2.7 |
| | 414732 | AW410976 | Hs.77152 | minichromosome maintenance deficient (S. | 2.7 |
| | 444207 | AI565004 | Hs.79572 | cathepsin D (lysosomal aspartyl protease | 2.7 |
| 25 | 427421 | AA402414 | Hs.3059 | coatamer protein complex, subunit beta | 2.7 |
| | 449655 | AI021987 | Hs.59970 | ESTs | 2.7 |
| | 422648 | D86983 | Hs.118893 | Melanoma associated gene | 2.7 |
| | 428494 | AA233439 | Hs.184634 | hypothetical protein FLJ20005 | 2.7 |
| | 406895 | X60648 | Hs.172550 | polypyrimidine tract binding protein (he | 2.7 |
| 30 | 453255 | AA278167 | Hs.19215 | Homo sapiens, clone IMAGE:3605822, mRNA | 2.7 |
| | 427348 | NM_014137 | Hs.177258 | PRO0650 protein | 2.7 |
| | 435370 | AI964074 | Hs.225838 | ESTs | 2.7 |
| | 407862 | BE548267 | Hs.50724 | Homo sapiens cDNA FLJ10934 fis, clone OV | 2.7 |
| | 411874 | AA096106 | Hs.20403 | ESTs | 2.7 |
| 35 | 421192 | AA833718 | Hs.204529 | KIAA1806 protein | 2.7 |
| | 435899 | W89093 | Hs.189914 | ESTs | 2.7 |
| | 414603 | R58394 | Hs.25119 | ESTs, Weakly similar to YEX0_YEAST HYPOT | 2.7 |
| | 453462 | AL037291 | Hs.236605 | ESTs, Moderately similar to ALLU4_HUMAN A | 2.7 |
| | 436554 | AI985810 | Hs.301173 | ESTs | 2.7 |
| 40 | 427528 | AU077143 | Hs.179565 | minichromosome maintenance deficient (S. | 2.7 |
| | 403881 | | | | 2.7 |
| | 431779 | AW971178 | Hs.268571 | apolipoprotein C-I | 2.7 |
| | 404984 | | | | 2.7 |
| | 448275 | BE514434 | Hs.20830 | kinesin-like 2 | 2.7 |
| 45 | 446839 | BE091926 | Hs.16244 | mitotic spindle coiled-coil related prot | 2.7 |
| | 411927 | BE274009 | Hs.772 | glycogen synthase 1 (muscle) | 2.7 |
| | 404756 | | | | 2.7 |
| | 447072 | D61594 | Hs.17279 | tyrosylprotein sulfotransferase 1 | 2.7 |
| | 422176 | H80977 | | gb:yu89a11.s1 Soares fetal liver spleen | 2.7 |
| 50 | 439627 | BE621702 | Hs.29076 | hypothetical protein FLJ21841 | 2.7 |
| | 436532 | AA721522 | | gb:nv54h12.r1 NCI_CGAP_Ew1 Homo sapiens | 2.7 |
| | 412833 | AW960547 | Hs.298262 | ribosomal protein S19 | 2.7 |
| | 457245 | AI745498 | Hs.204579 | ESTs | 2.7 |
| | 446861 | AI696519 | Hs.14427 | Homo sapiens cDNA: FLJ21800 fis, clone H | 2.7 |
| 55 | 453263 | R91778 | Hs.99369 | ESTs | 2.7 |
| | 459385 | BE380047 | | gb:601159362F2 NIH_MGC_53 Homo sapiens c | 2.7 |
| | 438764 | AA824524 | Hs.336452 | ESTs | 2.7 |
| | 429285 | AI971081 | Hs.20432 | ESTs, Weakly similar to I38022 hypotheti | 2.7 |
| | 424853 | BE549737 | Hs.132967 | Human EST clone 122887 mariner transposo | 2.7 |
| 60 | 430037 | BE409649 | Hs.227789 | mitogen-activated protein kinase-activat | 2.7 |
| | 449892 | N73608 | Hs.50309 | ESTs | 2.7 |
| | 454201 | AB023191 | Hs.44131 | KIAA0974 protein | 2.7 |
| | 452279 | AA286844 | Hs.61260 | hypothetical protein FLJ13164 | 2.7 |
| | 427954 | J03060 | Hs.247551 | metaxin 1 | 2.7 |
| 65 | 400371 | U80740 | | | 2.7 |
| | 452449 | AW068658 | Hs.20943 | ESTs | 2.7 |
| | 431114 | AA492400 | Hs.291015 | ESTs | 2.7 |
| | 417088 | M54915 | Hs.81170 | pim-1 oncogene | 2.7 |
| | 447674 | BE270640 | Hs.19192 | cyclin-dependent kinase 2 | 2.7 |
| 70 | 403680 | | | | 2.7 |
| | 454679 | AW813110 | | gb:CM4-ST0189-051099-021-r05 ST0189 Homo | 2.7 |
| | 411968 | AI207410 | Hs.69280 | Homo sapiens, clone IMAGE:3636299, mRNA, | 2.6 |
| | 422240 | R60594 | Hs.29002 | KIAA1706 protein | 2.6 |
| | 424368 | AB037766 | Hs.146085 | KIAA1345 protein | 2.6 |
| 75 | 405808 | | | | 2.6 |
| | 419700 | AF084935 | Hs.92357 | galactokinase 1 | 2.6 |
| | 435972 | W95088 | Hs.114198 | ESTs | 2.6 |
| | 453568 | S70782 | Hs.557 | adrenergic, alpha-1D-, receptor | 2.6 |
| | 443725 | AW245680 | Hs.9701 | growth arrest and DNA-damage-inducible, | 2.6 |
| 80 | 444156 | AW500059 | Hs.86437 | ESTs, Highly similar to AF219140 1 gastr | 2.6 |
| | 428209 | AA424197 | Hs.98947 | ESTs, Weakly similar to S33496 trypsin I | 2.6 |
| | 437640 | AA764893 | Hs.272155 | ESTs, Weakly similar to I38022 hypotheti | 2.6 |
| | 453948 | AI970797 | Hs.64859 | ESTs | 2.6 |
| | 415402 | AA164687 | Hs.177576 | mannosyl (alpha-1,3)-glycoprotein beta- | 2.6 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 425397 | J04088 | Hs.156346 | topoisomerase (DNA) II alpha (170kD) | 2.6 |
| | 418228 | AA962181 | Hs.111219 | ESTs, Moderately similar to ALU1_HUMAN A | 2.6 |
| | 401324 | | | | 2.6 |
| 5 | 425234 | AW152225 | Hs.165909 | ESTs, Weakly similar to I38022 hypotheti | 2.6 |
| | 443210 | AJ692649 | Hs.9451 | hypothetical protein MGC13168 | 2.6 |
| | 457244 | AA581385 | Hs.162473 | ESTs, Weakly similar to I38022 hypotheti | 2.6 |
| | 417144 | AA382104 | Hs.81337 | lectin, galactoside-binding, soluble, 9 | 2.6 |
| | 433933 | AJ754389 | Hs.133494 | Homo sapiens clone TCC01A00164 mRNA sequ | 2.6 |
| 10 | 437437 | AA226869 | Hs.16520 | hypothetical protein DKFZp762L0311 | 2.6 |
| | 434206 | AW136973 | Hs.288516 | ESTs, Weakly similar to S69890 mitogen i | 2.6 |
| | 400992 | | | | 2.6 |
| | 455530 | AW984744 | | gb:RC1-HN0015-040400-011-d03 HN0015 Homo | 2.6 |
| | 436139 | AA765786 | Hs.120936 | ESTs | 2.6 |
| 15 | 448330 | AL036449 | Hs.207163 | ESTs | 2.6 |
| | 412942 | AL120344 | Hs.75074 | mitogen-activated protein kinase-activat | 2.6 |
| | 432753 | NM_014075 | Hs.336938 | Homo sapiens PRO0593 mRNA, complete cds | 2.6 |
| | 433430 | AJ863735 | Hs.186755 | ESTs | 2.6 |
| | 436693 | AW973223 | Hs.303197 | B-cell CLL/lymphoma 7C | 2.6 |
| 20 | 429482 | AF076974 | Hs.203952 | transformation/transcription domain-asso | 2.6 |
| | 432715 | AA247152 | Hs.200483 | ESTs, Weakly similar to KIAA1074 protein | 2.6 |
| | 414217 | AJ309298 | Hs.279898 | Homo sapiens cDNA: FLJ23165 fis, clone I | 2.6 |
| | 434165 | AA971328 | Hs.95361 | myosin VIIA (Usher syndrome 1B (autosoma | 2.6 |
| | 414835 | AA156720 | Hs.185342 | ESTs | 2.6 |
| 25 | 424489 | T48851 | Hs.149250 | D-siglec precursor, | 2.6 |
| | 436496 | AA281959 | Hs.5210 | glia maturation factor, gamma | 2.6 |
| | 403797 | | | | 2.6 |
| | 434573 | AW372340 | Hs.159717 | ESTs | 2.6 |
| | 418841 | NM_002332 | Hs.89137 | low density lipoprotein-related protein | 2.6 |
| 30 | 415785 | RB2419 | Hs.23603 | ESTs, Moderately similar to ALU8_HUMAN A | 2.6 |
| | 450608 | AA010365 | Hs.193229 | ESTs | 2.6 |
| | 425304 | AA463844 | Hs.31339 | fibroblast growth factor 11 | 2.6 |
| | 432268 | BE311856 | Hs.274230 | 3'-phosphoadenosine 5'-phosphosulfate sy | 2.6 |
| | 410507 | AA355288 | Hs.40834 | transitional epithelia response protein | 2.6 |
| 35 | 427343 | AJ880044 | Hs.176977 | protein kinase C binding protein 2 | 2.6 |
| | 420917 | AW135716 | Hs.117330 | ESTs | 2.6 |
| | 414399 | L47345 | Hs.155202 | transcription elongation factor B (SIII) | 2.6 |
| | 446089 | AJ860021 | Hs.270651 | ESTs, Moderately similar to A47582 B-cel | 2.6 |
| | 440829 | AF136407 | Hs.7446 | chromosome 6 open reading frame 5 | 2.6 |
| 40 | 408475 | AA315514 | Hs.47986 | hypothetical protein MGC10940 | 2.6 |
| | 450946 | AA374569 | Hs.127698 | ESTs, Moderately similar to 2109260A B c | 2.6 |
| | 421462 | AF016495 | Hs.104624 | aquaporin 9 | 2.6 |
| | 434846 | AW295389 | Hs.119768 | ESTs | 2.6 |
| | 422887 | AJ751848 | Hs.49215 | ESTs | 2.6 |
| 45 | 417435 | NM_005181 | Hs.82129 | carbonic anhydrase III, muscle specific | 2.6 |
| | 437389 | AL359587 | Hs.271586 | hypothetical protein DKFZp762M115 | 2.5 |
| | 408981 | AW500797 | Hs.49427 | Gem-interacting protein | 2.5 |
| | 432180 | Y18418 | Hs.272822 | RuvB (E. coli homolog)-like 1 | 2.5 |
| | 418079 | R40058 | Hs.6911 | ESTs | 2.5 |
| 50 | 437820 | AA769062 | Hs.323836 | ESTs, Weakly similar to alternatively sp | 2.5 |
| | 439685 | AW956781 | Hs.293937 | ESTs, Weakly similar to FXD2_HUMAN FORKH | 2.5 |
| | 425681 | AB018297 | Hs.159183 | KIAA0754 protein | 2.5 |
| | 435177 | AJ018174 | Hs.42936 | ESTs | 2.5 |
| | 437323 | AA371145 | Hs.226627 | leptin receptor | 2.5 |
| 55 | 422114 | AW194851 | Hs.111801 | arsenate resistance protein ARS2 | 2.5 |
| | 448478 | AJ523218 | Hs.203456 | ESTs | 2.5 |
| | 426623 | AA382826 | Hs.132793 | ESTs | 2.5 |
| | 448764 | AJ568607 | Hs.182112 | ESTs | 2.5 |
| | 458385 | AJ051489 | Hs.246214 | ESTs | 2.5 |
| 60 | 403726 | N28939 | Hs.13434 | Homo sapiens clone 24418 mRNA sequence | 2.5 |
| | 444888 | AJ651039 | Hs.148559 | ESTs | 2.5 |
| | 456179 | H75490 | Hs.271930 | ESTs | 2.5 |
| | 424840 | D79987 | Hs.153479 | extra spindle poles, S. cerevisiae, homo | 2.5 |
| | 406273 | NM_000919 | Hs.83920 | peptidylglycine alpha-amidating monooxyg | 2.5 |
| 65 | 418054 | NM_002318 | Hs.83354 | lysyl oxidase-like 2 | 2.5 |
| | 445936 | BE543594 | Hs.61478 | hypothetical protein FLJ22329 | 2.5 |
| | 454967 | AW848276 | | gb:IL3-CT0214-150200-074-E06 CT0214 Homo | 2.5 |
| | 442303 | AA989289 | Hs.129169 | ESTs | 2.5 |
| | 456583 | AF179897 | Hs.104105 | Meis (mouse) homolog 2 | 2.5 |
| 70 | 434263 | N34895 | Hs.44648 | ESTs | 2.5 |
| | 416892 | L24498 | Hs.80409 | growth arrest and DNA-damage-inducible, | 2.5 |
| | 424528 | AW073971 | Hs.238954 | ESTs, Weakly similar to KIAA1204 protein | 2.5 |
| | 406038 | Y14443 | Hs.88219 | zinc finger protein 200 | 2.5 |
| | 413495 | Y12395 | Hs.315177 | interferon-related developmental regulat | 2.5 |
| 75 | 423098 | AA321980 | Hs.204682 | ESTs | 2.5 |
| | 410817 | AJ262789 | Hs.93659 | protein disulfide isomerase related prot | 2.5 |
| | 439841 | AF038961 | Hs.6710 | mannose-6-phosphate utilization defect 1 | 2.5 |
| | 453828 | AW970960 | Hs.293821 | ESTs | 2.5 |
| | 445034 | AW293376 | Hs.143659 | ESTs | 2.5 |
| 80 | 449620 | BE407797 | Hs.23794 | checkpoint with forkhead and ring finger | 2.5 |
| | 406876 | AJ382286 | Hs.180842 | ribosomal protein L13 | 2.5 |
| | 412370 | AW946614 | | gb:RC2-ET0021-280400-011-c05 ET0021 Homo | 2.5 |
| | 423642 | AW452650 | Hs.157148 | hypothetical protein MGC13204 | 2.5 |
| | 430357 | AW976789 | Hs.165607 | ESTs | 2.5 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| 5 | 414853 | U31116 | Hs.77501 | saroglycan, beta (43kD dystrophin-assoc | 2.5 |
| | 416097 | BE387371 | Hs.118964 | hypothetical protein FLJ20085 | 2.5 |
| | 428619 | AK002140 | Hs.187378 | hypothetical protein FLJ11278 | 2.5 |
| | 413976 | BE295452 | Hs.75655 | procollagen-proline, 2-oxoglutarate 4-di | 2.5 |
| | 445223 | AW291553 | Hs.254983 | ESTs | 2.5 |
| 10 | 423926 | X03833 | Hs.1722 | interleukin 1, alpha | 2.5 |
| | 410165 | BE560228 | Hs.71869 | apoptosis-associated speck-like protein | 2.5 |
| | 406474 | | | | 2.5 |
| | 433908 | AW298141 | Hs.157975 | ESTs | 2.5 |
| | 439755 | AW748482 | Hs.77873 | B7 homolog 3 | 2.5 |
| 15 | 437528 | N59646 | Hs.169745 | crumbs (Drosophila) homolog 1 | 2.5 |
| | 420734 | AW972872 | Hs.293736 | ESTs | 2.5 |
| | 415346 | Z43108 | | gb:HSC13E071 normalized infant brain cDN | 2.5 |
| | 419337 | AW291112 | Hs.209978 | ESTs | 2.5 |
| | 444606 | R09478 | Hs.18041 | ESTs | 2.5 |
| 20 | 430061 | AB037817 | Hs.230188 | KIAA1396 protein | 2.5 |
| | 413407 | AI356293 | Hs.75339 | inositol polyphosphate phosphatase-like | 2.5 |
| | 411965 | BE467339 | Hs.280115 | ESTs | 2.5 |
| | 409278 | AA346683 | Hs.52763 | anaphase-promoting complex subunit 7 | 2.5 |
| | 403142 | | | | 2.5 |
| 25 | 401714 | | | | 2.5 |
| | 425081 | X74794 | Hs.154443 | minichromosome maintenance deficient (S. | 2.5 |
| | 416505 | H66470 | Hs.16004 | ESTs | 2.5 |
| | 431518 | AA743462 | Hs.165337 | ESTs | 2.5 |
| | 448623 | BE613468 | Hs.107515 | ESTs, Weakly similar to T00329 hypotheti | 2.5 |
| 30 | 428301 | AW628666 | Hs.98440 | ESTs, Weakly similar to I38022 hypotheti | 2.5 |
| | 404366 | | | | 2.5 |
| | 449733 | R74546 | Hs.29438 | Homo sapiens cDNA FLJ12094 fis, clone HE | 2.5 |
| | 455853 | AI907673 | | gb:IL-BT152-080399-004 BT152 Homo sapien | 2.5 |
| | 402856 | AW939659 | | gb:RCD-OT0076-110100-031-c09 DT0076 Homo | 2.5 |
| 35 | 420751 | J03019 | Hs.99913 | adrenergic, beta-1-, receptor | 2.4 |
| | 436805 | AA731533 | Hs.270751 | ESTs | 2.4 |
| | 420285 | AA258124 | Hs.293878 | ESTs, Moderately similar to ZN91_HUMAN Z | 2.4 |
| | 453496 | AA442103 | Hs.33084 | solute carrier family 2 (facilitated glu | 2.4 |
| | 453853 | AL040600 | Hs.188083 | ESTs | 2.4 |
| 40 | 407909 | AW103986 | | gb:xd63e06.x1 NCI_CGAP_Ov23 Homo sapiens | 2.4 |
| | 454630 | BE142075 | | gb:CM3-HT0137-170999-012-402 HT0137 Homo | 2.4 |
| | 451026 | AA013218 | Hs.157492 | cer-d4 (mouse) homolog | 2.4 |
| | 420779 | L12398 | Hs.99922 | dopamine receptor D4 | 2.4 |
| | 438322 | AA804170 | Hs.221349 | ESTs | 2.4 |
| 45 | 455908 | BE156306 | | gb:QV0-HT0367-150200-114-h04 HT0367 Homo | 2.4 |
| | 419625 | U91616 | Hs.91640 | nuclear factor of kappa light polypeptid | 2.4 |
| | 440773 | AA352702 | Hs.332541 | Homo sapiens, Similar to RIKEN cDNA 2700 | 2.4 |
| | 450823 | T81223 | Hs.22011 | complement-c1q tumor necrosis factor-rel | 2.4 |
| | 447247 | AW369351 | Hs.287955 | Homo sapiens cDNA FLJ13090 fis, clone NT | 2.4 |
| 50 | 429109 | AL008637 | Hs.196352 | neutrophil cytosolic factor 4 (40kD) | 2.4 |
| | 451802 | AI817711 | Hs.209374 | ESTs | 2.4 |
| | 419417 | R92491 | Hs.39429 | ESTs | 2.4 |
| | 407094 | AF000574 | Hs.22405 | leukocyte immunoglobulin-like receptor, | 2.4 |
| | 423567 | BE252949 | Hs.59331 | hypothetical protein FLJ13633 | 2.4 |
| 55 | 427501 | AI369280 | Hs.131743 | ESTs | 2.4 |
| | 451773 | Z42044 | Hs.26996 | KIAA1278 protein | 2.4 |
| | 436845 | AA732297 | Hs.113928 | ESTs | 2.4 |
| | 431584 | AW295121 | Hs.266263 | Homo sapiens cDNA FLJ14115 fis, clone MA | 2.4 |
| | 440614 | AA781530 | Hs.127236 | hypothetical protein FLJ12879 | 2.4 |
| 60 | 423721 | AF176911 | Hs.132004 | cardiotrophin-like cytokine; neurotroph | 2.4 |
| | 452125 | BE312642 | Hs.28077 | GDP-mannose pyrophosphorylase B | 2.4 |
| | 419508 | AW997938 | Hs.90786 | ATP-binding cassette, sub-family C (CFTR | 2.4 |
| | 453446 | BE299996 | | gb:600944574F1 NIH_MGC_17 Homo sapiens c | 2.4 |
| | 419792 | AA250890 | Hs.190037 | ESTs | 2.4 |
| 65 | 452786 | R61362 | Hs.106642 | ESTs, Weakly similar to T09052 hypotheti | 2.4 |
| | 410447 | AW816134 | | gb:MR3-ST0220-290100-016-e04 ST0220 Homo | 2.4 |
| | 438662 | AA223599 | Hs.6351 | cleavage and polyadenylation specific fa | 2.4 |
| | 402408 | | | | 2.4 |
| | 443950 | NM_001425 | Hs.9999 | epithelial membrane protein 3 | 2.4 |
| 70 | 414625 | AA335738 | Hs.76686 | glutathione peroxidase 1 | 2.4 |
| | 403048 | | | | 2.4 |
| | 432088 | AA525454 | | gb:ni85c09.s1 NCI_CGAP_Pr20 Homo sapiens | 2.4 |
| | 431692 | AL021331 | Hs.267749 | unc93 (C.elegans) homolog A | 2.4 |
| | 455023 | AW850907 | | gb:ILL3-CT0220-310100-065-H11 CT0220 Homo | 2.4 |
| 75 | 426249 | F05422 | Hs.168352 | nucleoporin-like protein 1 | 2.4 |
| | 446795 | AI797713 | Hs.156471 | ESTs | 2.4 |
| | 414774 | X02419 | Hs.77274 | plasminogen activator, urokinase | 2.4 |
| | 414252 | AA346483 | Hs.126191 | ESTs | 2.4 |
| | 417918 | AA209205 | Hs.163754 | hypothetical protein FLJ12606 | 2.4 |
| 80 | 427550 | BE242818 | Hs.179606 | nuclear RNA helicase, DECD variant of DE | 2.4 |
| | 404020 | | | | 2.4 |
| | 407846 | AA426202 | Hs.40403 | Cbp/p300-interacting transactivator, wit | 2.4 |
| | 417222 | AI525424 | Hs.42053 | hypothetical protein MGC2383 | 2.4 |
| | 443639 | BE269042 | Hs.9661 | proteasome (prosome, macropain) subunit, | 2.4 |
| | 452706 | AW449390 | Hs.257150 | ESTs, Moderately similar to SUR1_HUMAN S | 2.4 |
| | 401676 | | | | 2.4 |
| | 428882 | AA436915 | Hs.131748 | ESTs, Moderately similar to ALU7_HUMAN A | 2.4 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 436277 | R88520 | Hs.120917 | ESTs | |
| | 426271 | AF026547 | Hs.169047 | chondroitin sulfate proteoglycan 3 (neur | 2.4 |
| | 405353 | | | | 2.4 |
| 5 | 409193 | AA131483 | | gb:zo08e05.r1 Stratagene neuroepithelium | 2.4 |
| | 431431 | AL096711 | Hs.252953 | Human DNA sequence from clone RP3-403A15 | 2.4 |
| | 407889 | R34556 | Hs.30800 | ESTs, Weakly similar to S65657 alpha-1C- | 2.4 |
| | 453335 | AW857376 | Hs.169238 | fucosyltransferase 3 (galactoside 3(4)-L | 2.4 |
| | 450621 | AW297288 | Hs.55918 | hypothetical protein FLJ11354 | 2.4 |
| 10 | 419652 | AL157485 | Hs.91973 | hypothetical protein | 2.4 |
| | 421151 | BE174431 | Hs.63386 | ESTs | 2.4 |
| | 437846 | AA773866 | Hs.244569 | esophagus cancer-related gene-2 | 2.4 |
| | 420681 | AA847602 | Hs.106510 | ESTs, Moderately similar to ALU2_HUMAN A | 2.4 |
| | 405288 | | | | 2.4 |
| 15 | 453527 | R49570 | Hs.180236 | ESTs | 2.4 |
| | 429875 | A091815 | | gb:qa58b06.s1 Soares_NhHMPu_S1 Homo sapi | 2.4 |
| | 436360 | A1962796 | Hs.136754 | ESTs | 2.4 |
| | 418592 | X99226 | Hs.284153 | Fanconi anemia, complementation group A | 2.4 |
| | 419991 | AJ000098 | Hs.94210 | eyes absent (Drosophila) homolog 1 | 2.4 |
| 20 | 449539 | W80363 | Hs.58446 | ESTs | 2.4 |
| | 419870 | AW403911 | Hs.266175 | phosphoprotein associated with GEMs | 2.4 |
| | 404584 | | | | 2.4 |
| | 454276 | AW294996 | Hs.255374 | ESTs | 2.4 |
| | 423746 | AW361817 | Hs.132370 | NADPH oxidase 1 | 2.4 |
| 25 | 415558 | AA885143 | Hs.125719 | ESTs | 2.4 |
| | 428141 | D50402 | Hs.182611 | solute carrier family 11 (proton-coupled | 2.4 |
| | 406953 | L36847 | | gb:Human (clone p17790) rearranged kluo | 2.4 |
| | 444471 | AB020684 | Hs.11217 | KIAA0877 protein | 2.4 |
| | 451031 | AJ360187 | Hs.4254 | ESTs | 2.4 |
| 30 | 455302 | AW997641 | | gb:RC6-BN0052-170200-011-D06 BN0052 Homo | 2.4 |
| | 449063 | AJ627352 | Hs.236547 | Homo sapiens, clone IMAGE:2905978, mRNA, | 2.4 |
| | 401048 | | | | 2.4 |
| | 434420 | AA688278 | Hs.194864 | hypothetical protein FLJ22578 | 2.4 |
| | 425848 | BE242709 | Hs.159637 | valyl-tRNA synthetase 2 | 2.4 |
| 35 | 449086 | AJ628357 | Hs.208037 | ESTs | 2.4 |
| | 415238 | R37780 | Hs.21422 | ESTs | 2.4 |
| | 448337 | AW206453 | Hs.3782 | ESTs | 2.4 |
| | 416991 | N36389 | Hs.141296 | KIAA0226 gene product | 2.3 |
| | 412600 | L28824 | Hs.74101 | spleen tyrosine kinase | 2.3 |
| 40 | 418385 | AW590613 | Hs.301040 | Homo sapiens, clone IMAGE:3357127, mRNA, | 2.3 |
| | 440769 | BE561793 | Hs.21446 | KIAA1716 protein | 2.3 |
| | 450437 | X13956 | Hs.24998 | hypothetical protein MGC10471 | 2.3 |
| | 412035 | N78559 | Hs.293629 | hypothetical protein MGC3121 | 2.3 |
| | 406739 | AJ566709 | Hs.182426 | ribosomal protein S2 | 2.3 |
| 45 | 418506 | AA084248 | Hs.85339 | G protein-coupled receptor 39 | 2.3 |
| | 410286 | AJ739159 | Hs.61898 | DKFZP586N2124 protein | 2.3 |
| | 443740 | R56434 | Hs.21062 | ESTs | 2.3 |
| | 405605 | | | | 2.3 |
| | 416913 | AW934714 | | gb:RC1-DT0001-031299-011-a11 DT0001 Homo | 2.3 |
| 50 | 426509 | M31166 | Hs.2050 | pentaxin-related gene, rapidly induced b | 2.3 |
| | 445828 | F05802 | Hs.81907 | ESTs | 2.3 |
| | 457195 | AB011099 | Hs.196647 | KIAA0527 protein | 2.3 |
| | 420372 | AW960049 | Hs.293660 | Homo sapiens, clone IMAGE:3535476, mRNA, | 2.3 |
| | 423198 | M81933 | Hs.1634 | cell division cycle 25A | 2.3 |
| 55 | 457730 | AW753613 | | gb:RC1-CT0268-060100-013-e01 CT0268 Homo | 2.3 |
| | 412014 | AJ620650 | Hs.43761 | ESTs, Weakly similar to A46010 X-linked | 2.3 |
| | 447131 | NM_004585 | Hs.17466 | retinoic acid receptor responder (tazaro | 2.3 |
| | 446288 | AW189209 | Hs.149708 | ESTs | 2.3 |
| | 436954 | AA740151 | Hs.130425 | ESTs | 2.3 |
| 60 | 411658 | AW855598 | | gb:CM1-CT0278-031199-032-e08 CT0278 Homo | 2.3 |
| | 404240 | | | | 2.3 |
| | 456094 | H95091 | | gb:yw57a09.r1 Soares_placenta_8to9weeks_ | 2.3 |
| | 416951 | AA190926 | Hs.190785 | ESTs, Moderately similar to S65657 alpha | 2.3 |
| | 406737 | AJ356586 | | gb:qy15h09.x1 NCI_CGAP_Bm23 Homo sapien | 2.3 |
| 65 | 458453 | AJ097452 | Hs.135095 | ESTs | 2.3 |
| | 452330 | AJ879127 | Hs.191979 | KIAA1733 protein | 2.3 |
| | 408523 | AW833259 | Hs.314287 | ESTs | 2.3 |
| | 455470 | AW947992 | | gb:PMO-MT0011-240300-001-c09 MT0011 Homo | 2.3 |
| | 436323 | R17697 | Hs.140963 | ESTs, Weakly similar to I38022 hypotheti | 2.3 |
| 70 | 450000 | AJ952797 | Hs.10888 | hypothetical protein FLJ21709 | 2.3 |
| | 416171 | H23896 | Hs.125790 | leucine-rich repeat-containing 2 | 2.3 |
| | 419134 | T89863 | Hs.221771 | ESTs | 2.3 |
| | 445933 | AV655733 | Hs.293860 | spinster-like protein | 2.3 |
| | 422089 | AA523172 | Hs.103135 | ESTs, Weakly similar to SFR4_HUMAN SPLIC | 2.3 |
| 75 | 449911 | AJ262106 | Hs.12653 | ESTs | 2.3 |
| | 417079 | U65590 | Hs.81134 | interleukin 1 receptor antagonist | 2.3 |
| | 411742 | AW247593 | Hs.71819 | eukaryotic translation initiation factor | 2.3 |
| | 435615 | Y15065 | Hs.4975 | potassium voltage-gated channel, KQT-like | 2.3 |
| | 423491 | AA191765 | Hs.129673 | eukaryotic translation initiation factor | 2.3 |
| 80 | 407182 | AA312551 | Hs.230157 | ESTs | 2.3 |
| | 411448 | AA178955 | Hs.271439 | ESTs, Weakly similar to I38022 hypotheti | 2.3 |
| | 438644 | AJ126162 | Hs.129037 | ESTs | 2.3 |
| | 432691 | U29725 | Hs.3080 | mitogen-activated protein kinase 7 | 2.3 |
| | 452198 | AJ097560 | Hs.61210 | ESTs, Weakly similar to I38022 hypotheti | 2.3 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 411125 | AA151647 | Hs.68877 | cytochrome b-245, alpha polypeptide | 2.3 |
| | 404054 | | | | 2.3 |
| | 430458 | AA479300 | Hs.225706 | ESTs, Weakly similar to I38022 hypothe | 2.3 |
| | 440210 | AW674562 | Hs.125296 | ESTs | 2.3 |
| 5 | 446727 | AB011095 | Hs.16032 | KIAA0523 protein | 2.3 |
| | 453775 | NM_002916 | Hs.35120 | replication factor C (activator 1) 4 (37 | 2.3 |
| | 438379 | N23018 | Hs.171391 | C-terminal binding protein 2 | 2.3 |
| | 449919 | AJ674685 | Hs.200141 | ESTs | 2.3 |
| | 415293 | R49462 | Hs.106541 | ESTs | 2.3 |
| 10 | 441126 | NM_000429 | Hs.323715 | methionine adenosyltransferase I, alpha | 2.3 |
| | 408203 | AA053137 | Hs.42390 | nasopharyngeal carcinoma susceptibility | 2.3 |
| | 434941 | AW073202 | Hs.334825 | Homo sapiens cDNA FLJ14752 fis, clone NT | 2.3 |
| | 450748 | AI733093 | Hs.130016 | ESTs | 2.3 |
| | 404185 | | | | 2.3 |
| 15 | 418327 | U70370 | Hs.84136 | paired-like homeodomain transcription fa | 2.3 |
| | 451370 | AI791929 | Hs.300782 | ESTs | 2.3 |
| | 400034 | | | | 2.3 |
| | 407723 | AW071161 | Hs.252873 | ESTs | 2.3 |
| | 431320 | AW969474 | Hs.183070 | ESTs | 2.3 |
| 20 | 429271 | AF039850 | Hs.198515 | dead ringer (Drosophila)-like 1 | 2.3 |
| | 453707 | AW003879 | Hs.126522 | Homo sapiens, clone MGC:16722, mRNA, com | 2.3 |
| | 419225 | U70073 | | gb:HSU70073 Human Homo sapiens cDNA clon | 2.3 |
| | 444656 | AI277924 | Hs.145199 | ESTs | 2.3 |
| | 405741 | | | | 2.3 |
| 25 | 400917 | | | | 2.3 |
| | 432567 | AA736777 | Hs.293770 | ESTs | 2.3 |
| | 437949 | U78519 | Hs.41654 | ESTs, Weakly similar to A46010 X-linked | 2.3 |
| | 450514 | AC005785 | Hs.25059 | A kinase (PRKA) anchor protein 8 | 2.3 |
| 30 | 418400 | BE243026 | Hs.301989 | KIAA0246 protein | 2.3 |
| | 444019 | BE173977 | Hs.10098 | putative nucleolar RNA helicase | 2.3 |
| | 406326 | | | | 2.3 |
| | 412077 | N51107 | Hs.47199 | ESTs, Weakly similar to FLJ00004 protein | 2.3 |
| | 427647 | W19744 | Hs.180059 | Homo sapiens cDNA FLJ20653 fis, clone KA | 2.3 |
| | 414528 | AA148950 | Hs.188836 | ESTs | 2.3 |
| 35 | 414854 | BE546797 | Hs.51483 | ESTs, Weakly similar to hypothetical pro | 2.3 |
| | 420352 | BE258835 | | gb:601117374F1 NIH_MGC_16 Homo sapiens c | 2.3 |
| | 439467 | AW292275 | Hs.158365 | ESTs | 2.3 |
| | 402627 | | | | 2.3 |
| 40 | 451711 | AK000461 | Hs.26890 | cat eye syndrome chromosome region, cand | 2.3 |
| | 424308 | AW975531 | Hs.154443 | minichromosome maintenance deficient (S. | 2.3 |
| | 423869 | BE409301 | Hs.134012 | C1q-related factor | 2.3 |
| | 405915 | | | | 2.3 |
| | 431503 | NM_012129 | Hs.258576 | claudin 12 | 2.3 |
| 45 | 423306 | W88562 | Hs.108198 | ESTs | 2.3 |
| | 443232 | AF161521 | Hs.9081 | phenylalanyl-tRNA synthetase beta-subuni | 2.3 |
| | 433064 | D79991 | Hs.30002 | SH3-containing protein SH3GLB2; KIAA1848 | 2.3 |
| | 434437 | AI912566 | Hs.187813 | ESTs | 2.3 |
| | 436191 | BE407866 | Hs.170253 | hypothetical protein FLJ23282 | 2.3 |
| 50 | 420006 | H14429 | Hs.94300 | serologically defined colon cancer antig | 2.3 |
| | 447942 | F12628 | Hs.334786 | hypothetical protein MGC16040 | 2.3 |
| | 403166 | | | | 2.3 |
| | 422119 | AI277829 | Hs.111862 | KIAA0590 gene product | 2.3 |
| | 403751 | | | | 2.3 |
| 55 | 426451 | AI908165 | Hs.169946 | GATA-binding protein 3 | 2.3 |
| | 427413 | BE547647 | Hs.177781 | hypothetical protein MGC5618 | 2.3 |
| | 409091 | AW970386 | Hs.269423 | ESTs | 2.3 |
| | 440491 | R35252 | Hs.24944 | ESTs, Weakly similar to 2109260A B cell | 2.3 |
| | 427722 | AK000123 | Hs.180479 | hypothetical protein FLJ20116 | 2.3 |
| 60 | 405747 | | | | 2.3 |
| | 438210 | AA780519 | Hs.311601 | EST | 2.3 |
| | 404652 | | | | 2.3 |
| | 423524 | AF055989 | Hs.129738 | potassium voltage-gated channel, Shaw-re | 2.2 |
| | 426793 | X89887 | Hs.172350 | HIR (histone cell cycle regulation defec | 2.2 |
| 65 | 444424 | AI654684 | Hs.196377 | ESTs | 2.2 |
| | 434031 | BE384165 | Hs.23723 | pseudouridylyl synthase 1 | 2.2 |
| | 427650 | AW501245 | Hs.252259 | ribosomal protein S3 | 2.2 |
| | 435220 | D50030 | Hs.104 | HGF activator | 2.2 |
| | 438279 | AA805166 | Hs.154762 | HIV-1 rev binding protein 2 | 2.2 |
| 70 | 424668 | D83702 | Hs.151573 | cryptochrome 1 (photolyase-like) | 2.2 |
| | 429961 | BE246829 | Hs.226770 | DKFZP566C0424 protein | 2.2 |
| | 442065 | AI831229 | Hs.128417 | hypothetical protein FLJ14009 | 2.2 |
| | 415198 | AW009480 | Hs.943 | natural killer cell transcript 4 | 2.2 |
| | 420536 | AL117455 | Hs.275438 | histone deacetylase 7A | 2.2 |
| 75 | 411263 | BE297802 | Hs.69360 | kinesin-like 6 (mitotic centromere-assoc | 2.2 |
| | 443753 | AW367578 | Hs.134749 | ESTs | 2.2 |
| | 423243 | AA351938 | Hs.23964 | sin3-associated polypeptide, 18kD | 2.2 |
| | 446572 | AV659151 | Hs.282961 | ESTs | 2.2 |
| | 412247 | AF022375 | Hs.73793 | vascular endothelial growth factor | 2.2 |
| 80 | 421040 | AA715026 | Hs.135280 | ESTs | 2.2 |
| | 426212 | S71824 | Hs.167988 | neural cell adhesion molecule 1 | 2.2 |
| | 455584 | BE007420 | | gb:PM3-BN0142-200300-001-c04 BN0142 Homo | 2.2 |
| | 406851 | AA609784 | Hs.180255 | major histocompatibility complex, class | 2.2 |
| | 444153 | AK001610 | Hs.10414 | hypothetical protein FLJ10748 | 2.2 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 419575 | U43431 | Hs.91175 | topoisomerase (DNA) III alpha | 2.2 |
| | 418572 | L44284 | Hs.159743 | ESTs | 2.2 |
| | 456261 | AA210718 | Hs.104157 | ESTs, Weakly similar to KIAA0694 protein | 2.2 |
| 5 | 415737 | AA167626 | Hs.118743 | ESTs | 2.2 |
| | 447554 | AJ391598 | Hs.36119 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.2 |
| | 405159 | | | | 2.2 |
| | 442177 | AW661820 | Hs.211413 | ESTs | 2.2 |
| | 446139 | H77395 | Hs.39749 | ESTs | 2.2 |
| 10 | 458339 | AW976853 | Hs.172843 | ESTs | 2.2 |
| | 401876 | | | | 2.2 |
| | 439566 | AF086387 | | gb:Homo sapiens full length insert cDNA | 2.2 |
| | 425079 | H09963 | Hs.2257 | vitronectin (serum spreading factor, som | 2.2 |
| | 441837 | AA361743 | Hs.179881 | core-binding factor, beta subunit | 2.2 |
| 15 | 430644 | AB015419 | Hs.247710 | preprolactin-releasing peptide | 2.2 |
| | 431474 | AL133990 | Hs.190642 | ESTs | 2.2 |
| | 407739 | NM_002285 | Hs.38070 | lymphoid nuclear protein related to AF4 | 2.2 |
| | 424244 | AV647184 | Hs.143601 | hypothetical protein hCLA-iso | 2.2 |
| | 438057 | AW294544 | Hs.125785 | ESTs, Weakly similar to CORB MOUSE CORNI | 2.2 |
| 20 | 412715 | NM_000947 | Hs.74519 | primase, polypeptide 2A (58kD) | 2.2 |
| | 422365 | AF035537 | Hs.115521 | REV3 (yeast homolog)-like, catalytic sub | 2.2 |
| | 404170 | | | | 2.2 |
| | 406902 | M32074 | | gb:Human retinoic acid receptor gamma 2 | 2.2 |
| | 437902 | AA770599 | Hs.144055 | ESTs | 2.2 |
| | 401012 | | | | 2.2 |
| 25 | 446502 | AI302654 | Hs.208024 | ESTs | 2.2 |
| | 442554 | AW467376 | Hs.129640 | ESTs | 2.2 |
| | 443021 | AA368546 | Hs.8904 | Ig superfamily protein | 2.2 |
| | 421141 | AW117261 | Hs.125914 | ESTs | 2.2 |
| 30 | 443070 | BE388662 | Hs.8984 | Homo sapiens chromosome 14 BAC 98L12 | 2.2 |
| | 446566 | H95741 | Hs.17914 | membrane-spanning 4-domains, subfamily A | 2.2 |
| | 427695 | R88483 | Hs.172862 | ESTs | 2.2 |
| | 426503 | AA380153 | | gb:EST93093 Skin tumor I Homo sapiens cD | 2.2 |
| | 431468 | AW248431 | Hs.256526 | nuclear prelamin A recognition factor | 2.2 |
| 35 | 416185 | AW975861 | Hs.47367 | KIAA1785 protein | 2.2 |
| | 437319 | BE410958 | Hs.56406 | Homo sapiens cDNA FLJ13549 fis, clone PL | 2.2 |
| | 402064 | | | | 2.2 |
| | 413335 | AJ613318 | Hs.48442 | ESTs | 2.2 |
| | 408212 | AA297567 | Hs.43728 | hypothetical protein | 2.2 |
| 40 | 406169 | | | | 2.2 |
| | 451099 | R52795 | Hs.25954 | interleukin 13 receptor, alpha 2 | 2.2 |
| | 407335 | AA631047 | Hs.158761 | Homo sapiens cDNA FLJ13054 fis, clone NT | 2.2 |
| | 409715 | W42591 | Hs.23892 | ESTs | 2.2 |
| | 431921 | N46466 | Hs.58879 | ESTs | 2.2 |
| 45 | 443823 | BE089782 | Hs.9877 | hypothetical protein | 2.2 |
| | 432458 | AI968598 | Hs.78768 | malignant cell expression-enhanced gene/ | 2.2 |
| | 419726 | U50330 | Hs.1274 | bone morphogenetic protein 1 | 2.2 |
| | 423178 | AI033140 | Hs.124983 | Homo sapiens mRNA; cDNA DKFZp564C142 (fr | 2.2 |
| | 451089 | AA903705 | Hs.4190 | Homo sapiens cDNA: FLJ23269 fis, clone C | 2.2 |
| 50 | 415216 | AI825905 | Hs.193211 | Homo sapiens cDNA FLJ11421 fis, clone HE | 2.2 |
| | 442242 | AV647908 | Hs.90424 | Homo sapiens cDNA: FLJ23285 fis, clone H | 2.2 |
| | 441830 | AA383104 | Hs.42954 | hypothetical protein DKFZp564D0372 | 2.2 |
| | 406660 | X65371 | Hs.172550 | polypyrimidine tract binding protein (he | 2.2 |
| | 443378 | AW392550 | Hs.9280 | proteasome (prosome, macropain) subunit, | 2.2 |
| 55 | 432558 | R97268 | Hs.177269 | ESTs | 2.2 |
| | 408146 | R45621 | Hs.81057 | hypothetical protein MGC2718 | 2.2 |
| | 419865 | NM_007020 | Hs.93502 | U1-snRNP binding protein homolog (70kD) | 2.2 |
| | 439444 | AI277652 | Hs.54578 | ESTs, Weakly similar to I38022 hypotheti | 2.2 |
| 60 | 438407 | AI457122 | Hs.129673 | eukaryotic translation initiation factor | 2.2 |
| | 450184 | W31096 | Hs.237617 | Homo sapiens, clone IMAGE:3447394, mRNA, | 2.2 |
| | 409130 | BE076601 | Hs.75658 | phosphorylase, glycogen; brain | 2.2 |
| | 428844 | AW972635 | Hs.301904 | hypothetical protein FLJ12671 | 2.2 |
| | 429489 | AF008203 | Hs.204039 | aristless-like homeobox 3 | 2.2 |
| | 433042 | AW193534 | Hs.281895 | Homo sapiens cDNA FLJ11660 fis, clone HE | 2.2 |
| 65 | 440658 | H29142 | Hs.143032 | ESTs, Weakly similar to neuronal thread | 2.2 |
| | 408204 | AA454501 | Hs.43666 | protein tyrosine phosphatase type IVA, m | 2.2 |
| | 427498 | NM_003926 | Hs.178728 | methyl-CpG binding domain protein 3 | 2.2 |
| | 408006 | H57654 | Hs.303345 | ESTs, Weakly similar to I38022 hypotheti | 2.2 |
| | 445703 | AV654845 | Hs.27 | glycine dehydrogenase (decarboxylating; | 2.2 |
| 70 | 431446 | AW294929 | Hs.255369 | Homo sapiens cDNA FLJ10265 fis, clone HE | 2.2 |
| | 456660 | AA909249 | Hs.112282 | solute carrier family 30 (zinc transport | 2.2 |
| | 433099 | NM_002504 | Hs.3187 | nuclear transcription factor, X-box bind | 2.2 |
| | 415857 | AA866115 | Hs.127797 | Homo sapiens cDNA FLJ11381 fis, clone HE | 2.2 |
| | 415245 | N59650 | Hs.27252 | ESTs | 2.2 |
| 75 | 443657 | R14973 | | gb:yf4210.s1 Soares fetal liver spleen | 2.2 |
| | 402521 | AW501216 | Hs.108945 | KIAA0515 protein | 2.2 |
| | 414819 | BE177320 | Hs.156148 | hypothetical protein FLJ13231 | 2.2 |
| | 446530 | AV658909 | Hs.282642 | ESTs | 2.2 |
| | 415797 | AI291896 | Hs.72800 | ESTs | 2.2 |
| 80 | 414812 | X72755 | Hs.77367 | monokine induced by gamma interferon | 2.2 |
| | 453028 | AB006532 | Hs.31442 | RecQ protein-like 4 | 2.2 |
| | 412133 | U83460 | Hs.73614 | solute carrier family 31 (copper transpo | 2.2 |
| | 407881 | AW072003 | Hs.40968 | heparan sulfate (glucosamine) 3-O-sulfot | 2.2 |
| | 437033 | AW248364 | Hs.5409 | RNA polymerase I subunit | 2.2 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| 5 | 422732 | AA577455 | Hs.24937 | transformer-2 alpha (htra-2 alpha) | 2.2 |
| | 416388 | AJ417358 | Hs.73677 | ESTs | 2.2 |
| | 452849 | AF044924 | Hs.30792 | hook2 protein | 2.2 |
| | 446615 | BE513202 | Hs.15589 | PPAR binding protein | 2.2 |
| | 428361 | NM_015905 | Hs.183858 | transcriptional intermediary factor 1 | 2.2 |
| 10 | 446279 | AA490770 | Hs.182382 | ESTs | 2.2 |
| | 422938 | NM_001809 | Hs.1594 | centromere protein A (17kD) | 2.2 |
| | 403969 | | | | 2.2 |
| | 410423 | AW402432 | Hs.63489 | protein tyrosine phosphatase, non-recept | 2.2 |
| | 429736 | AF125304 | Hs.212680 | tumor necrosis factor receptor superfam | 2.2 |
| 15 | 447091 | AW089648 | Hs.157779 | ESTs, Weakly similar to CA17_HUMAN COLLA | 2.2 |
| | 422017 | NM_003877 | Hs.110776 | STAT induced STAT inhibitor-2 | 2.2 |
| | 426728 | NM_007118 | Hs.171957 | triple functional domain (PTPRF interact | 2.2 |
| | 438726 | AB033103 | Hs.6385 | KIAA1277 protein | 2.2 |
| | 453315 | BE544203 | Hs.24831 | ESTs | 2.2 |
| 20 | 423244 | AL039379 | Hs.209602 | ESTs, Weakly similar to ubiquitous TPR m | 2.2 |
| | 433610 | AA806822 | Hs.112547 | ESTs | 2.2 |
| | 429451 | BE409861 | Hs.202833 | heme oxygenase (decycling) 1 | 2.2 |
| | 417980 | R32235 | | gb:yh67f08.r1 Soares placenta Nb2HP Homo | 2.2 |
| | 406347 | | | | 2.2 |
| 25 | 414406 | BE297904 | | gb:601177814F1 NIH_MGC_17 Homo sapiens c | 2.2 |
| | 401827 | | | | 2.2 |
| | 446913 | AA430650 | Hs.16529 | transmembrane 4 superfamily member (tet | 2.2 |
| | 452294 | AJ871925 | Hs.117895 | ESTs, Moderately similar to A47582 B-cel | 2.2 |
| | 404084 | | | | 2.2 |
| 30 | 456786 | AK002084 | Hs.132851 | hypothetical protein FLJ11222 | 2.2 |
| | 435031 | AI632091 | Hs.116877 | ESTs | 2.2 |
| | 442609 | AL020996 | Hs.8518 | selenoprotein N | 2.1 |
| | 439732 | AW629604 | Hs.167641 | hypothetical protein from EUROIMAGE 1703 | 2.1 |
| | 421506 | BE302796 | Hs.105097 | thymidine kinase 1, soluble | 2.1 |
| 35 | 439253 | AF086064 | Hs.332252 | ESTs | 2.1 |
| | 409669 | AW177551 | Hs.220255 | hypothetical protein MGC13098 | 2.1 |
| | 429574 | BE268321 | Hs.208912 | hypothetical protein MGC861 | 2.1 |
| | 437470 | AL390147 | Hs.134742 | hypothetical protein DKFZp547D065 | 2.1 |
| | 408945 | AW015089 | Hs.4964 | DKFZP586J1624 protein | 2.1 |
| 40 | 447687 | AI627947 | Hs.150186 | hypothetical protein DKFZp566K1946 | 2.1 |
| | 459584 | AJ910884 | Hs.207898 | ESTs | 2.1 |
| | 439130 | AA306090 | Hs.124707 | ESTs | 2.1 |
| | 428180 | AI129767 | Hs.182874 | guanine nucleotide binding protein (G pr | 2.1 |
| | 442028 | AJ239437 | Hs.48945 | ESTs | 2.1 |
| 45 | 430968 | AW972830 | | gb:EST384925 MAGE resequences, MAGL Homo | 2.1 |
| | 443609 | AV650231 | Hs.282941 | ESTs, Highly similar to A Chain A, Human | 2.1 |
| | 417164 | AA338283 | Hs.81361 | heterogeneous nuclear ribonucleoprotein | 2.1 |
| | 444534 | AW271626 | Hs.42294 | ESTs | 2.1 |
| | 438391 | AI262248 | Hs.25027 | ESTs | 2.1 |
| 50 | 442003 | AW297497 | Hs.201891 | ESTs | 2.1 |
| | 456278 | BE300369 | Hs.289308 | hypothetical protein MGC4126 | 2.1 |
| | 416976 | BE243985 | Hs.80680 | major vault protein | 2.1 |
| | 417810 | D28419 | Hs.82609 | hydroxymethylbilane synthase | 2.1 |
| | 445242 | BE156478 | Hs.21108 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.1 |
| 55 | 452712 | AW838616 | | gb:RC5-LT0054-140200-013-D01 LT0054 Homo | 2.1 |
| | 434926 | BE543269 | Hs.50252 | mitochondrial ribosomal protein L32 | 2.1 |
| | 421564 | AB007864 | Hs.105850 | KIAA0404 protein | 2.1 |
| | 424927 | AW973666 | Hs.153850 | hypothetical protein C321D2.4 | 2.1 |
| | 432742 | AA564453 | Hs.162339 | ESTs | 2.1 |
| 60 | 435958 | H98180 | Hs.117975 | ESTs | 2.1 |
| | 421531 | AA713505 | Hs.291769 | ESTs | 2.1 |
| | 410431 | BE261320 | Hs.158196 | transcriptional adaptor 3 (ADA3, yeast h | 2.1 |
| | 420503 | AI570943 | Hs.337546 | ESTs | 2.1 |
| | 448127 | AI478416 | Hs.282883 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.1 |
| 65 | 452897 | BE066058 | Hs.269233 | ESTs, Moderately similar to I78885 serin | 2.1 |
| | 447112 | H17800 | Hs.7154 | ESTs | 2.1 |
| | 406577 | | | | 2.1 |
| | 437162 | AW005505 | Hs.5464 | thyroid hormone receptor coactivating pr | 2.1 |
| | 451460 | AI797550 | Hs.209652 | ESTs | 2.1 |
| 70 | 447402 | H54520 | Hs.18490 | hypothetical protein FLJ20452 | 2.1 |
| | 435828 | AA700705 | Hs.13852 | ESTs | 2.1 |
| | 436396 | AI683487 | Hs.152213 | wingless-type MMTV integration site fami | 2.1 |
| | 420582 | BE047878 | Hs.99093 | Homo sapiens chromosome 19, cosmid R2837 | 2.1 |
| | 452020 | AA722012 | Hs.255757 | ESTs, Weakly similar to AT2A_HUMAN POTEN | 2.1 |
| 75 | 415586 | Z45481 | | gb:HSC2QE041 normalized infant brain cDN | 2.1 |
| | 452620 | AA436504 | Hs.119286 | ESTs | 2.1 |
| | 457066 | BE244613 | Hs.158272 | ESTs, Weakly similar to CA13 MOUSE COLLA | 2.1 |
| | 435472 | AW972330 | Hs.283022 | triggering receptor expressed on myeloid | 2.1 |
| | 431741 | AA514783 | Hs.191701 | ESTs | 2.1 |
| 80 | 446840 | AW294828 | Hs.209203 | ESTs | 2.1 |
| | 440818 | AI147060 | Hs.146726 | ESTs | 2.1 |
| | 410174 | AA306007 | Hs.59461 | DKFZP434C245 protein | 2.1 |
| | 400822 | | | | 2.1 |
| | 412760 | AW379030 | Hs.41324 | ESTs | 2.1 |
| | 410653 | BE383768 | Hs.65238 | 95 kDa retinoblastoma protein binding pr | 2.1 |
| | 426925 | NM_001196 | Hs.315689 | Homo sapiens cDNA: FLJ22373 fis, clone H | 2.1 |
| | 424242 | AA337476 | Hs.293984 | hypothetical protein MGC13102 | 2.1 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 452560 | BE077084 | Hs.336432 | ESTs | |
| | 456437 | AI924228 | Hs.115185 | ESTs, Moderately similar to PC4259 ferr | 2.1 |
| | 458922 | BE501831 | Hs.282053 | ESTs | 2.1 |
| 5 | 439231 | AW581935 | Hs.141480 | Homo sapiens mRNA; cDNA DKFZp434N079 (fr | 2.1 |
| | 419488 | AA316241 | Hs.90691 | nucleophosmin/nucleoplasm 3 | 2.1 |
| | 411829 | AW865749 | | gb:QV3-SN0021-100500-185-c03 SN0021 Homo | 2.1 |
| | 457192 | AL135682 | Hs.22452 | Homo sapiens mRNA for KIAA1737 protein, | 2.1 |
| | 422128 | AW981145 | | gb:QV0-OT0033-010400-182-a07 OT0033 Homo | 2.1 |
| 10 | 452571 | W31518 | Hs.34665 | ESTs | 2.1 |
| | 423699 | H41850 | Hs.131846 | PCAF associated factor 65 alpha | 2.1 |
| | 406610 | | | | 2.1 |
| | 453638 | AW814996 | | gb:MR1-ST0206-170400-024-h09 ST0206 Homo | 2.1 |
| | 418856 | AA362858 | | gb:EST72900 Ovary II Homo sapiens cDNA 5 | 2.1 |
| 15 | 437623 | D63880 | Hs.5719 | chromosome condensation-related SMC-asso | 2.1 |
| | 410908 | AA121686 | Hs.10592 | ESTs | 2.1 |
| | 420221 | N25991 | Hs.43725 | ESTs | 2.1 |
| | 424739 | AA346108 | Hs.221610 | ESTs | 2.1 |
| | 425398 | AL049689 | Hs.156369 | hypothetical protein similar to tenascin | 2.1 |
| 20 | 424901 | Z11933 | Hs.182505 | POU domain, class 3, transcription facto | 2.1 |
| | 411096 | U80034 | Hs.68583 | mitochondrial intermediate peptidase | 2.1 |
| | 415635 | F13168 | | gb:HSC3JF101 normalized infant brain cDN | 2.1 |
| | 418181 | U37012 | Hs.83727 | cleavage and polyadenylation specific fa | 2.1 |
| | 407103 | AA424881 | Hs.256301 | hypothetical protein MGC13170 | 2.1 |
| 25 | 454369 | AW752571 | | gb:IL3-CT0213-170100-055-F02 CT0213 Homo | 2.1 |
| | 400021 | | | | 2.1 |
| | 439228 | N51700 | | gb:yy72d01.s1 Soares_multiple_sclerosis_ | 2.1 |
| | 456505 | AA504595 | Hs.111418 | ESTs | 2.1 |
| | 405258 | | | | 2.1 |
| 30 | 444645 | AI184564 | Hs.101654 | ESTs | 2.1 |
| | 430246 | AI269069 | Hs.109268 | hypothetical protein FLJ12552 | 2.1 |
| | 458687 | AW024815 | Hs.170088 | GLUT4 enhancer factor | 2.1 |
| | 403857 | | | | 2.1 |
| | 400258 | | | | 2.1 |
| 35 | 422221 | AA306649 | Hs.169370 | FYN oncogene related to SRC, FGR, YES | 2.1 |
| | 441054 | AA913591 | Hs.126480 | ESTs | 2.1 |
| | 452700 | AI859390 | Hs.288940 | five-span transmembrane protein M83 | 2.1 |
| | 454806 | AW809752 | | gb:MR4-ST0124-181299-020-b06 ST0124 Homo | 2.1 |
| | 448954 | AB014564 | Hs.22616 | KIAA0664 protein | 2.1 |
| 40 | 443148 | AI034357 | Hs.211194 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 2.1 |
| | 453486 | AL039201 | Hs.173554 | ubiquinol-cytochrome c reductase core pr | 2.1 |
| | 437695 | AA769202 | Hs.192142 | ESTs | 2.1 |
| | 425449 | X52056 | Hs.157441 | spleen focus forming virus (SFFV) provir | 2.1 |
| | 447270 | AC002551 | Hs.331 | general transcription factor IIIC, polyp | 2.1 |
| 45 | 435677 | AA694142 | Hs.293726 | ESTs, Weakly similar to TSGA RAT TESTIS | 2.1 |
| | 436382 | AW977063 | Hs.250181 | ESTs | 2.1 |
| | 435837 | AI689210 | Hs.187276 | Homo sapiens cDNA FLJ11431 fis, clone HE | 2.1 |
| | 458287 | AA987556 | Hs.12867 | ESTs | 2.1 |
| | 423794 | BE551781 | Hs.231895 | ESTs | 2.1 |
| 50 | 408049 | AW076098 | Hs.74316 | desmoplakin (DPI, DP1) | 2.1 |
| | 402721 | | | | 2.1 |
| | 451999 | AW176401 | Hs.27424 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypep | 2.1 |
| | 417541 | AI992191 | Hs.180040 | hypothetical protein FLJ22439 | 2.1 |
| | 414857 | AIW402389 | Hs.920 | modulator recognition factor I | 2.1 |
| 55 | 435760 | AF231922 | Hs.213004 | chromosome 21 open reading frame 62 | 2.1 |
| | 428086 | AL1110193 | Hs.224137 | hypothetical protein | 2.1 |
| | 447853 | AI434204 | Hs.164285 | ESTs, Weakly similar to AFG1_YEAST AFG1 | 2.1 |
| | 419034 | NM_002110 | Hs.89555 | hemopoietic cell kinase | 2.1 |
| | 431019 | NM_005249 | Hs.2714 | forkhead box G1B | 2.1 |
| 60 | 421064 | AI245432 | Hs.101382 | tumor necrosis factor, alpha-induced pro | 2.1 |
| | 416435 | AI431301 | Hs.179703 | KIAA0129 gene product | 2.1 |
| | 437014 | AA808757 | Hs.222531 | ESTs, Weakly similar to S59501 interfero | 2.1 |
| | 459369 | T83080 | | gb:yd40e03.r1 Soares fetal liver spleen | 2.1 |
| | 402239 | | | | 2.1 |
| 65 | 412280 | AW205116 | Hs.272814 | hypothetical protein DKFZp434E1723 | 2.1 |
| | 426012 | AA367507 | Hs.75874 | pregnancy-associated plasma protein A | 2.1 |
| | 438885 | AI886558 | Hs.184987 | ESTs | 2.1 |
| | 426076 | AW962714 | | gb:EST374787 MAGE resequences, MAGG Homo | 2.1 |
| | 404561 | | | | 2.1 |
| 70 | 442932 | AA457211 | Hs.8858 | bromodomain adjacent to zinc finger doma | 2.1 |
| | 408175 | W29089 | Hs.19066 | hypothetical protein DKFZp667O2416 | 2.1 |
| | 423867 | AA331886 | | gb:EST35757 Embryo, 8 week I Homo sapien | 2.1 |
| | 458604 | W37944 | Hs.4007 | Sarcolemmal-associated protein | 2.1 |
| | 409650 | T08490 | Hs.288969 | HSCARG protein | 2.1 |
| 75 | 401729 | | | | 2.1 |
| | 433675 | AW977653 | Hs.75319 | ribonucleotide reductase M2 polypeptide | 2.1 |
| | 456741 | W37608 | Hs.184492 | ESTs | 2.1 |
| | 417037 | BE083936 | Hs.80976 | antigen identified by monoclonal antibod | 2.1 |
| | 415079 | R43179 | Hs.22895 | hypothetical protein FLJ23548 | 2.1 |
| 80 | 439262 | AA832333 | Hs.333045 | ESTs | 2.1 |
| | 403108 | | | | 2.1 |
| | 436718 | AW015227 | Hs.289053 | hypothetical protein FLJ14733 | 2.1 |
| | 440696 | AI762757 | Hs.187660 | putative Rab5 GDP/GTP exchange factor ho | 2.1 |
| | 409745 | AA077391 | | gb:7B14E12 Chromosome 7 Fetal Brain cDNA | 2.1 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 453485 | BE620712 | Hs.33026 | hypothetical protein PP2447 | 2.1 |
| | 418177 | N44967 | Hs.5663 | ESTs | 2.1 |
| | 457292 | AI921270 | Hs.334882 | hypothetical protein FLJ14251 | 2.1 |
| | 454434 | AA083558 | Hs.261286 | ESTs | 2.1 |
| 5 | 406085 | | | | 2.1 |
| | 424441 | X14850 | Hs.147097 | H2A histone family, member X | 2.1 |
| | 422726 | U11690 | Hs.1572 | faciogenital dysplasia (Aarskog-Scott sy | 2.1 |
| | 424576 | BE154142 | Hs.96833 | ESTs | 2.1 |
| 10 | 423660 | AL045228 | Hs.130831 | Homo sapiens mRNA: cDNA DKFZp434L137 (fr | 2.1 |
| | 403509 | AF231919 | Hs.18759 | KJAA0539 gene product | 2.1 |
| | 441940 | AW298115 | Hs.128152 | ESTs | 2.1 |
| | 439190 | AW978693 | Hs.293811 | ESTs | 2.1 |
| | 417791 | AW965339 | Hs.111471 | ESTs | 2.1 |
| | 423701 | AA329856 | Hs.143022 | ESTs | 2.1 |
| 15 | 427239 | BE270447 | Hs.174070 | ubiquitin carrier protein | 2.1 |
| | 459642 | BE243103 | | gb:TCAA2E0949 Pediatric acute myelogeno | 2.1 |
| | 450385 | AI631024 | Hs.24948 | synuclein, alpha interacting protein (sy | 2.1 |
| | 425159 | NM_004341 | Hs.154868 | carbamoyl-phosphate synthetase 2, aspart | 2.1 |
| 20 | 425591 | AW294734 | Hs.279727 | Homo sapiens cDNA FLJ14035 fis, clone HE | 2.1 |
| | 445101 | T75202 | Hs.12314 | Homo sapiens mRNA: cDNA DKFZp586C1019 (f | 2.1 |
| | 412811 | H06382 | Hs.21400 | ESTs | 2.1 |
| | 426369 | AF134157 | Hs.169487 | Kreisler (mouse) maf-related leucine zip | 2.1 |
| | 435924 | AW029203 | Hs.191952 | ESTs | 2.1 |
| 25 | 418388 | R72332 | Hs.29258 | Homo sapiens cDNA FLJ11364 fis, clone HE | 2.1 |
| | 452235 | AL039743 | Hs.28514 | testes development-related NYD-SP21 | 2.1 |
| | 452313 | Y00486 | Hs.28914 | adenine phosphoribosyltransferase | 2.1 |
| | 450704 | H85157 | Hs.40696 | ESTs | 2.1 |
| | 427539 | AA405205 | Hs.97960 | ESTs, Weakly similar to T51146 ring-box | 2.1 |
| 30 | 402028 | | | | 2.1 |
| | 405362 | | | | 2.1 |
| | 414718 | H95348 | Hs.107987 | ESTs | 2.1 |
| | 433424 | R68252 | Hs.163566 | ESTs | 2.1 |
| | 444875 | AI200759 | Hs.44737 | ESTs | 2.0 |
| 35 | 449523 | NM_000579 | Hs.54443 | chemokine (C-C motif) receptor 5 | 2.0 |
| | 456072 | H54381 | | gb:yq89a03.s1 Soares fetal liver spleen | 2.0 |
| | 436331 | AI239495 | Hs.120189 | ESTs | 2.0 |
| | 448418 | Z43704 | Hs.21192 | Homo sapiens clone 25155 mRNA sequence | 2.0 |
| | 447250 | AI878909 | Hs.17883 | protein phosphatase 1G (formerly 2C), ma | 2.0 |
| 40 | 448192 | R43915 | Hs.4958 | ESTs | 2.0 |
| | 448966 | AW372914 | Hs.86149 | phosphoinositol 3-phosphate-binding prot | 2.0 |
| | 408605 | AF025374 | Hs.46465 | T-cell, immune regulator 1 | 2.0 |
| | 410790 | AW803357 | | gb:IL2-UM0079-090300-050-A08 UM0079 Homo | 2.0 |
| | 436872 | X15624 | | gb:Human H1 RNA | 2.0 |
| 45 | 432238 | AL133057 | Hs.274135 | Homo sapiens mRNA: cDNA DKFZp434K1815 (f | 2.0 |
| | 446307 | T50083 | Hs.9094 | ESTs | 2.0 |
| | 436588 | AA759233 | Hs.126506 | ESTs | 2.0 |
| | 452487 | AW207659 | Hs.6630 | Homo sapiens cDNA FLJ13329 fis, clone OV | 2.0 |
| | 430420 | AW140027 | Hs.26373 | Homo sapiens cDNA: FLJ23449 fis, clone H | 2.0 |
| 50 | 432036 | AF224266 | Hs.272373 | interleukin 20 | 2.0 |
| | 414460 | L00727 | Hs.898 | dystrophin myotonic-protein kinase | 2.0 |
| | 433507 | AI817336 | Hs.191791 | ESTs | 2.0 |
| | 427964 | AA418082 | Hs.98286 | ESTs, Weakly similar to T20655 hypothei | 2.0 |
| | 443108 | W86975 | Hs.203707 | ESTs | 2.0 |
| 55 | 434504 | AI887341 | Hs.121590 | hypothetical protein FLJ12827 | 2.0 |
| | 454310 | AW818390 | Hs.175613 | homolog of Xenopus Caspase | 2.0 |
| | 443566 | AI290284 | Hs.159872 | ESTs | 2.0 |
| | 449722 | BE280074 | Hs.23960 | cyclin B1 | 2.0 |
| 60 | 452682 | AA456193 | Hs.9071 | progesterone membrane binding protein | 2.0 |
| | 412362 | AW945484 | Hs.184252 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 2.0 |
| | 429341 | X73874 | Hs.2393 | phosphorylase kinase, alpha 1 (muscle) | 2.0 |
| | 435863 | AF255346 | Hs.62919 | Jun dimerization protein p21SNFT | 2.0 |
| | 400774 | R58624 | Hs.2186 | eukaryotic translation elongation factor | 2.0 |
| | 453944 | AW975369 | Hs.292570 | Homo sapiens, clone IMAGE:3502107, mRNA, | 2.0 |
| 65 | 419227 | BE537383 | Hs.89739 | cholinergic receptor, nicotinic, beta po | 2.0 |
| | 448529 | T26460 | Hs.22550 | ESTs | 2.0 |
| | 443206 | AB011420 | Hs.9075 | serine/threonine kinase 17a (apoptosis-i | 2.0 |
| | 439360 | AA448488 | Hs.336629 | ribosomal protein L44 | 2.0 |
| | 436660 | AI658870 | Hs.184513 | ESTs | 2.0 |
| 70 | 449030 | AI365582 | Hs.57100 | Homo sapiens mRNA for FLJ00016 protein, | 2.0 |
| | 411048 | AK001742 | Hs.67991 | hypothetical protein DKFZp434G0522 | 2.0 |
| | 406624 | AF052762 | | gb:Homo sapiens clone csneg8-1 immunoglo | 2.0 |
| | 450666 | T99968 | Hs.18799 | ESTs, Weakly similar to I38022 hypothei | 2.0 |
| | 445143 | BE245342 | Hs.306079 | sec61 homolog | 2.0 |
| | 437698 | R61837 | Hs.7990 | ESTs, Moderately similar to I84505 calci | 2.0 |
| 75 | 426607 | AA382330 | Hs.124223 | ESTs | 2.0 |
| | 449246 | AW411209 | Hs.23363 | hypothetical protein FLJ10983 | 2.0 |
| | 422564 | AI148006 | Hs.222120 | ESTs | 2.0 |
| | 432682 | AI376400 | Hs.159588 | ESTs | 2.0 |
| 80 | 422140 | BE295918 | Hs.112193 | mutS (E. coli) homolog 5 | 2.0 |
| | 408215 | BE614290 | Hs.43812 | syntactin 10 | 2.0 |
| | 417129 | AI381800 | Hs.300684 | calcitonin gene-related peptide-receptor | 2.0 |
| | 442772 | AW503680 | Hs.5957 | Homo sapiens clone 24416 mRNA sequence | 2.0 |
| | 434928 | AW015595 | Hs.4267 | Homo sapiens clones 24714 and 24715 mRNA | 2.0 |

| | | | | | |
|----|-------------|---------------------------------------|---|--|-----|
| | 411380 | AW841619 | | gb:RC1-CN0017-120200-012-b09 CN0017 Homo | 2.0 |
| | 430603 | AA148164 | Hs.247280 | HBV associated factor | 2.0 |
| | 425905 | AB032959 | Hs.318584 | novel C3HC4 type Zinc finger (ring finger) | 2.0 |
| 5 | 401125 | | | | 2.0 |
| | 412939 | AW411491 | Hs.2186 | eukaryotic translation elongation factor | 2.0 |
| | 448740 | BE250632 | Hs.8026 | sestrin 2 | 2.0 |
| | 454390 | AB020713 | Hs.56966 | KIAA0906 protein | 2.0 |
| | 415012 | NM_004383 | Hs.77793 | c-src tyrosine kinase | 2.0 |
| 10 | 410407 | X66839 | Hs.63287 | carbonic anhydrase IX | 2.0 |
| | 403478 | | | | 2.0 |
| | 455485 | AJ393037 | Hs.97871 | Homo sapiens, clone IMAGE:3845253, mRNA, | 2.0 |
| | 430294 | AI538226 | Hs.32976 | guanine nucleotide binding protein 4 | 2.0 |
| | 411669 | BE612676 | Hs.303116 | stromal cell-derived factor 2-like 1 | 2.0 |
| 15 | 451944 | AW445218 | Hs.210876 | ESTs | 2.0 |
| | 436395 | AJ227900 | | gb:Homo sapiens partial mRNA; ID EE2-16B | 2.0 |
| | 456457 | AA252905 | Hs.194477 | E3 ubiquitin ligase SMURF2 | 2.0 |
| | 449123 | D50920 | Hs.23106 | KIAA0130 gene product | 2.0 |
| | 409214 | AW405967 | Hs.333388 | Homo sapiens, clone IMAGE:3957135, mRNA, | 2.0 |
| 20 | 437619 | AW351491 | Hs.334853 | hypothetical protein FLJ23544 | 2.0 |
| | 453348 | BE272318 | Hs.8595 | hypothetical protein FLJ12438 | 2.0 |
| | 424382 | AA351898 | Hs.23539 | ESTs | 2.0 |
| | 447079 | AA280057 | Hs.105280 | ESTs, Weakly similar to dJ963K23.2 [Hsa] | 2.0 |
| 25 | 449501 | AJ652924 | Hs.231942 | ESTs | 2.0 |
| | 422893 | X98411 | Hs.121555 | myosin IF | 2.0 |
| | 412125 | Y17114 | Hs.73393 | eyes absent (Drosophila) homolog 4 | 2.0 |
| | 434845 | BE267057 | Hs.325321 | hypothetical protein R32184_1 | 2.0 |
| | 410422 | AL042014 | Hs.334698 | Homo sapiens, clone MGC:15203, mRNA, com | 2.0 |
| 30 | 430255 | AK000703 | Hs.323822 | Homo sapiens mRNA for KIAA1551 protein, | 2.0 |
| | 451656 | BE327088 | Hs.212752 | ESTs | 2.0 |
| | 442068 | BE312873 | Hs.314932 | ESTs | 2.0 |
| | 446846 | AW197626 | Hs.271901 | ESTs, Moderately similar to S08686 finger | 2.0 |
| | 442690 | AJ014727 | Hs.160047 | ESTs, Weakly similar to B28096 line-1 pr | 2.0 |
| | 454277 | AW295069 | Hs.31743 | ESTs, Weakly similar to Z157_HUMAN ZINC | 2.0 |
| 35 | 426910 | AA470023 | Hs.190089 | ESTs, Moderately similar to ALU1_HUMAN A | 2.0 |
| | 402798 | | | | 2.0 |
| | 404554 | | | | 2.0 |
| | TABLE 258: | | | | |
| 40 | Pkey: | Unique Eos probeset identifier number | | | |
| | CAT number: | Gene cluster number | | | |
| | Accession: | Genbank accession numbers | | | |
| | Pkey | CAT Number | Accession | | |
| 45 | 407909 | 1025254_1 | AW103986 BE156395 BE156391 BE156190 BE156184 BE156388 BE156394 | | |
| | 408432 | 1058667_1 | AW195262 R27868 AW811262 | | |
| | 409193 | 110747_1 | AA131483 AA065156 AA076448 | | |
| | 409745 | 115237_1 | AA077391 AJ347618 AJ361453 AJ088754 AW207491 AW960912 AA921874 AA286833 AA150722 BE152353 AW188822 BE152450 | | |
| | 410447 | 1203929_1 | AW816134 BE063456 AW748795 BE150839 | | |
| 50 | 410790 | 1221131_1 | AW803357 AW803423 AW812233 R06814 | | |
| | 411256 | 1236790_1 | AW834039 AW834040 AW834047 AW845410 BE003128 AW852479 | | |
| | 411380 | 1242343_1 | AW841619 AW851958 AW851851 AW851985 | | |
| | 411632 | 1252361_1 | AW854829 AW854805 AW854841 AW854825 AW854822 AW854830 AW854835 AW854826 | | |
| | 411658 | 1252987_1 | AW855598 AW855608 BE148763 BE148764 AW855645 AW855615 AW855596 AW855610 AW855601 AW855605 | | |
| 55 | 411829 | 1260309_1 | AW865749 BE179419 BE179492 | | |
| | 412225 | 1284108_1 | AW902042 N77591 | | |
| | 412370 | 1291952_1 | AW946614 AW946622 AW946663 AW946667 AW946615 AW946619 | | |
| | 412391 | 1292625_1 | AW947710 AW947698 AW947697 AW947713 | | |
| | 413257 | 1355963_1 | BE075035 BE074999 BE075006 BE075005 BE075032 BE075008 BE075037 | | |
| 60 | 413604 | 1379715_1 | R51767 BE152515 Z44834 H23397 | | |
| | 414406 | 1443333_1 | BE297904 BE294312 | | |
| | 414550 | 1460990_1 | BE379808 | | |
| | 415346 | 1534581_1 | Z43108 F06295 R13085 | | |
| | 415406 | 1536026_1 | T26510 F07926 R53367 | | |
| 65 | 415586 | 1540116_1 | Z45481 F12393 T74437 | | |
| | 415635 | 1540853_1 | F13168 R21289 T77628 | | |
| | 416871 | 1625761_1 | H98716 N90792 N24283 | | |
| | 416913 | 163001_1 | AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499 | | |
| | 417980 | 1712954_1 | R32235 R32247 R32219 | | |
| 70 | 418333 | 173_2 | W92113 AA702794 BE044316 W91984 AA679375 T94184 AA679335 BE503126 AW502118 BE467367 AA584550 AW139964 R93353 AW088477 | | |
| | 418856 | 179649_1 | AJ887846 AW502624 W81697 W81696 AA447817 AA447667 F13631 AW268271 AA055366 AW629027 AA677404 AA831618 AI124782 AA889402 | | |
| | 419217 | 182954_1 | AA765804 AA765530 AA055698 AA594019 AI267368 AA456946 R93354 AF264624 AW668618 AA601493 | | |
| | 419225 | 1830274_1 | AA362858 AW863761 AA229428 | | |
| 75 | 419311 | 183793_1 | AA504571 AA235243 AA411737 AW969068 AA406543 | | |
| | 420352 | 192979_1 | U70073 | | |
| | 422128 | 211994_1 | AA689591 AW974261 AA236240 AJ077451 AA631399 AW974262 | | |
| | 422156 | 212379_1 | BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280 | | |
| 80 | 422176 | 212714_1 | AW881145 AA490718 M85637 AA304575 T06067 AA331991 | | |
| | 423756 | 231725_1 | N34524 AA305071 AW954803 AA502335 AJ433430 AI203597 AW026670 AW265323 AW850787 AA317554 AW993643 AW835572 AW385512 | | |
| | 423867 | 232732_1 | AI334966 W32951 H62656 H53902 R88904 AW835732 | | |
| | 425189 | 247825_1 | H80977 BE147695 AA305496 AW962366 AA436754 | | |
| | | | AA828125 AA834883 AA330555 | | |
| | | | AA331886 AW962659 AW962655 T89841 | | |
| | | | H16622 R17322 AA351959 | | |

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|----|--------------|---|--|
| 5 | 425517 | 252729_1 | AF121179 BE162736 AA358827 |
| | 426076 | 260504_1 | AW962714 AA369277 AA369278 |
| | 426413 | 266650_1 | AA377823 AW954494 AI022688 |
| | 426503 | 268283_1 | AA380153 AA380233 AW963529 |
| | 426531 | 268760_1 | AA381071 AA381084 AA380862 |
| | 429875 | 310034_1 | AI091815 AA460162 AA460761 |
| | 430968 | 326269_1 | AW972830 AA527647 AA489820 AA570362 |
| | 432088 | 341195_1 | AA525454 H74039 R89502 T77379 |
| 10 | 433532 | 368950_1 | AW975367 AA598607 AA742735 |
| | 434559 | 38889_1 | AF147315 AW173079 T53029 |
| | 435065 | 399329_1 | BE064391 BE064395 AA663613 N99644 |
| | 436190 | 41555_1 | AK001059 AA633055 |
| | 436395 | 41905_1 | AJ227900 AI094933 AW051119 F00947 |
| 15 | 436532 | 421802_1 | AA721522 AW975443 T93070 |
| | 436722 | 425758_1 | AW975977 AA729469 AA747132 |
| | 436872 | 42851_1 | X15624 |
| | 437034 | 431713_1 | AA742643 AA808575 AW976668 |
| | 439086 | 46852_1 | AF085947 H70981 H78989 |
| 20 | 439228 | 47001_1 | N51700 AF086051 N51792 |
| | 439518 | 47334_1 | W76326 AF086341 W72300 |
| | 439546 | 47360_1 | AF088056 W76297 W72448 |
| | 439566 | 47387_1 | AF086387 W77884 W72711 |
| | 439710 | 47550_1 | AF086543 W96291 W96225 |
| 25 | 443657 | 576685_1 | R14973 R14967 AI081006 |
| | 444168 | 593829_1 | AW379879 AI126285 H12014 |
| | 444386 | 604004_1 | BE065183 AI144398 BE065367 |
| | 451129 | 859870_1 | BE072881 BE072946 AI762181 |
| | 452712 | 928309_1 | AW838616 AW838660 BE144343 AI914520 AW888910 BE184854 BE184784 |
| 30 | 453446 | 967533_1 | BE299996 BE297115 BE270415 BE295214 BE296526 |
| | 453638 | 975649_1 | AW814996 AL047199 AW850979 |
| | 453746 | 979731_1 | AL120611 BE006190 BE006189 |
| | 454377 | 114761_1 | AA076811 AW814764 |
| | 454389 | 115682_1 | AW752571 AW847602 AA077979 |
| 35 | 454606 | 1226149_2 | AW809752 AW810271 AW809944 AW810319 AW810215 AW810368 AW810167 |
| | 454630 | 1227352_1 | BE142075 BE142148 BE142189 AW816249 BE142147 BE142002 BE142406 BE142094 BE142074 BE142347 BE142000 BE142375 |
| | | | AW811189 BE142133 |
| | 454631 | 1227443_1 | AW811324 AW811325 AW811326 AW811333 AW811329 AW811328 AW811332 AW811339 AW811335 |
| | 454679 | 1228929_1 | AW813110 AW813113 |
| 40 | 454967 | 1247021_1 | AW848276 AW848416 AW848160 AW847945 AW847947 AW848063 AW848113 |
| | 455023 | 1249188_1 | AW850907 AW850901 AW850877 |
| | 455302 | 1276542_1 | AW997641 AW891777 |
| | 455470 | 1292849_1 | AW947992 AW947967 AW947950 AW947957 AW947953 AW947973 AW947966 AW947971 AW947947 AW947970 AW947995 AW947979 AW947952 |
| | | | AW947956 |
| 45 | 455514 | 1321649_1 | AW983871 BE090302 AW983867 AW983845 AW983860 AW983853 AW983852 |
| | 455530 | 1322298_1 | AW984744 AW984759 |
| | 455584 | 1334741_1 | BE007420 BE007419 BE007421 BE007422 |
| | 455778 | 1364506_1 | BE088746 BE088802 BE088755 BE088876 BE088947 BE088881 BE088952 |
| | 455908 | 1382301_1 | BE156306 BE156188 BE156298 BE156377 BE156374 |
| 50 | 456072 | 1470256_1 | H54381 H54463 BE393262 |
| | 456094 | 1504780_1 | H95091 C01228 |
| | 457374 | 328758_1 | AA493662 AW897396 BE154814 |
| | 457578 | 359618_1 | AA578027 |
| | 457730 | 393905_1 | AW753613 AW753857 BE150374 BE150693 BE150394 AA808851 AA650159 AA654653 BE150419 |
| 55 | TABLE 25C: | | |
| | Pkey: | Unique number corresponding to an Eos probeset | |
| | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. | |
| | Strand: | Indicates DNA strand from which exons were predicted. | |
| 60 | NI_position: | Indicates nucleotide positions of predicted exons. | |
| | Pkey | Ref | Strand |
| | 400822 | 7465000 | Plus |
| | 400859 | 9757499 | Minus |
| 65 | 400917 | 7283186 | Minus |
| | 400992 | 8096828 | Plus |
| | 401012 | 7230838 | Minus |
| | 401048 | 7232177 | Plus |
| | 401125 | 8570296 | Minus |
| 70 | 401324 | 9863791 | Plus |
| | 401384 | 6850939 | Minus |
| | 401558 | 7139678 | Plus |
| | 401626 | 8575943 | Minus |
| | 401676 | 9965536 | Plus |
| 75 | 401714 | 6715702 | Plus |
| | 401729 | 8134856 | Minus |
| | 401827 | 2262095 | Plus |
| | 401876 | 8099107 | Plus |
| | 402028 | 7139781 | Plus |
| 80 | 402064 | 8117294 | Plus |
| | 402239 | 7690131 | Plus |
| | 402408 | 9796239 | Minus |
| | 402424 | 9796344 | Minus |

| | | | | |
|----|--------|---------|-------|---|
| | 402516 | 9798099 | Minus | 195342-195511 |
| | 402604 | 9909420 | Plus | 20393-20767 |
| | 402627 | 9931216 | Plus | 12136-12272,16487-16628,17654-17798,18494-18621,18933-19089,20669-20790,21134-21298,22866-22973,23686-23820,26626-26895,29279-29469 |
| 5 | 402721 | 8969253 | Minus | 144428-144715 |
| | 402798 | 3355547 | Plus | 23596-23867 |
| | 402856 | 9801288 | Minus | 90119-90411 |
| | 403048 | 4210991 | Plus | 44275-44592,49656-49955 |
| 10 | 403108 | 8980955 | Plus | 93253-93667 |
| | 403142 | 9444521 | Plus | 89286-90131 |
| | 403166 | 9838127 | Minus | 67762-67940,68695-68856,70394-70507 |
| | 403478 | 9958258 | Plus | 116458-116564 |
| | 403680 | 7331517 | Minus | 157184-157415 |
| 15 | 403751 | 7229815 | Minus | 158794-160929 |
| | 403790 | 8084957 | Minus | 87826-87947,89835-90002 |
| | 403797 | 8099896 | Minus | 123065-125008 |
| | 403857 | 7708910 | Minus | 2524-3408 |
| | 403881 | 7710245 | Minus | 107250-107685,108924-109213 |
| 20 | 403961 | 7596976 | Minus | 110393-110603 |
| | 403969 | 8569909 | Plus | 31237-31375,32405-32506 |
| | 404020 | 8655966 | Minus | 174449-174663 |
| | 404054 | 3548785 | Plus | 66713-69175 |
| | 404084 | 9944055 | Plus | 2795-2969 |
| 25 | 404108 | 8247074 | Minus | 63603-64942 |
| | 404170 | 9930793 | Plus | 168836-169248 |
| | 404185 | 4572584 | Minus | 129171-129327 |
| | 404240 | 5002624 | Minus | 116132-116407,116653-116922 |
| | 404295 | 9856663 | Minus | 75747-75947 |
| 30 | 404299 | 5738652 | Minus | 3826-4025 |
| | 404366 | 9964977 | Plus | 96589-96801 |
| | 404554 | 7243881 | Plus | 42637-42839 |
| | 404561 | 9795980 | Minus | 69039-70100 |
| | 404584 | 9857511 | Plus | 138651-139153 |
| 35 | 404589 | 9931665 | Minus | 32824-32985 |
| | 404642 | 9796810 | Plus | 102999-103145 |
| | 404652 | 9796969 | Minus | 108172-108296 |
| | 404721 | 9856648 | Minus | 173763-174294 |
| | 404756 | 7706327 | Plus | 82849-83627 |
| 40 | 404802 | 4581357 | Minus | 30093-30600 |
| | 404984 | 6939882 | Plus | 87221-87505 |
| | 405159 | 9966252 | Plus | 79659-79804 |
| | 405258 | 7329310 | Plus | 129930-130076 |
| | 405288 | 6139075 | Minus | 126268-126436 |
| 45 | 405353 | 2811095 | Plus | 118525-118892 |
| | 405362 | 2337862 | Minus | 105008-105142,105980-106091,140445-140556,142519-142641 |
| | 405558 | 1621110 | Plus | 4502-4644,5983-6083 |
| | 405588 | 5002511 | Plus | 46180-46366 |
| | 405605 | 5836195 | Minus | 117070-117270 |
| 50 | 405701 | 4263751 | Plus | 93243-93364 |
| | 405741 | 9966947 | Minus | 156747-156875,156936-157208 |
| | 405747 | 8469069 | Minus | 153933-154060 |
| | 405771 | 7018349 | Plus | 91191-91254,91510-91589 |
| | 405808 | 9929207 | Plus | 109758-111166 |
| 55 | 405884 | 6758747 | Plus | 62383-62583 |
| | 405915 | 7712162 | Minus | 43717-43859 |
| | 406028 | 8312303 | Minus | 177469-177829 |
| | 406085 | 9123888 | Plus | 18665-18843 |
| | 406169 | 6684220 | Minus | 12620-14251 |
| 60 | 406267 | 7528342 | Minus | 2570-2731 |
| | 406326 | 9212385 | Plus | 84508-84655 |
| | 406347 | 9255981 | Plus | 90900-91091 |
| | 406474 | 9795567 | Plus | 52758-53211 |
| | 406577 | 7711730 | Plus | 11377-11509 |
| 65 | 406610 | 8312226 | Plus | 13096-13334 |

TABLE 26A: ABOUT 582 GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS TISSUES

Table 26A lists about 582 genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal CNS to "average" glioblastoma was greater than or equal to 3. The "average" normal CNS level was set to the 75th percentile amongst various normal CNS tissues. The "average" glioblastoma level was set to the 85th percentile amongst various tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of 75th percentile normal central nervous system tissue to 85th percentile tumor

| | | | | | |
|----|--------|----------|-----------|---|-------|
| 80 | Pkey | ExAccn | UnigenelD | Unigene Title | R1 |
| | 453655 | AW960427 | Hs.79059 | transforming growth factor, beta receptor | 136.7 |
| | 417275 | XG3578 | Hs.295449 | parvalbumin | 29.0 |
| | 430829 | AW451999 | Hs.194024 | ESTs | 25.7 |
| | 410657 | AF063228 | Hs.65248 | dynein, cytoplasmic, intermediate polype | 22.6 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 419954 | D14720 | Hs.93883 | myelin protein zero (Charcot-Marie-Tooth | 21.2 |
| | 459247 | N46243 | Hs.110373 | ESTs, Highly similar to T42626 secreted | 18.5 |
| | 416133 | NM_001683 | Hs.89512 | ATPase, Ca++ transporting, plasma membra | 15.5 |
| | 416018 | AW138239 | Hs.78977 | proprotein convertase subtilisin/kexin 1 | 15.2 |
| 5 | 417167 | AW206437 | Hs.4290 | ESTs | 14.8 |
| | 433940 | H05129 | Hs.7459 | cyclic AMP-regulated phosphoprotein, 21 | 13.4 |
| | 413324 | V00571 | Hs.75294 | corticotropin releasing hormone | 13.1 |
| | 439830 | AA846666 | Hs.151489 | ESTs, Weakly similar to XE7_HUMAN PROTEI | 12.6 |
| 10 | 408068 | AW148652 | Hs.167398 | ESTs | 12.6 |
| | 412636 | NM_004415 | Hs.74316 | desmoplakin (DPI, DPII) | 12.5 |
| | 429096 | AB011106 | Hs.196012 | KIAA0534 protein | 12.2 |
| | 412638 | AA910199 | Hs.203838 | ESTs | 12.2 |
| | 423690 | AA329648 | Hs.23804 | ESTs, Weakly similar to PN0099 son3 prot | 12.1 |
| | 456844 | AI264155 | Hs.152981 | CDP-diacylglycerol synthase (phosphatida | 11.9 |
| 15 | 418318 | U47732 | Hs.84072 | transmembrane 4 superfamily member 3 | 10.9 |
| | 442593 | R39804 | Hs.31961 | ESTs | 10.8 |
| | 446353 | AI290919 | Hs.153661 | ESTs | 10.4 |
| | 420290 | AW977318 | Hs.194480 | ESTs | 10.3 |
| 20 | 414220 | BE298094 | | gb:601118231F1 NIH_MGC_17 Homo sapiens c | 10.3 |
| | 414290 | AI568801 | Hs.71721 | ESTs | 10.2 |
| | 426365 | AA376667 | Hs.10283 | RNA binding motif protein 8B | 10.0 |
| | 414937 | R38898 | Hs.12382 | ESTs | 10.0 |
| | 419643 | F06066 | Hs.91791 | chromosome 11 open reading frame 25 | 9.5 |
| 25 | 407173 | T64349 | | gb:yc10d08.s1 Stratagene lung (937210) H | 9.5 |
| | 412454 | R55745 | Hs.167330 | ESTs | 9.5 |
| | 439366 | AF100143 | Hs.6540 | fibroblast growth factor 13 | 9.4 |
| | 415315 | F12240 | Hs.250655 | prothymosin, alpha (gene sequence 28) | 9.3 |
| | 441790 | AW294909 | Hs.132208 | ESTs | 9.2 |
| 30 | 448117 | H49129 | Hs.172982 | ESTs | 9.1 |
| | 400661 | | | | 9.0 |
| | 433558 | AA833757 | Hs.201769 | ESTs, Weakly similar to T24435 hypotheti | 9.0 |
| | 412453 | R20205 | Hs.167330 | ESTs | 9.0 |
| | 408920 | AL120071 | Hs.48998 | fibronectin leucine rich transmembrane p | 8.9 |
| 35 | 409031 | AA376836 | Hs.76728 | ESTs | 8.7 |
| | 428106 | BE620016 | Hs.182470 | PTD010 protein | 8.3 |
| | 446544 | AI631932 | Hs.7047 | ESTs, Weakly similar to Unknown (H.sapie | 8.2 |
| | 423479 | NM_014326 | Hs.129208 | death-associated protein kinase 2 | 8.2 |
| 40 | 439480 | AL038511 | Hs.125316 | ESTs, Weakly similar to S33990 finger pr | 8.2 |
| | 418036 | Z37976 | Hs.83337 | latent transforming growth factor beta b | 8.0 |
| | 456490 | U83171 | Hs.97203 | small inducible cytokine subfamily A (Cy | 8.0 |
| | 410200 | AA082557 | Hs.101915 | Stargardt disease 3 (autosomal dominant) | 8.0 |
| | 414602 | AW630088 | Hs.76550 | Homo sapiens mRNA; cDNA DKFZp564B1264 (f | 8.0 |
| | 408428 | NM_014787 | Hs.44896 | DnaJ (Hsp40) homolog, subfamily B, membe | 7.9 |
| 45 | 437073 | AI885608 | Hs.94122 | ESTs | 7.9 |
| | 408434 | AW195317 | Hs.107716 | hypothetical protein FLJ22344 | 7.9 |
| | 438150 | AA037534 | Hs.79059 | transforming growth factor, beta recepto | 7.9 |
| | 440209 | H05049 | Hs.22263 | neurexin 3 | 7.8 |
| | 408119 | W26213 | Hs.101672 | ESTs, Weakly similar to T00331 hypotheti | 7.8 |
| 50 | 417421 | AL138201 | Hs.82120 | nuclear receptor subfamily 4, group A, m | 7.8 |
| | 410587 | AA370706 | Hs.86412 | chromosome 9 open reading frame 5 | 7.8 |
| | 429611 | AI889077 | Hs.211388 | Homo sapiens BAC clone CTB-60N22 from 7q | 7.7 |
| | 405800 | | | | 7.7 |
| | 421750 | AK000768 | Hs.107872 | hypothetical protein FLJ20761 | 7.7 |
| 55 | 426356 | BE536836 | Hs.98682 | hypothetical protein FKSG32 | 7.7 |
| | 423440 | R25234 | Hs.143434 | contactin 1 | 7.7 |
| | 445148 | AI214510 | Hs.146304 | ESTs | 7.6 |
| | 416294 | D86980 | Hs.79170 | KIAA0227 protein | 7.6 |
| | 424087 | N69333 | Hs.143434 | contactin 1 | 7.6 |
| 60 | 437479 | R61866 | Hs.101277 | ESTs | 7.5 |
| | 405071 | | | | 7.5 |
| | 421224 | AW402154 | Hs.125812 | ESTs | 7.4 |
| | 442025 | AW887434 | Hs.11810 | CDA11 protein | 7.4 |
| | 459476 | BE185844 | | gb:ILS-HT0731-110500-087-c08 HT0731 Homo | 7.2 |
| 65 | 430573 | AA744550 | Hs.136345 | ESTs | 7.1 |
| | 401836 | | | | 7.1 |
| | 448958 | AB020651 | Hs.22653 | KIAA0844 protein | 7.1 |
| | 430152 | AB001325 | Hs.234642 | aquaporin 3 | 7.1 |
| | 419474 | AW968619 | Hs.155849 | ESTs | 7.1 |
| 70 | 401780 | | | | 7.1 |
| | 446052 | AA358760 | | gb:EST67699 Fetal lung II Homo sapiens c | 7.0 |
| | 423605 | AF047826 | Hs.129887 | cadherin 19, type 2 | 7.0 |
| | 433098 | AW190593 | Hs.151143 | ESTs | 7.0 |
| | 449511 | AI436187 | Hs.296261 | guanine nucleotide binding protein (G pr | 6.9 |
| 75 | 451285 | AW137912 | Hs.227583 | Homo sapiens chromosome X map Xp11.23 L- | 6.8 |
| | 428414 | AL049980 | Hs.184216 | DKFZP564C152 protein | 6.8 |
| | 419273 | BE271180 | Hs.293490 | ESTs, Weakly similar to I38022 hypotheti | 6.8 |
| | 443155 | R54485 | Hs.23772 | ESTs | 6.8 |
| | 450561 | R49674 | Hs.25909 | ESTs | 6.8 |
| 80 | 433068 | NM_006456 | Hs.288215 | sialyltransferase | 6.8 |
| | 440729 | AA904739 | Hs.128204 | ESTs | 6.8 |
| | 448426 | BE018315 | Hs.280776 | tankyrase, TRF1-interacting ankyrin-refa | 6.7 |
| | 423589 | AA328082 | Hs.209569 | ESTs | 6.6 |
| | 415681 | AI379882 | Hs.72630 | ESTs | 6.5 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 413510 | F13044 | | gb:HSC3H101 normalized infant brain cDN | 6.4 |
| | 427992 | Y15014 | Hs.181353 | UDP-Gal:betaGlcNAc beta 1,3-galactosyltr | 6.4 |
| | 453344 | BE349075 | Hs.44571 | ESTs | 6.4 |
| 5 | 450642 | R39773 | Hs.7130 | copine IV | 6.4 |
| | 432251 | AW972983 | Hs.232165 | polycythemia rubra vera 1; cell surface | 6.4 |
| | 429322 | D86984 | Hs.199243 | KIAA0231 protein | 6.4 |
| | 444927 | AW016637 | Hs.199425 | ESTs | 6.4 |
| | 447482 | AB033059 | Hs.18705 | KIAA1233 protein | 6.4 |
| 10 | 400332 | S66407 | Hs.248032 | FLT4 | 6.4 |
| | 440703 | AL137663 | Hs.7378 | Homo sapiens mRNA; cDNA DKFZp434G227 (fr | 6.3 |
| | 446129 | AW244073 | Hs.145946 | ESTs | 6.3 |
| | 454076 | AW204712 | Hs.61957 | ESTs | 6.3 |
| | 425526 | AA359933 | | gb:EST69040 Fetal lung II Homo sapiens c | 6.3 |
| 15 | 421913 | AI934365 | Hs.109439 | osteoglycin (osteoinductive factor, mime | 6.3 |
| | 434273 | AA913143 | Hs.26303 | ESTs | 6.3 |
| | 408480 | AI350337 | Hs.164568 | fibroblast growth factor 7 (keratinocyte | 6.2 |
| | 451301 | AI769514 | Hs.209890 | EST | 6.2 |
| | 430754 | AW862610 | Hs.157068 | ESTs | 6.2 |
| | 438356 | AA805530 | Hs.48527 | ESTs | 6.2 |
| 20 | 422743 | BE304678 | Hs.119598 | ribosomal protein L3 | 6.2 |
| | 453355 | AW295374 | Hs.31412 | Homo sapiens cDNA FLJ11422 fis, clone HE | 6.2 |
| | 426388 | AW081394 | Hs.97103 | ESTs | 6.2 |
| | 452502 | AI904296 | | gb:PM-BT046-220199-286_1 BT046 Homo sapi | 6.2 |
| | 402546 | | | | 6.1 |
| 25 | 457534 | AI761307 | Hs.232226 | ESTs | 6.1 |
| | 408165 | AL137573 | Hs.43143 | Homo sapiens mRNA; cDNA DKFZp564A2463 (fr | 6.1 |
| | 404958 | | | | 6.1 |
| | 432501 | BE546532 | Hs.25682 | Homo sapiens mRNA for KIAA1863 protein, | 6.1 |
| 30 | 442979 | AW440782 | Hs.174743 | ESTs | 6.1 |
| | 422262 | AL022315 | Hs.113987 | lectin, galactoside-binding, soluble, 2 | 6.0 |
| | 408713 | NM_001248 | Hs.47042 | ectonucleoside triphosphate diphosphohyd | 6.0 |
| | 454065 | BE394588 | | gb:601311808F1 NIH_MGC_44 Homo sapiens c | 6.0 |
| | 430004 | U27768 | Hs.227571 | regulator of G-protein signalling 4 | 6.0 |
| 35 | 401521 | | | | 5.9 |
| | 425087 | R62424 | Hs.126059 | ESTs | 5.9 |
| | 446298 | AF187813 | Hs.14637 | kidney- and liver-specific gene | 5.9 |
| | 417761 | R13727 | Hs.21435 | ESTs | 5.9 |
| | 424806 | AA382523 | Hs.105689 | MSTP031 protein | 5.9 |
| 40 | 441695 | T12411 | Hs.183745 | hypothetical protein FLJ13456 | 5.9 |
| | 457483 | AB034694 | Hs.272558 | endomucin-1 | 5.9 |
| | 417175 | R44558 | Hs.94002 | ESTs | 5.9 |
| | 437483 | AL390174 | | gb:Homo sapiens mRNA; cDNA DKFZp547J184 | 5.8 |
| | 436427 | AI344378 | Hs.143399 | ESTs | 5.8 |
| 45 | 411939 | AI365585 | Hs.146246 | ESTs | 5.8 |
| | 459053 | AI807052 | Hs.210361 | ESTs | 5.8 |
| | 411052 | AW814950 | | gb:MR1-ST0206-130400-023-d06 ST0206 Homo | 5.7 |
| | 431063 | Z98949 | Hs.326843 | hypothetical protein bk125H2.1 | 5.7 |
| | 450382 | AA397658 | Hs.60257 | Homo sapiens cDNA FLJ13598 fis, clone PL | 5.7 |
| 50 | 408478 | NM_000806 | Hs.45740 | gamma-aminobutyric acid (GABA) A recepto | 5.7 |
| | 442676 | AI733585 | Hs.130897 | ESTs | 5.7 |
| | 446443 | AV659082 | Hs.134228 | ESTs | 5.7 |
| | 400865 | | | | 5.7 |
| | 459080 | AW192083 | Hs.290855 | ESTs | 5.7 |
| 55 | 407952 | AI215902 | Hs.88845 | ESTs, Highly similar to T50835 hypotheti | 5.6 |
| | 431984 | AL080239 | Hs.272284 | Human DNA sequence from clone GS1-256O22 | 5.6 |
| | 425705 | AF007833 | Hs.159265 | kruppel-related zinc finger protein hckr | 5.6 |
| | 442238 | AW135374 | Hs.270949 | ESTs, Moderately similar to F41925 hypot | 5.6 |
| | 422994 | AW891802 | Hs.296276 | ESTs | 5.6 |
| 60 | 457148 | AF091035 | Hs.184627 | KIAA0118 protein | 5.6 |
| | 428356 | AL046991 | Hs.10338 | ESTs | 5.6 |
| | 415927 | AL120168 | Hs.78919 | Kell blood group precursor (McLeod pheno | 5.6 |
| | 402092 | | | | 5.5 |
| | 440526 | AI832243 | Hs.211471 | ESTs | 5.5 |
| 65 | 444409 | AI792140 | Hs.49265 | ESTs | 5.5 |
| | 417877 | AI025829 | Hs.86320 | ESTs | 5.5 |
| | 458238 | AW071521 | Hs.333541 | beta-amyloid binding protein precursor | 5.4 |
| | 430702 | U56979 | Hs.250651 | H factor 1 (complement) | 5.4 |
| | 456189 | H91010 | Hs.44940 | ESTs | 5.4 |
| 70 | 427424 | AA402453 | Hs.113011 | ESTs | 5.4 |
| | 437354 | AA749215 | Hs.291886 | ESTs | 5.4 |
| | 455617 | BE078070 | | gb:CM1-BT0614-160300-149-R02 BT0614 Homo | 5.4 |
| | 429290 | AF203032 | Hs.198760 | neurofilament, heavy polypeptide (200kD) | 5.4 |
| | 427861 | AA813185 | Hs.98183 | ESTs | 5.3 |
| 75 | 408556 | U49516 | Hs.46362 | 5-hydroxytryptamine (serotonin) receptor | 5.3 |
| | 444209 | AI753134 | Hs.146494 | ESTs | 5.3 |
| | 422831 | R02504 | Hs.332943 | ESTs | 5.3 |
| | 403180 | | | | 5.3 |
| | 418026 | BE379727 | Hs.83213 | fatty acid binding protein 4, adipocyte | 5.3 |
| 80 | 430339 | W28608 | Hs.239625 | integral membrane protein 2B | 5.3 |
| | 431596 | T34708 | Hs.272927 | Sec23 (S. cerevisiae) homolog A | 5.2 |
| | 431930 | AB035301 | Hs.272211 | cadherin 7, type 2 | 5.2 |
| | 437403 | AI208149 | Hs.121196 | ESTs | 5.2 |
| | 438285 | AA782845 | Hs.22790 | ESTs | 5.2 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 439901 | N73885 | Hs.124169 | ESTs | 5.2 |
| | 438507 | AA809052 | Hs.211275 | ESTs | 5.2 |
| | 449222 | AW293984 | Hs.197621 | ESTs | 5.2 |
| 5 | 402834 | AK001507 | Hs.306084 | Homo sapiens clone FLB6914 PRO1821 mRNA, | 5.2 |
| | 419042 | T81429 | Hs.221065 | ESTs | 5.2 |
| | 436777 | AA731199 | Hs.293130 | ESTs | 5.2 |
| | 445071 | AI280246 | Hs.149504 | ESTs | 5.1 |
| | 408016 | AW136827 | Hs.256096 | ESTs | 5.1 |
| 10 | 412047 | AA934589 | Hs.49696 | ESTs | 5.1 |
| | 436953 | AW959074 | Hs.23648 | Homo sapiens cDNA FLJ13097 fis, clone NT | 5.1 |
| | 436773 | AW078629 | Hs.82110 | PC4 and SFRS1 interacting protein 1 | 5.1 |
| | 409263 | AA069573 | Hs.50319 | ESTs | 5.1 |
| | 453830 | AA534296 | Hs.20953 | ESTs | 5.1 |
| 15 | 459580 | AA022888 | Hs.176065 | ESTs | 5.1 |
| | 417616 | R07728 | Hs.268668 | ESTs | 5.1 |
| | 423457 | F08208 | Hs.283844 | similar to rat tricarboxylate carrier-li | 5.1 |
| | 441535 | AL135735 | Hs.7885 | phosphatidylinositol binding clathrin as | 5.0 |
| | 416490 | AF090116 | Hs.79348 | regulator of G-protein signalling 7 | 5.0 |
| 20 | 417284 | N62889 | Hs.107242 | Homo sapiens cDNA FLJ12965 fis, clone NT | 5.0 |
| | 447135 | TS8148 | | gb:yb98g06.s1 Stratagene lung (937210) H | 5.0 |
| | 448605 | AL109678 | Hs.21597 | Homo sapiens mRNA full length insert cDN | 5.0 |
| | 442240 | AI791883 | Hs.292719 | ESTs | 4.9 |
| | 459399 | BE407712 | Hs.153998 | creatine kinase, mitochondrial 1 (ubiqui | 4.9 |
| 25 | 427972 | AA864870 | Hs.181304 | putative gene product | 4.9 |
| | 432944 | AA570687 | Hs.38512 | ESTs | 4.9 |
| | 440198 | BE560093 | | gb:601345159F1 NIH_MGC_8 Homo sapiens cD | 4.9 |
| | 444047 | AI097452 | Hs.135095 | ESTs | 4.9 |
| | 416040 | AW819158 | Hs.289044 | Homo sapiens cDNA FLJ12048 fis, clone HE | 4.9 |
| 30 | 444922 | AI921750 | Hs.144871 | Homo sapiens cDNA FLJ13752 fis, clone PL | 4.8 |
| | 436670 | AI690021 | Hs.201536 | ESTs | 4.8 |
| | 448072 | AI459306 | Hs.24908 | ESTs | 4.8 |
| | 408936 | AL138043 | Hs.293549 | ESTs | 4.8 |
| | 412622 | AW664708 | Hs.171959 | ESTs | 4.8 |
| 35 | 414943 | D80647 | Hs.124193 | ESTs | 4.8 |
| | 429254 | H10133 | Hs.91846 | hypothetical protein DKFZp761C121 | 4.8 |
| | 453567 | AI742835 | Hs.33368 | hypothetical protein FLJ11175 | 4.8 |
| | 407906 | AA369665 | Hs.41185 | Homo sapiens mRNA; cDNA DKFZp564O1262 (I | 4.8 |
| | 441028 | AI333660 | Hs.17558 | Homo sapiens cDNA FLJ14446 fis, clone HE | 4.7 |
| 40 | 405130 | | | | 4.7 |
| | 455225 | AW996689 | | gb:OV3-BN0046-150400-151-g09 BN0046 Homo | 4.7 |
| | 446218 | AV657159 | | gb:AV657159 GLC Homo sapiens cDNA clone | 4.7 |
| | 443347 | AI052543 | Hs.133244 | melanoma-derived leucine zipper, extra-n | 4.7 |
| | 402176 | | | | 4.7 |
| 45 | 416577 | BE063207 | Hs.79381 | grancalcin | 4.7 |
| | 436221 | AK001781 | Hs.296543 | Homo sapiens cDNA FLJ10919 fis, clone OV | 4.7 |
| | 420480 | AL137361 | Hs.98173 | hypothetical protein | 4.7 |
| | 400800 | Y10262 | Hs.46925 | eyes absent (Drosophila) homolog 3 | 4.6 |
| | 435161 | AF124150 | Hs.272091 | ESTs | 4.6 |
| 50 | 404793 | | | | 4.6 |
| | 430895 | U66581 | Hs.248121 | G protein-coupled receptor 22 | 4.6 |
| | 438571 | AW020775 | Hs.56022 | ESTs | 4.6 |
| | 445924 | AI264671 | Hs.164166 | ESTs | 4.6 |
| | 444585 | AW170015 | Hs.6594 | ESTs | 4.6 |
| 55 | 421044 | AF061871 | Hs.311736 | Human DNA sequence from clone RP1-238D15 | 4.6 |
| | 418274 | AI458587 | Hs.128677 | Human DNA sequence from clone RP1-50024 | 4.6 |
| | 425475 | W56339 | Hs.107057 | ESTs | 4.6 |
| | 434311 | BE543469 | Hs.266263 | Homo sapiens cDNA FLJ14115 fis, clone MA | 4.5 |
| | 414272 | AI651603 | Hs.46988 | ESTs | 4.5 |
| 60 | 446235 | AI564022 | Hs.138207 | ESTs | 4.5 |
| | 414327 | BE408145 | Hs.185254 | ESTs, Weakly similar to T24435 hypotheti | 4.5 |
| | 414630 | BE410857 | | gb:601301177F1 NIH_MGC_21 Homo sapiens c | 4.5 |
| | 414456 | H74314 | | gb:yu56e10.r1 Soares fetal liver spleen | 4.5 |
| | 401024 | | | | 4.5 |
| 65 | 414699 | AI815523 | Hs.76930 | synuclein, alpha (non A4 component of am | 4.5 |
| | 423449 | AI497900 | Hs.33067 | ESTs | 4.5 |
| | 405138 | | | | 4.5 |
| | 413544 | BE147225 | | gb:PM2-HT0225-031299-003-f11 HT0225 Homo | 4.5 |
| | 453880 | AI803166 | Hs.28462 | ESTs, Weakly similar to I38022 hypotheti | 4.5 |
| 70 | 433521 | T66087 | Hs.112482 | Homo sapiens unknown mRNA sequence | 4.4 |
| | 441184 | AA922009 | Hs.150269 | ESTs | 4.4 |
| | 429876 | AB028977 | Hs.225974 | KIAA1054 protein | 4.4 |
| | 445481 | AW661846 | Hs.148836 | ESTs | 4.4 |
| | 452340 | NM_002202 | Hs.505 | ISL1 transcription factor, LIM/homeodoma | 4.4 |
| 75 | 404769 | | | | 4.4 |
| | 444331 | AW193342 | Hs.24144 | ESTs | 4.4 |
| | 429726 | AW628326 | Hs.27151 | ESTs | 4.4 |
| | 449093 | AB035356 | Hs.22998 | neurexin 1 | 4.4 |
| | 451959 | AA056203 | Hs.27337 | hypothetical protein FLJ20623 | 4.4 |
| 80 | 415716 | N59294 | Hs.179662 | nucleosome assembly protein 1-like 1 | 4.4 |
| | 417888 | R23053 | | gb:yh31a05.r1 Soares placenta Nb2HP Homo | 4.4 |
| | 419656 | AB002314 | Hs.92025 | KIAA0316 gene product | 4.4 |
| | 425864 | U56420 | Hs.159903 | olfactory receptor, family 5, subfamily | 4.4 |
| | 435078 | AW518888 | Hs.40937 | ESTs | 4.4 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 413493 | BE14444 | | gb:MR0-HT0168-141199-002-f09 HT0168 Homo | 4.3 |
| | 432712 | AB016247 | Hs.288031 | sterol-C5-desaturase (fungal ERG3, delta | 4.3 |
| | 459650 | R25754 | Hs.301185 | ESTs | 4.3 |
| 5 | 404828 | | | | 4.3 |
| | 423782 | AA472209 | Hs.323117 | ESTs | 4.3 |
| | 426867 | AA460967 | Hs.22668 | ESTs | 4.3 |
| | 426802 | AA385182 | Hs.46699 | ESTs | 4.3 |
| | 457353 | X65633 | Hs.248144 | melanocortin 2 receptor (adrenocorticotr | 4.3 |
| 10 | 412112 | BE180342 | | gb:RC3-HT0622-130400-012-a07 HT0622 Homo | 4.3 |
| | 401522 | N47812 | Hs.306198 | CGI-35 protein | 4.3 |
| | 419055 | AI365384 | Hs.11571 | Homo sapiens cDNA FLJ11570 fis, clone HE | 4.3 |
| | 410171 | H07892 | Hs.12431 | ESTs | 4.3 |
| | 419564 | U08989 | Hs.91139 | solute carrier family 1 (neuronal/epithe | 4.3 |
| 15 | 458789 | AL157468 | Hs.325825 | Homo sapiens cDNA FLJ20848 fis, clone AD | 4.3 |
| | 455040 | AW852286 | | gb:QV0-CT0225-100400-187-d08 CT0225 Homo | 4.3 |
| | 438533 | AI440266 | Hs.170673 | ESTs, Weakly similar to T24832 hypotheti | 4.3 |
| | 459005 | AA447679 | Hs.144558 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 4.3 |
| | 418489 | U76421 | Hs.85302 | adenosine deaminase, RNA-specific, B1 (h | 4.2 |
| 20 | 433389 | AF038171 | | gb:Homo sapiens clone 23671 mRNA sequenc | 4.2 |
| | 454356 | AW390363 | Hs.11522 | hypothetical protein from Xq28 | 4.2 |
| | 442339 | BE299668 | Hs.227591 | ESTs, Weakly similar to 1901303A Leu zip | 4.2 |
| | 421249 | AA285362 | | gb:HTH277 HTCDL1 Homo sapiens cDNA 5'/3' | 4.2 |
| | 443998 | AI620661 | Hs.296276 | ESTs | 4.2 |
| 25 | 452197 | AW023595 | Hs.232048 | ESTs | 4.2 |
| | 451117 | AA015752 | Hs.205173 | ESTs | 4.2 |
| | 404501 | AW247252 | Hs.75514 | nucleoside phosphorylase | 4.2 |
| | 410378 | R23324 | Hs.41693 | DnaJ (Hsp40) homolog, subfamily B, membe | 4.2 |
| | 422528 | AB011182 | Hs.118087 | KIAA0610 protein | 4.2 |
| 30 | 440323 | AA970614 | Hs.127992 | ESTs | 4.2 |
| | 425767 | AF054176 | Hs.159483 | chromosome 1 open reading frame 7 | 4.1 |
| | 434460 | AA478486 | Hs.3852 | KIAA0368 protein | 4.1 |
| | 410362 | H04811 | Hs.93164 | proprotein convertase subtilisin/kexin 1 | 4.1 |
| | 413121 | T96090 | Hs.142678 | ESTs | 4.1 |
| 35 | 409403 | AA668224 | Hs.6634 | Homo sapiens cDNA: FLJ22547 fis, clone H | 4.1 |
| | 450235 | AA007512 | Hs.17538 | ESTs | 4.1 |
| | 449754 | H00820 | Hs.30977 | ESTs, Weakly similar to B34087 hypotheti | 4.1 |
| | 421813 | BE048255 | | gb:tz49b05.y1 NCI_CGAP_Bm52 Homo sapien | 4.1 |
| 40 | 408496 | AI683802 | Hs.136182 | ESTs | 4.1 |
| | 430261 | AA305127 | Hs.237225 | hypothetical protein HT023 | 4.1 |
| | 434101 | AA625205 | Hs.259599 | KIAA1622 protein | 4.1 |
| | 451837 | T92157 | Hs.16970 | ESTs | 4.1 |
| | 411772 | BE170301 | | gb:QV4-HT0536-040500-193-f05 HT0536 Homo | 4.1 |
| 45 | 437630 | AI252782 | Hs.153026 | SWAP-70 protein | 4.1 |
| | 430212 | AA469153 | | gb:nc67f04.s1 NCI_CGAP_Pr1 Homo sapiens | 4.1 |
| | 400216 | | | | 4.0 |
| | 429830 | AI537278 | Hs.225841 | DKFZP434D193 protein | 4.0 |
| | 453165 | S74727 | Hs.32042 | aspartoacylase (aminoacylase 2, Canavan | 4.0 |
| | 418047 | R37633 | Hs.4847 | ESTs | 4.0 |
| 50 | 405354 | | | | 4.0 |
| | 427931 | AW206512 | Hs.186996 | ESTs | 4.0 |
| | 428775 | AA434579 | Hs.143691 | ESTs | 4.0 |
| | 449422 | AA001373 | Hs.59821 | ESTs | 4.0 |
| | 453864 | AW021407 | Hs.21068 | hypothetical protein | 4.0 |
| 55 | 456407 | AW968614 | | gb:EST380690 MAGE resequences, MAGJ Homo | 4.0 |
| | 441869 | NM_003947 | Hs.8004 | huntingtin-associated protein interactin | 4.0 |
| | 420784 | T65158 | Hs.102399 | ESTs, Moderately similar to S65657 alpha | 4.0 |
| | 425195 | AA352026 | Hs.94319 | VPS10 domain receptor protein | 4.0 |
| | 429628 | H09604 | Hs.13268 | ESTs | 4.0 |
| 60 | 410087 | F12079 | Hs.332579 | ESTs | 4.0 |
| | 409840 | AW502122 | | gb:UI-HF-BR0p-ajr-c-08-0-UI.r1 NIH_MGC_5 | 4.0 |
| | 452854 | AA437061 | Hs.14060 | prokineticin 1 precursor | 4.0 |
| | 419910 | AA662913 | Hs.190173 | ESTs, Weakly similar to A46010 X-linked | 4.0 |
| | 427443 | AA402713 | Hs.97872 | ESTs | 4.0 |
| 65 | 414990 | C17758 | Hs.221652 | Homo sapiens cDNA FLJ14323 fis, clone PL | 3.9 |
| | 412678 | AA115575 | Hs.114914 | ESTs | 3.9 |
| | 405629 | | | | 3.9 |
| | 420299 | AI056871 | Hs.15276 | ESTs | 3.9 |
| | 453098 | Z25935 | Hs.86379 | ESTs | 3.9 |
| 70 | 435752 | AF230801 | | gb:Homo sapiens growth hormone receptor | 3.9 |
| | 441005 | Z41305 | Hs.303172 | Homo sapiens mRNA: cDNA DKFZp547G133 (fr | 3.9 |
| | 414516 | AI307802 | Hs.135560 | ESTs, Weakly similar to T43458 hypotheti | 3.9 |
| | 442257 | AW503831 | Hs.323370 | Human EST clone 25267 mariner transposon | 3.9 |
| | 422563 | BE299342 | Hs.19348 | hypothetical protein FLJ13119 | 3.9 |
| 75 | 406697 | M21388 | Hs.123017 | Human unproductively rearranged Ig mu-ch | 3.9 |
| | 443850 | AW014723 | Hs.334612 | ESTs | 3.9 |
| | 412677 | AW029608 | Hs.17384 | ESTs | 3.9 |
| | 422788 | AL117352 | Hs.120828 | Human DNA sequence from clone RPS-876B10 | 3.9 |
| | 405377 | | | | 3.9 |
| 80 | 414376 | BE393856 | Hs.66915 | ESTs, Weakly similar to 16.7Kd protein [| 3.9 |
| | 453341 | AI758912 | Hs.296341 | adenylyl cyclase-associated protein 2 | 3.9 |
| | 431960 | AW241821 | Hs.301927 | c6.1A | 3.9 |
| | 416854 | H40164 | Hs.80296 | Purkinje cell protein 4 | 3.9 |
| | 427264 | AA400117 | Hs.125747 | ESTs | 3.9 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 422746 | NM_004484 | Hs.119651 | glypican 3 | 3.9 |
| | 452346 | BE243534 | | gb:TCBAP1D0885 Pediatric pre-B cell acut | 3.9 |
| | 414666 | NM_004466 | Hs.76828 | glypican 5 | 3.8 |
| 5 | 418217 | AJ910647 | Hs.13442 | ESTs | 3.8 |
| | 419118 | AA234223 | Hs.139204 | ESTs | 3.8 |
| | 445017 | AJ205493 | Hs.176860 | ESTs | 3.8 |
| | 405867 | | | | 3.8 |
| | 422760 | BE409561 | | gb:601299865F1 NIH_MGC_21 Homo sapiens c | 3.8 |
| 10 | 453863 | X02544 | Hs.572 | orosomucoid 1 | 3.8 |
| | 457821 | H47166 | Hs.124322 | ESTs, Weakly similar to A47582 B-cell gr | 3.8 |
| | 457330 | AB013818 | Hs.247220 | peroxisome biogenesis factor 10 | 3.8 |
| | 435600 | AL047034 | Hs.119747 | ESTs | 3.8 |
| | 456083 | U46922 | Hs.77252 | fragile histidine triad gene | 3.8 |
| 15 | 413341 | H78472 | Hs.191325 | ESTs, Weakly similar to T18967 hypotheti | 3.8 |
| | 449057 | AB037784 | Hs.22941 | KIAA1363 protein | 3.8 |
| | 421855 | F06504 | Hs.27384 | ESTs, Moderately similar to ALU4_HUMAN A | 3.8 |
| | 414764 | AW013887 | Hs.72047 | ESTs | 3.8 |
| | 404391 | | | | 3.7 |
| 20 | 433629 | R13140 | Hs.13359 | ESTs | 3.7 |
| | 424738 | AJ963740 | Hs.46826 | ESTs | 3.7 |
| | 401315 | | | | 3.7 |
| | 407706 | AA191085 | Hs.26612 | ESTs, Moderately similar to S23650 retro | 3.7 |
| | 440530 | AA888646 | Hs.174187 | ESTs | 3.7 |
| 25 | 433930 | AA620338 | Hs.273781 | ESTs | 3.7 |
| | 409662 | AW452320 | Hs.279726 | ESTs | 3.7 |
| | 437268 | AJ754847 | Hs.227571 | regulator of G-protein signalling 4 | 3.7 |
| | 445688 | AJ248205 | Hs.153244 | ESTs | 3.7 |
| | 408593 | R19566 | Hs.197617 | ESTs | 3.7 |
| 30 | 417091 | AA193283 | Hs.291990 | ESTs | 3.7 |
| | 448556 | AW885606 | Hs.5064 | ESTs | 3.7 |
| | 423135 | N67655 | Hs.26411 | ESTs | 3.7 |
| | 400135 | | | | 3.7 |
| | 459150 | BE155356 | | gb:PM1-HT0350-160300-009-d06 HT0350 Homo | 3.7 |
| 35 | 457221 | AW383197 | Hs.218260 | ESTs | 3.7 |
| | 451660 | AJ807927 | Hs.249601 | ESTs | 3.7 |
| | 401600 | BE247275 | Hs.151787 | U5 snRNP-specific protein, 116 kD | 3.7 |
| | 446818 | AJ342668 | Hs.279765 | ESTs | 3.7 |
| | 447795 | AW295151 | Hs.163612 | ESTs | 3.7 |
| 40 | 427562 | R56424 | Hs.26534 | ESTs | 3.6 |
| | 412258 | AA376768 | Hs.324841 | hypothetical protein FLJ22622 | 3.6 |
| | 454339 | AW381880 | | gb:QV4-HT0316-091199-028-d05 HT0316 Homo | 3.6 |
| | 439274 | AF086092 | Hs.48372 | ESTs | 3.6 |
| | 452381 | H23329 | Hs.290880 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.6 |
| 45 | 422897 | AA679784 | Hs.4290 | ESTs | 3.6 |
| | 429656 | X05608 | Hs.211584 | neurofilament, light polypeptide (68kD) | 3.6 |
| | 421908 | AW935200 | Hs.285814 | sprouty (Drosophila) homolog 4 | 3.6 |
| | 407978 | AW385129 | Hs.41717 | phosphodiesterase 1A, calmodulin-depende | 3.6 |
| | 426452 | AW614271 | Hs.121647 | ESTs, Highly similar to AC006014 8 simil | 3.6 |
| 50 | 400685 | | | | 3.6 |
| | 417154 | AJ674701 | Hs.21388 | ESTs | 3.6 |
| | 447176 | Z42549 | Hs.160893 | ESTs | 3.6 |
| | 423893 | AL031709 | Hs.134846 | Human DNA sequence from clone 316G12 on | 3.6 |
| | 449231 | BE410360 | Hs.298573 | KIAA1720 protein | 3.6 |
| 55 | 411607 | AW853498 | | gb:RC1-CT0252-170200-025-h02 CT0252 Homo | 3.6 |
| | 405977 | | | | 3.6 |
| | 441470 | BE503874 | Hs.301986 | ESTs | 3.6 |
| | 423568 | NM_005256 | Hs.129818 | growth arrest-specific 2 | 3.6 |
| 60 | 441235 | AJ884585 | Hs.135570 | Homo sapiens cDNA: FLJ21268 fis, clone C | 3.6 |
| | 450236 | AW162998 | Hs.24684 | KIAA1376 protein | 3.6 |
| | 425364 | AF052150 | Hs.155959 | Homo sapiens clone 24533 mRNA sequence | 3.6 |
| | 426775 | AA384564 | Hs.108829 | ESTs | 3.6 |
| | 414831 | M31158 | Hs.77439 | protein kinase, cAMP-dependent, regulato | 3.6 |
| | 416876 | AW501916 | Hs.117897 | ESTs | 3.6 |
| 65 | 400878 | | | | 3.6 |
| | 425153 | AW023193 | Hs.27046 | ESTs | 3.6 |
| | 432222 | AJ204995 | | gb:an03c03.x1 Stratagene schizo brain S1 | 3.5 |
| | 415047 | F13142 | | gb:HSC3/D031 normalized infant brain cDN | 3.5 |
| | 401532 | | | | 3.5 |
| 70 | 446495 | D60923 | Hs.153460 | ESTs | 3.5 |
| | 431325 | AW026751 | Hs.5794 | ESTs, Weakly similar to 2109260A B cell | 3.5 |
| | 445898 | AF070623 | Hs.13423 | Homo sapiens clone 24468 mRNA sequence | 3.5 |
| | 455901 | BE155527 | | gb:PM1-HT0350-190400-013-b08 HT0350 Homo | 3.5 |
| | 416421 | AA134006 | Hs.79306 | eukaryotic translation initiation factor | 3.5 |
| 75 | 455697 | BE067952 | | gb:CM0-BT0365-061299-122-g09 BT0365 Homo | 3.5 |
| | 405678 | | | | 3.5 |
| | 418207 | C14685 | Hs.34772 | ESTs | 3.5 |
| | 425383 | D83407 | Hs.156007 | Down syndrome critical region gene 1-lik | 3.5 |
| | 417027 | AA192306 | Hs.23926 | triadin | 3.5 |
| 80 | 408367 | AK001178 | Hs.44424 | homolog of rat orphan transporter v7-3 | 3.5 |
| | 417702 | R09935 | Hs.191146 | ESTs | 3.5 |
| | 445687 | W80382 | Hs.149297 | ESTs | 3.5 |
| | 408776 | AA057365 | Hs.63356 | ESTs, Weakly similar to I38022 hypotheti | 3.5 |
| | 413164 | BE068494 | | gb:MR1-BT0371-050500-009-a12 BT0371 Homo | 3.5 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 414593 | BE386764 | | gb:601273249F1 NIH_MGC_20 Homo sapiens c | 3.5 |
| | 453220 | AB033089 | Hs.32452 | Homo sapiens mRNA for KIAA1263 protein, | 3.5 |
| | 415621 | AJ648602 | Hs.55468 | ESTs | 3.5 |
| 5 | 454437 | AJ248173 | Hs.191460 | hypothetical protein MGC12936 | 3.5 |
| | 446066 | AJ343931 | Hs.149383 | ESTs | 3.5 |
| | 423374 | AB037770 | Hs.127656 | KIAA1349 protein | 3.5 |
| | 419347 | C15944 | Hs.90005 | superiorcervical ganglia, neural specifi | 3.5 |
| | 418516 | NM_006218 | Hs.85701 | phosphoinositide-3-kinase, catalytic, al | 3.5 |
| 10 | 451776 | W45679 | Hs.169854 | hypothetical protein SP192 | 3.5 |
| | 432305 | M62402 | Hs.274313 | insulin-like growth factor binding prote | 3.5 |
| | 456995 | T89832 | Hs.170278 | ESTs | 3.5 |
| | 403323 | | | | 3.5 |
| | 425022 | M95724 | Hs.154207 | centromere protein C 1 | 3.5 |
| | 439394 | AA149250 | Hs.56105 | ESTs | 3.5 |
| 15 | 433803 | AI823593 | Hs.27688 | ESTs | 3.4 |
| | 450715 | AI266484 | Hs.31570 | ESTs, Weakly similar to KIAA1324 protein | 3.4 |
| | 411474 | AW848427 | | gb:fl3-CT0214-150200-075-H10 CT0214 Homo | 3.4 |
| | 415076 | NM_000857 | Hs.77890 | guanylate cyclase 1, soluble, beta 3 | 3.4 |
| 20 | 423826 | U20325 | Hs.1707 | cocaine- and amphetamine-regulated trans | 3.4 |
| | 459495 | BE544158 | | gb:601076707F1 NIH_MGC_12 Homo sapiens c | 3.4 |
| | 427173 | BE255017 | Hs.97540 | ESTs | 3.4 |
| | 408112 | AW451982 | Hs.248613 | ESTs | 3.4 |
| | 446092 | N33522 | Hs.145894 | ESTs | 3.4 |
| 25 | 416868 | AI656856 | Hs.292597 | ESTs | 3.4 |
| | 458234 | BE551408 | Hs.127196 | ESTs | 3.4 |
| | 419555 | AA244416 | | gb:nc07d11.s1 NCI_CGAP_Pr1 Homo sapiens | 3.4 |
| | 414314 | BE312991 | | gb:601150275F1 NIH_MGC_19 Homo sapiens c | 3.4 |
| | 400425 | AY004252 | Hs.287385 | PR domain containing 12 | 3.4 |
| 30 | 414366 | BE549143 | | gb:601076456F1 NIH_MGC_12 Homo sapiens c | 3.4 |
| | 434053 | AW445136 | Hs.134946 | ESTs | 3.4 |
| | 449997 | AI683052 | Hs.201577 | KIAA1829 protein | 3.4 |
| | 433461 | AI636047 | Hs.197623 | ESTs | 3.4 |
| | 428006 | AA418743 | Hs.98306 | KIAA1862 protein | 3.4 |
| 35 | 424695 | U58331 | Hs.151899 | sarcoglycan, delta (35kD dystrophin-asso | 3.4 |
| | 443294 | AI733625 | Hs.133053 | ESTs | 3.4 |
| | 428212 | AW444451 | Hs.134812 | ESTs | 3.4 |
| | 457673 | AA551569 | Hs.272034 | hypothetical protein PRO2822 | 3.4 |
| | 446390 | AA233393 | Hs.14992 | hypothetical protein FLJ11151 | 3.4 |
| 40 | 428536 | AI143139 | Hs.2288 | visinin-like 1 | 3.3 |
| | 426597 | AA382250 | Hs.145601 | ESTs | 3.3 |
| | 410366 | AI267589 | Hs.302689 | hypothetical protein | 3.3 |
| | 458258 | AW406546 | Hs.127971 | ESTs | 3.3 |
| | 401738 | | | | 3.3 |
| 45 | 409038 | T97490 | Hs.50002 | small inducible cytokine subfamily A (Cy | 3.3 |
| | 425785 | T27017 | Hs.159528 | Homo sapiens clone 24400 mRNA sequence | 3.3 |
| | 433328 | AW298159 | Hs.23644 | ESTs, Weakly similar to S65824 reverse t | 3.3 |
| | 414541 | BE293116 | Hs.76392 | aldehyde dehydrogenase 1 family, member | 3.3 |
| | 434998 | AW975157 | Hs.26037 | ESTs | 3.3 |
| 50 | 456359 | AI967991 | Hs.93574 | homeo box D3 | 3.3 |
| | 426527 | NM_001037 | Hs.170238 | sodium channel, voltage-gated, type I, b | 3.3 |
| | 454267 | AA437199 | Hs.656 | cell division cycle 25C | 3.3 |
| | 400302 | N48056 | Hs.1915 | folate hydrolase (prostate-specific memb | 3.3 |
| | 434077 | AF116659 | Hs.321151 | Homo sapiens PRO1412 mRNA, complete cds | 3.3 |
| 55 | 436602 | AI793222 | Hs.166817 | ESTs | 3.3 |
| | 449204 | AB000099 | Hs.23251 | Down syndrome critical region gene 4 | 3.3 |
| | 417935 | R53697 | Hs.170044 | ESTs | 3.3 |
| | 423310 | AA325225 | Hs.124023 | Homo sapiens cDNA FLJ14218 fis, clone NT | 3.3 |
| | 436624 | T64297 | Hs.5241 | fatty acid binding protein 1, liver | 3.3 |
| 60 | 453406 | AI192987 | Hs.61784 | hypothetical protein FLJ14451 | 3.3 |
| | 420164 | AW339037 | Hs.24908 | ESTs | 3.3 |
| | 447826 | AW779317 | Hs.258556 | ESTs | 3.3 |
| | 419875 | AA853410 | Hs.93557 | proenkephalin | 3.3 |
| | 444612 | AW138111 | Hs.22902 | ESTs | 3.3 |
| 65 | 418504 | BE159718 | Hs.85335 | Homo sapiens mRNA; cDNA DKFZp564D1462 (f | 3.2 |
| | 415242 | R45986 | Hs.295014 | ESTs | 3.2 |
| | 418188 | AW139413 | Hs.151880 | ESTs | 3.2 |
| | 430355 | NM_006219 | Hs.239818 | phosphoinositide-3-kinase, catalytic, be | 3.2 |
| | 421640 | AW966652 | | gb:EST378726 MAGE resequences, MAGI Homo | 3.2 |
| 70 | 432359 | AA076049 | Hs.274415 | Homo sapiens cDNA FLJ10229 fis, clone HE | 3.2 |
| | 408806 | AW847814 | Hs.289005 | Homo sapiens cDNA: FLJ21532 fis, clone C | 3.2 |
| | 400409 | AF153341 | Hs.283954 | Homo sapiens winged helix/forkhead trans | 3.2 |
| | 446015 | T30968 | Hs.13531 | hypothetical protein FLJ10971 | 3.2 |
| | 425495 | AA358454 | Hs.78026 | ESTs, Weakly similar to similar to ankyr | 3.2 |
| 75 | 403092 | | | | 3.2 |
| | 452971 | AI873878 | Hs.91789 | ESTs | 3.2 |
| | 454186 | BE141030 | | gb:MR0-HT0067-201099-002-h11 HT0067 Homo | 3.2 |
| | 401485 | | | | 3.2 |
| | 401949 | | | | 3.2 |
| 80 | 457452 | AW972675 | | gb:EST384766 MAGE resequences, MAGL Homo | 3.2 |
| | 454100 | AI693231 | Hs.126043 | chromosome 21 open reading frame 51 | 3.2 |
| | 448440 | AA173467 | Hs.62402 | p21/Cdc42/Rac1-activated kinase 1 (yeast | 3.2 |
| | 421200 | AA284811 | Hs.264433 | ESTs | 3.2 |
| | 430142 | NM_000437 | Hs.234392 | platelet-activating factor acetylhydrola | 3.2 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 433197 | AB040889 | Hs.281022 | KIAA1456 protein | 3.2 |
| | 443509 | AV645470 | | gb:AV645470 GLC Homo sapiens cDNA clone | 3.2 |
| | 440827 | A1733110 | Hs.128128 | ESTs | 3.2 |
| 5 | 432799 | NM_016161 | Hs.278960 | alpha-1,4-N-acetylglucosaminyltransferase | 3.2 |
| | 409257 | AW370362 | | gb:RC1-BT0255-181099-012-007 BT0255 Homo | 3.2 |
| | 459235 | BE246010 | Hs.271468 | Homo sapiens mRNA for FLJ00038 protein, | 3.2 |
| | 416789 | AA223439 | Hs.79933 | cydin I | 3.2 |
| | 429809 | AL162010 | Hs.223603 | Homo sapiens mRNA; cDNA DKFZp761D09121 (| 3.2 |
| 10 | 420156 | AW449258 | Hs.6187 | ESTs | 3.2 |
| | 455577 | BE008341 | | gb:RC2-BN0127-240300-011-b05 BN0127 Homo | 3.2 |
| | 400617 | AF151064 | Hs.36069 | hypothetical protein | 3.2 |
| | 437129 | AL049327 | Hs.302057 | Homo sapiens mRNA; cDNA DKFZp564E016 (fr | 3.2 |
| | 451820 | AW058357 | Hs.337353 | ESTs | 3.2 |
| 15 | 457535 | AA609685 | Hs.278672 | membrane component, chromosome 11, surfa | 3.2 |
| | 419956 | AL137939 | Hs.40096 | ESTs | 3.1 |
| | 456235 | AA203637 | | gb:zx58b12.r1 Soares_fetal_liver_spleen_ | 3.1 |
| | 423930 | AA332697 | Hs.42721 | ESTs | 3.1 |
| | 403796 | | | | 3.1 |
| 20 | 414085 | AA114016 | Hs.75746 | aldehyde dehydrogenase 1 family, member | 3.1 |
| | 445886 | A1793176 | Hs.145596 | ESTs | 3.1 |
| | 414401 | A1760159 | Hs.124833 | ESTs | 3.1 |
| | 441573 | BE563966 | Hs.6529 | ESTs, Weakly similar to I78885 serine/th | 3.1 |
| | 450725 | R71389 | Hs.175951 | ESTs | 3.1 |
| 25 | 458805 | A1282933 | Hs.23294 | hypothetical protein FLJ14393 | 3.1 |
| | 417868 | A1078534 | Hs.122592 | ESTs | 3.1 |
| | 458391 | A1792628 | Hs.133273 | ESTs | 3.1 |
| | 423346 | A1267677 | Hs.127416 | synaptojanin 1 | 3.1 |
| | 454486 | AW857077 | | gb:RC1-CT0302-140300-016-004 CT0302 Homo | 3.1 |
| 30 | 408341 | AW182952 | Hs.249957 | ESTs | 3.1 |
| | 410669 | AW805749 | Hs.318885 | superoxide dismutase 2, mitochondrial | 3.1 |
| | 404907 | | | | 3.1 |
| | 434910 | A1333863 | Hs.215474 | ESTs, Moderately similar to alternative | 3.1 |
| | 436990 | A1149729 | Hs.120557 | ESTs | 3.1 |
| 35 | 441921 | A1733376 | Hs.164478 | hypothetical protein FLJ21939 similar to | 3.1 |
| | 454673 | AW812807 | | gb:RC3-ST0186-070100-016-c04 ST0186 Homo | 3.1 |
| | 429470 | A1878901 | Hs.203862 | guanine nucleotide binding protein (G pr | 3.1 |
| | 404345 | AA730407 | Hs.159156 | protocadherin 11 | 3.1 |
| | 408217 | A433201 | Hs.279860 | tumor protein, translationally-controlled | 3.1 |
| 40 | 417313 | AA195602 | | gb:zr32f09.r1 Soares_NhHMPu_S1 Homo sapi | 3.1 |
| | 427322 | AK002017 | Hs.176227 | hypothetical protein FLJ11155 | 3.1 |
| | 411003 | AA181018 | Hs.13056 | hypothetical protein FLJ13920 | 3.1 |
| | 425339 | AA936330 | Hs.198113 | ESTs | 3.1 |
| | 426716 | NM_006379 | Hs.171921 | sema domain, immunoglobulin domain (Ig), | 3.1 |
| 45 | 449078 | AK001256 | Hs.22975 | KIAA1576 protein | 3.1 |
| | 429608 | U49250 | Hs.210862 | T-box, brain, 1 | 3.1 |
| | 442308 | AA989402 | Hs.111 | fibroblast growth factor 9 (glia-activat | 3.1 |
| | 428465 | AW970976 | Hs.293653 | ESTs | 3.1 |
| | 411666 | AF106564 | Hs.71346 | neurofilament 3 (150kD medium) | 3.1 |
| 50 | 447965 | AW292577 | Hs.94445 | ESTs | 3.1 |
| | 413918 | AW015898 | Hs.71245 | ESTs | 3.1 |
| | 419682 | H13139 | Hs.92282 | paired-like homeodomain transcription fa | 3.1 |
| | 425810 | A1923627 | Hs.31903 | ESTs | 3.1 |
| | 427865 | AA416931 | Hs.126065 | ESTs | 3.1 |
| 55 | 429060 | AW139155 | Hs.194995 | hypothetical protein DKFZp434O0320 | 3.1 |
| | 430708 | U78308 | Hs.278485 | olfactory receptor, family 1, subfamily | 3.1 |
| | 448084 | AA467800 | Hs.271000 | ESTs, Weakly similar to I38022 hypotheti | 3.1 |
| | 454506 | AW847346 | | gb:RC0-CT0205-240999-021-e01 CT0205 Homo | 3.1 |
| | 414629 | AA345824 | Hs.76688 | carboxylesterase 1 (monocyte/macrophage | 3.0 |
| 60 | 422963 | M79141 | Hs.13234 | ESTs | 3.0 |
| | 417696 | BE241624 | Hs.82401 | CD69 antigen (p60, early T-cell activati | 3.0 |
| | 448175 | BE296174 | Hs.225160 | hypothetical protein FLJ13102 | 3.0 |
| | 414686 | BE409757 | Hs.23189 | ESTs, Moderately similar to TBB2_HUMAN T | 3.0 |
| | 458360 | A1027207 | Hs.132253 | ESTs | 3.0 |
| 65 | 451829 | AW964081 | Hs.247377 | ESTs | 3.0 |
| | 445179 | A1949743 | Hs.224768 | ESTs | 3.0 |
| | 433090 | A1720050 | Hs.145362 | immortalization-upregulated protein | 3.0 |
| | 432018 | AA524447 | Hs.152377 | ESTs | 3.0 |
| | 407988 | N47760 | Hs.285107 | hypothetical protein FLJ13397 | 3.0 |
| | 405911 | | | | 3.0 |
| 70 | 418808 | A1821836 | Hs.10359 | ESTs | 3.0 |
| | 431900 | AW972048 | Hs.192534 | ESTs | 3.0 |
| | 452893 | H18017 | Hs.22869 | ESTs, Moderately similar to KIAA1395 pro | 3.0 |
| | 423952 | AW877787 | Hs.136102 | KIAA0853 protein | 3.0 |
| 75 | 412000 | AW576555 | Hs.15780 | ATP-binding cassette, sub-family A (ABC1 | 3.0 |
| | 405793 | | | | 3.0 |
| | 410711 | AB002316 | Hs.65746 | KIAA0318 protein | 3.0 |
| | 411279 | AW884776 | | gb:QV4-OT0067-010300-121-d01 OT0067 Homo | 3.0 |
| | 423957 | AW978309 | Hs.136235 | Homo sapiens cDNA FLJ13542 fs, clone PL | 3.0 |
| 80 | 427071 | AA397958 | Hs.192719 | ESTs | 3.0 |
| | 434961 | AW974956 | | gb:EST387061 MAGE resequences, MAGN Homo | 3.0 |

TABLE 26B:

Pkey: Unique Eos probeset identifier number

| CAT number: Accession: | | Gene cluster number Genbank accession numbers | |
|---------------------------|--------------|---|--|
| Pkey | CAT Number | Accession | |
| 5 | 409257 | 1112994_1 | AW370362 AW809101 |
| | 409840 | 1156071_1 | AW502122 AW502125 AW501663 AW501720 |
| | 411052 | 1230374_1 | AW814950 R98513 H69459 BE176242 H54583 |
| | 411279 | 1237516_1 | AW884776 AW935737 AW835261 AW835247 AW835246 AW835263 AW835240 AW835258 |
| 10 | 411474 | 1247047_2 | AW848427 AW848890 AW848159 AW848118 AW848634 AW848285 AW848086 AW848485 AW848283 AW848162 |
| | 411607 | 1251251_1 | AW853498 AW853442 AW853590 AW853433 AW853592 |
| | 411772 | 1257386_1 | BE170301 AW861539 AW904851 BE154336 BE154090 BE154275 |
| | 412112 | 1277883_1 | BE180342 BE180347 AW901900 BE180222 BE180218 BE180226 BE180413 BE180416 AW901899 BE180228 AW901897 BE180224 AW901898 |
| 15 | 413164 | 1351422_1 | BE180223 BE180219 BE180346 BE180343 BE180418 BE180225 BE180221 BE180341 AW901894 BE180217 BE180227 AW901891 BE180345 |
| | | | AW893614 AW893615 H85799 H83501 BE180220 |
| | | | BE068494 BE068414 BE068332 BE068347 BE068706 BE068623 BE068450 BE068480 BE068350 BE068295 BE068498 BE068765 BE068328 |
| | | | BE068778 BE068671 BE068526 BE068493 BE068433 BE068740 BE068306 BE068631 BE068580 BE068445 BE068567 BE068521 BE068549 |
| | | | BE068392 BE068307 BE068692 BE068473 BE068754 BE068476 BE068585 BE068626 BE068591 BE068745 BE068434 BE068759 BE068628 |
| 20 | | | BE068723 BE068529 BE068689 BE068383 BE068422 BE068470 BE068522 BE068618 BE068354 BE068748 BE068683 BE068303 BE068602 |
| | | | BE068739 BE068374 BE068302 BE068625 BE068596 BE068663 BE068429 BE068605 BE068693 BE068672 BE068401 BE068579 BE068329 |
| | | | BE068390 BE068419 BE068393 BE068447 BE068675 BE068311 BE068540 BE068301 BE068543 BE068719 BE068369 BE068324 BE068588 |
| | | | BE068568 BE068317 BE068384 BE068547 BE068674 BE068436 BE068321 BE068361 BE068676 BE068499 BE068299 BE068352 BE068410 |
| | | | BE068293 BE068418 BE068552 BE068598 BE068327 BE068550 BE068712 BE068661 BE068733 BE068525 BE068752 BE068357 BE068330 |
| | | | BE068565 BE068538 BE068340 BE068537 BE068761 BE068632 BE068758 |
| 25 | 413493 | 1373555_1 | BE144444 BE144430 |
| | 413510 | 1374377_1 | F13044 T77009 BE145525 BE145493 |
| | 413544 | 1375671_1 | BE147225 BE147205 BE147234 |
| | 414220 | 1426940_1 | BE298094 BE267860 |
| | 414314 | 1435028_1 | BE312991 BE272945 |
| | 414366 | 1438636_1 | BE549143 BE390613 BE277344 |
| 30 | 414456 | 1447655_1 | H74314 BE299593 |
| | 414593 | 1464909_1 | BE386764 BE387560 |
| | 414630 | 1468083_1 | BE410857 BE390605 |
| | 415047 | 1517450_1 | F13142 Z42926 F06135 F06147 H08517 D51360 T75341 |
| 35 | 417313 | 166644_1 | AA195602 W01148 N40632 |
| | 417888 | 1706092_1 | R23053 R79884 R76271 |
| | 419555 | 185884_1 | AA244416 AA244401 |
| | 421249 | 200649_1 | AA285362 AW752386 AW847156 AA285373 AW879575 AW879558 |
| | 421640 | 204833_1 | AW966652 AW966653 AA294989 AA385977 |
| 40 | 421813 | 207654_1 | BE048255 AA313083 AA298419 |
| | 422760 | 221034_1 | BE409561 BE162756 AW73798 |
| | 425526 | 252776_1 | AA359933 AA358889 AW955306 AW962995 AW837746 AW837755 AW837697 |
| | 430212 | 314437_1 | AA469153 AI718503 AA469225 |
| | 432222 | 343347_1 | AI204995 AW827539 AW969908 AW440776 AA528756 |
| 45 | 433389 | 36497_1 | AF038171 Z43209 F07347 |
| | 434961 | 396357_1 | AW974956 AA781075 AA654944 |
| | 435752 | 41050_1 | AF230801 AF230800 AA401795 AA398260 |
| | 437483 | 43756_1 | AL390174 AW898817 |
| | 440198 | 48824_2 | BE560093 |
| 50 | 443509 | 57199_1 | AV645470 T84636 T82805 |
| | 446052 | 65988_1 | AA358760 AA158850 AW062737 AW062738 AV656291 |
| | 446218 | 66686_1 | AV657159 BE145509 BE145512 BE145505 BE145507 |
| | 447135 | 70963_1 | T58148 AW516579 AW059603 |
| | 452346 | 912205_1 | BE243534 BE243752 AI880228 L44326 |
| 55 | 452502 | 919733_1 | AI904296 BE007223 R30687 |
| | 454065 | 998401_1 | BE394588 AW024754 BE183166 BE183167 |
| | 454186 | 1049791_1 | BE141030 BE141474 BE141467 BE141753 BE141024 BE141761 AW177583 AW177579 AW177582 AW177585 AW177587 AW807582 AW177581 |
| | | | BE141477 BE141520 BE141456 BE141492 BE141028 BE141775 BE141489 BE141751 AW177599 BE141750 AW177597 BE141512 BE141460 |
| 60 | 454339 | 1122972_1 | AW381980 BE152244 BE152235 BE152238 BE152232 |
| | 454486 | 1215703_1 | AW857077 AW861268 AW847383 AW79587 |
| | 454506 | 1219857_1 | AW847346 AW847395 AW847408 AW847385 AW847342 AW847396 AW847339 AW801718 AW801787 |
| | 454673 | 1228669_1 | AW812807 AW812815 AW812802 |
| | 455040 | 1250028_1 | AW852286 AW851934 AW852096 AW852274 |
| 65 | 455225 | 1252318_1 | AW996689 AW996380 AW996453 BE085650 AW868687 BE085595 |
| | 455577 | 1333898_1 | BE006341 BE006307 BE006311 |
| | 455617 | 1346117_1 | BE078070 BE061030 BE077927 |
| | 455697 | 1351148_1 | BE067952 BE067945 BE067942 BE067943 BE067949 BE067954 BE067944 BE067953 BE067956 BE067946 |
| | 455901 | 1381569_1 | BE155527 BE155503 BE155188 BE155126 |
| 70 | 456235 | 168686_1 | AA203637 AA832266 H67452 |
| | 456407 | 184986_1 | AW968614 AA243209 AA281411 |
| | 457452 | 339381_1 | AW972675 AA541366 AA523039 |
| | 459150 | 919196_1 | BE155356 BE153488 BE153461 BE155059 BE155210 BE155413 BE153577 BE153688 BE155063 BE155347 AI903640 BE155492 |
| 75 | TABLE 26C: | | |
| | Pkey: | Unique number corresponding to an Eos probe set | |
| | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA | |
| | Strand: | sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. | |
| | NI_position: | Indicates DNA strand from which exons were predicted. | |
| 80 | | Indicates nucleotide positions of predicted exons. | |
| | Pkey | Ref | Strand |
| | 400661 | 8118474 | Plus |
| | 400685 | 8118768 | Minus |
| | | | NI_position |
| | | | 84912-85187 |
| | | | 72969-73050, 73713-73800 |

| | | | | |
|----|--------|---------|-------|---|
| 5 | 400865 | 1945037 | Minus | 44482-45526 |
| | 400878 | 9864757 | Plus | 31493-32842 |
| | 401024 | 8117489 | Plus | 60551-60802 |
| | 401315 | 9212516 | Minus | 198960-199619 |
| | 401485 | 7341723 | Plus | 68009-68209,68841-69077 |
| | 401521 | 7705251 | Plus | 9127-9234 |
| | 401532 | 7798785 | Plus | 124414-124950,125050-125418 |
| | 401738 | 2982169 | Minus | 41547-41757 |
| 10 | 401780 | 7249190 | Minus | 28397-28617,28920-29045,29135-29296,29411-29567,29705-29787,30224-30573 |
| | 401836 | 7534063 | Plus | 71981-72084 |
| | 401949 | 3492889 | Plus | 160728-161660 |
| | 402092 | 7249154 | Minus | 107533-108094 |
| | 402176 | 7543687 | Minus | 10-750 |
| 15 | 402546 | 7637348 | Plus | 24673-25170 |
| | 403092 | 8954241 | Plus | 174720-175016,175104-175406,175508-175813 |
| | 403180 | 7523976 | Minus | 63603-63759 |
| | 403323 | 8348082 | Minus | 120366-120845 |
| | 403796 | 8099896 | Minus | 75073-77664 |
| 20 | 404391 | 3135305 | Minus | 26030-26173,27852-27997 |
| | 404769 | 8099713 | Minus | 175801-176823 |
| | 404793 | 7232206 | Minus | 61087-61590 |
| | 404828 | 6580415 | Minus | 26291-27253 |
| | 404907 | 7331453 | Minus | 102880-103828 |
| 25 | 404958 | 7407941 | Minus | 2731-4531 |
| | 405071 | 7708797 | Minus | 11115-11552 |
| | 405130 | 8516045 | Plus | 150235-150449 |
| | 405138 | 8576241 | Plus | 90303-90516 |
| | 405354 | 2642452 | Plus | 52213-53089 |
| 30 | 405377 | 5649375 | Plus | 216656-216848 |
| | 405629 | 4508116 | Minus | 101678-101866 |
| | 405678 | 4079670 | Plus | 151821-152027 |
| | 405793 | 1405887 | Minus | 89197-89453 |
| | 405800 | 2791346 | Plus | 19271-19813 |
| 35 | 405867 | 6758731 | Minus | 74553-75173 |
| | 405911 | 6758795 | Plus | 101008-101643 |
| | 405977 | 8247789 | Minus | 135548-136177 |

40 TABLE 27A: ABOUT 533 CNS-ENRICHED GENES SIGNIFICANTLY DOWN-REGULATED IN GLIOBLASTOMA COMPARED TO NORMAL ADULT CNS TISSUES

45 Table 27A lists about 533 CNS-enriched genes significantly down-regulated in glioblastoma compared to normal adult CNS tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal CNS to "average" glioblastoma was greater than or equal to 2. The "average" normal CNS level was set to the 75th percentile amongst various normal CNS tissues. The "average" glioblastoma level was set to the 85th percentile amongst various tumor samples. To enrich for CNS specific genes, the ratio of "average" CNS to "average" non-CNS normal adult tissues was calculated to be greater than or equal to 2. The "average" CNS level was set to the 85th percentile amongst various CNS tissues. The "average" normal non-CNS adult tissue level was set to the 85th percentile amongst various non-CNS normal tissues. In order to

45 remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratios were evaluated.

50 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of 75th percentile normal central nervous system tissue to 85th percentile tumor
 R2: Ratio of 85th percentile central nervous system tissue to 85th percentile normal body tissue

| | | | | | | |
|----|--------|-----------|-----------|--|------|------|
| 55 | Pkey | ExAccn | UnigenelD | Unigene Title | R1 | R2 |
| | 417275 | X63578 | Hs.295449 | parvalbumin | 29.0 | 30.0 |
| | 430829 | AW451999 | Hs.194024 | ESTs | 25.7 | 6.2 |
| | 410657 | AF063228 | Hs.65248 | dynein, cytoplasmic, intermediate polype | 22.6 | 25.8 |
| | 419954 | D14720 | Hs.93883 | myelin protein zero (Charcot-Marie-Tooth | 21.2 | 30.3 |
| 60 | 416133 | NM_001683 | Hs.89512 | ATPase, Ca ⁺⁺ transporting, plasma membra | 15.5 | 16.8 |
| | 416018 | AW138239 | Hs.78977 | proprotein convertase subtilisin/kexin 1 | 15.2 | 18.0 |
| | 417167 | AW206437 | Hs.4290 | ESTs | 14.8 | 17.7 |
| | 433940 | H05129 | Hs.7459 | cyclic AMP-regulated phosphoprotein, 21 | 13.4 | 18.1 |
| | 413324 | V00571 | Hs.75294 | corticotropin releasing hormone | 13.1 | 18.0 |
| 65 | 439830 | AA846666 | Hs.151489 | ESTs, Weakly similar to XE7_HUMAN PROTEI | 12.6 | 16.5 |
| | 408068 | AW148652 | Hs.167398 | ESTs | 12.6 | 16.9 |
| | 429096 | AB011106 | Hs.196012 | KIAA0534 protein | 12.2 | 21.1 |
| | 412638 | AA910199 | Hs.203838 | ESTs | 12.2 | 16.0 |
| | 442593 | R39804 | Hs.31961 | ESTs | 10.8 | 15.0 |
| 70 | 446353 | AI290919 | Hs.153661 | ESTs | 10.4 | 13.2 |
| | 426365 | AA376667 | Hs.10283 | RNA binding motif protein 8B | 10.0 | 5.9 |
| | 414937 | R38698 | Hs.12382 | ESTs | 10.0 | 10.8 |
| | 419643 | F06066 | Hs.91791 | chromosome 11 open reading frame 25 | 9.5 | 10.9 |
| | 412454 | R55745 | Hs.167330 | ESTs | 9.5 | 14.1 |
| 75 | 439366 | AF100143 | Hs.6540 | fibroblast growth factor 13 | 9.4 | 12.3 |
| | 441790 | AW294909 | Hs.132208 | ESTs | 9.2 | 3.2 |
| | 448117 | H49129 | Hs.172982 | ESTs | 9.1 | 12.8 |
| | 433558 | AA833757 | Hs.201769 | ESTs, Weakly similar to T24435 hypotheti | 9.0 | 14.7 |
| | 412453 | R20205 | Hs.167330 | ESTs | 9.0 | 13.7 |
| 80 | 408920 | AL120071 | Hs.48998 | fibronectin leucine rich transmembrane p | 8.9 | 17.3 |
| | 409031 | AA376836 | Hs.76728 | ESTs | 8.7 | 8.6 |
| | 446544 | AI631932 | Hs.7047 | ESTs, Weakly similar to Unknown [H.sapie | 8.2 | 20.0 |
| | 439480 | AL038511 | Hs.125316 | ESTs, Weakly similar to S33990 finger pr | 8.2 | 8.3 |
| | 410200 | AA082557 | Hs.101915 | Stargardt disease 3 (autosomal dominant) | 8.0 | 8.9 |

| | | | | | | |
|----|--------|-----------|-----------|--|-----|------|
| | 408428 | NM_014787 | Hs.44896 | DnaJ (Hsp40) homolog, subfamily B, membe | 7.9 | 9.6 |
| | 437073 | AI885608 | Hs.94122 | ESTs | 7.9 | 11.3 |
| | 408434 | AW195317 | Hs.107716 | hypothetical protein FLJ22344 | 7.9 | 16.4 |
| 5 | 440209 | H05049 | Hs.22269 | neurexin 3 | 7.8 | 34.3 |
| | 408119 | W26213 | Hs.101672 | ESTs, Weakly similar to T00331 hypothe | 7.8 | 9.0 |
| | 429611 | AI889077 | Hs.211388 | Homo sapiens BAC clone CTB-60N22 from 7q | 7.7 | 5.0 |
| | 423440 | R25234 | Hs.143434 | contactin 1 | 7.7 | 9.9 |
| | 445148 | AI214510 | Hs.146304 | ESTs | 7.6 | 9.1 |
| 10 | 416294 | D86980 | Hs.79170 | KIAA0227 protein | 7.6 | 7.6 |
| | 424087 | N69333 | Hs.143434 | contactin 1 | 7.6 | 10.3 |
| | 437479 | R61866 | Hs.101277 | ESTs | 7.5 | 9.3 |
| | 430573 | AA744550 | Hs.136345 | ESTs | 7.1 | 2.8 |
| | 448958 | AB020651 | Hs.22653 | KIAA0844 protein | 7.1 | 10.4 |
| 15 | 419474 | AW968619 | Hs.155849 | ESTs | 7.1 | 3.0 |
| | 423605 | AF047826 | Hs.129887 | cadherin 19, type 2 | 7.0 | 6.9 |
| | 433098 | AW190593 | Hs.151143 | ESTs | 7.0 | 9.2 |
| | 449511 | AI436187 | Hs.296261 | guanine nucleotide binding protein (G pr | 6.9 | 3.1 |
| | 428414 | AL049980 | Hs.184216 | DKFZP564C152 protein | 6.8 | 5.0 |
| 20 | 443155 | R54485 | Hs.23772 | ESTs | 6.8 | 3.5 |
| | 450561 | R49674 | Hs.25909 | ESTs | 6.8 | 8.1 |
| | 433068 | NM_006456 | Hs.288215 | sialyltransferase | 6.8 | 2.0 |
| | 423589 | AA328082 | Hs.209569 | ESTs | 6.6 | 10.5 |
| | 415681 | AI379882 | Hs.72630 | ESTs | 6.5 | 9.0 |
| 25 | 413510 | F13044 | | gb:HSC3HH101 normalized infant brain cDN | 6.4 | 7.1 |
| | 427992 | Y15014 | Hs.181353 | UDP-Gal4betaGlcNAc beta 1,3-galactosyltr | 6.4 | 9.5 |
| | 450642 | R39773 | Hs.7130 | copine IV | 6.4 | 5.7 |
| | 429322 | D86984 | Hs.199243 | KIAA0231 protein | 6.4 | 8.2 |
| | 447482 | AB033059 | Hs.18705 | KIAA1233 protein | 6.4 | 2.3 |
| 30 | 446129 | AW244073 | Hs.145946 | ESTs | 6.3 | 8.3 |
| | 421913 | AI934365 | Hs.109439 | osteoglycin (osteoinductive factor, mime | 6.3 | 2.1 |
| | 434273 | AA913143 | Hs.26303 | ESTs | 6.2 | 10.3 |
| | 408480 | AI350337 | Hs.164568 | fibroblast growth factor 7 (keratinocyte | 6.2 | 3.5 |
| | 451301 | AI769514 | Hs.209890 | EST | 6.2 | 12.4 |
| 35 | 438356 | AA805530 | Hs.48527 | ESTs | 6.2 | 8.1 |
| | 426388 | AW081394 | Hs.97103 | ESTs | 6.2 | 8.6 |
| | 452502 | AI904296 | | gb:PM-BT046-Z20199-286_1 BT046 Homo sapi | 6.1 | 2.8 |
| | 408165 | AL137573 | Hs.43143 | Homo sapiens mRNA; cDNA DKFZp564A2463 (f | 6.1 | 6.3 |
| | 442979 | AW440782 | Hs.174743 | ESTs | 6.1 | 6.3 |
| 40 | 408713 | NM_001248 | Hs.47042 | ectonucleoside triphosphate diphosphohyd | 6.0 | 3.8 |
| | 430004 | U27768 | Hs.227571 | regulator of G-protein signalling 4 | 5.9 | 21.4 |
| | 425087 | R62424 | Hs.126059 | ESTs | 5.9 | 8.1 |
| | 441695 | T12411 | Hs.183745 | hypothetical protein FLJ13456 | 5.9 | 3.1 |
| | 417175 | R44558 | Hs.94002 | ESTs | 5.8 | 12.5 |
| 45 | 437483 | AL390174 | | gb:Homo sapiens mRNA; cDNA DKFZp547J184 | 5.8 | 2.2 |
| | 436427 | AI344378 | Hs.143399 | ESTs | 5.8 | 13.8 |
| | 450382 | AA397658 | Hs.60257 | Homo sapiens cDNA FLJ13598 fis, clone PL | 5.7 | 4.4 |
| | 408478 | NM_000806 | Hs.45740 | gamma-aminobutyric acid (GABA) A recepto | 5.7 | 12.5 |
| | 442676 | AI733585 | Hs.130897 | ESTs | 5.7 | 6.8 |
| 50 | 446443 | AV659082 | Hs.134228 | ESTs | 5.7 | 6.4 |
| | 459080 | AW192083 | Hs.290855 | ESTs | 5.6 | 15.6 |
| | 431984 | AL080239 | Hs.272284 | Human DNA sequence from clone GS1-256022 | 5.6 | 8.2 |
| | 428356 | AL046991 | Hs.10338 | ESTs | 5.6 | 6.2 |
| | 417877 | AI025829 | Hs.86320 | ESTs | 5.4 | 4.9 |
| 55 | 429290 | AF203032 | Hs.198760 | neurofilament, heavy polypeptide (200kD) | 5.3 | 13.1 |
| | 408556 | U49516 | Hs.46362 | 5-hydroxytryptamine (serotonin) receptor | 5.3 | 6.6 |
| | 431930 | AB035301 | Hs.272211 | cadherin 7, type 2 | 5.2 | 6.0 |
| | 438285 | AA782845 | Hs.22790 | ESTs | 5.2 | 7.3 |
| | 439901 | N73885 | Hs.124169 | ESTs | 5.2 | 2.7 |
| 60 | 449222 | AW293984 | Hs.197621 | ESTs | 5.2 | 8.1 |
| | 408016 | AW136827 | Hs.256096 | ESTs | 5.1 | 2.5 |
| | 436853 | AW959074 | Hs.23648 | Homo sapiens cDNA FLJ13097 fis, clone NT | 5.1 | 3.0 |
| | 436773 | AW078629 | Hs.82110 | PC4 and SFRS1 interacting protein 1 | 5.1 | 7.3 |
| | 409263 | AA089573 | Hs.50319 | ESTs | 5.1 | 12.9 |
| 65 | 453830 | AA534296 | Hs.20953 | ESTs | 5.1 | 3.4 |
| | 441535 | AL135735 | Hs.7885 | phosphatidylinositol binding clathrin as | 5.0 | 4.8 |
| | 416490 | AF090116 | Hs.79348 | regulator of G-protein signalling 7 | 5.0 | 20.1 |
| | 417284 | N62889 | Hs.107242 | Homo sapiens cDNA FLJ12965 fis, clone NT | 5.0 | 3.9 |
| | 448505 | AL109678 | Hs.21597 | Homo sapiens mRNA full length insert cDN | 5.0 | 6.1 |
| 70 | 442240 | AI791883 | Hs.292719 | ESTs | 4.9 | 6.7 |
| | 427972 | AA864870 | Hs.181304 | putative gene product | 4.9 | 5.2 |
| | 416040 | AW819158 | Hs.289044 | Homo sapiens cDNA FLJ12048 fis, clone HE | 4.9 | 2.8 |
| | 444922 | AI921750 | Hs.144871 | Homo sapiens cDNA FLJ13752 fis, clone PL | 4.8 | 3.7 |
| | 408936 | AL138043 | Hs.293549 | ESTs | 4.8 | 6.6 |
| 75 | 414943 | D80647 | Hs.124193 | ESTs | 4.8 | 3.1 |
| | 429254 | H10133 | Hs.91846 | hypothetical protein DKFZp761C121 | 4.8 | 2.3 |
| | 407906 | AA369665 | Hs.41185 | Homo sapiens mRNA; cDNA DKFZp564O1262 (f | 4.8 | 9.1 |
| | 416577 | BE063207 | Hs.79381 | granulatin | 4.7 | 2.2 |
| | 420480 | AL137361 | Hs.98173 | hypothetical protein | 4.7 | 2.8 |
| 80 | 404793 | | | | 4.6 | 2.2 |
| | 430895 | U66581 | Hs.248121 | G protein-coupled receptor 22 | 4.6 | 7.4 |
| | 438571 | AW020775 | Hs.56022 | ESTs | 4.6 | 5.4 |
| | 444585 | AW170015 | Hs.6594 | ESTs | 4.6 | 6.0 |
| | 414272 | AI651603 | Hs.46988 | ESTs | 4.5 | 2.2 |

| | | | | | | |
|----|--------|-----------|-----------|--|-----|------|
| 5 | 414699 | AJ815523 | Hs.76930 | synuclein, alpha (non A4 component of am | 4.5 | 30.9 |
| | 423449 | A497900 | Hs.33087 | ESTs | 4.5 | 20.8 |
| | 433521 | T66087 | Hs.112482 | Homo sapiens unknown mRNA sequence | 4.4 | 2.0 |
| | 429876 | AB028977 | Hs.225974 | KIAA1054 protein | 4.4 | 19.2 |
| | 429726 | AW626326 | Hs.27151 | ESTs | 4.4 | 10.2 |
| 10 | 449093 | AB035356 | Hs.22998 | neurexin 1 | 4.4 | 9.4 |
| | 415716 | N59294 | Hs.179662 | nucleosome assembly protein 1-like 1 | 4.4 | 15.1 |
| | 419656 | AB002314 | Hs.92025 | KIAA0316 gene product | 4.4 | 8.2 |
| | 425864 | U56420 | Hs.159903 | olfactory receptor, family 5, subfamily | 4.4 | 2.4 |
| | 435078 | AW518888 | Hs.40937 | ESTs | 4.4 | 5.7 |
| 15 | 432712 | AB016247 | Hs.288031 | sterol-C5-desaturase (fungal ERG3, delta | 4.3 | 5.9 |
| | 426867 | AA460967 | Hs.22668 | ESTs | 4.3 | 6.0 |
| | 412112 | BE180342 | | gb:RC3-HT0622-130400-012-a07 HT0622 Homo | 4.3 | 3.2 |
| | 410171 | H07892 | Hs.12431 | ESTs | 4.3 | 5.3 |
| | 442339 | BE299668 | Hs.227591 | ESTs, Weakly similar to 1901303A Leu zip | 4.2 | 5.0 |
| 20 | 421249 | AA285362 | | gb:HTH277 HTC0L1 Homo sapiens cDNA 5'3' | 4.2 | 3.5 |
| | 422528 | AB011182 | Hs.118087 | KIAA0610 protein | 4.2 | 3.9 |
| | 434460 | AA478486 | Hs.3852 | KIAA0368 protein | 4.1 | 8.3 |
| | 410362 | H04811 | Hs.93164 | proprotein convertase subtilisin/kexin 1 | 4.1 | 7.0 |
| | 449754 | H00820 | Hs.30977 | ESTs, Weakly similar to B34087 hypotheti | 4.1 | 3.9 |
| 25 | 408496 | AJ683802 | Hs.136182 | ESTs | 4.1 | 4.7 |
| | 434101 | AA625205 | Hs.259599 | KIAA1622 protein | 4.1 | 6.3 |
| | 430212 | AA469153 | | gb:nc67104.s1 NC1_CGAP_Prl Homo sapiens | 4.0 | 2.5 |
| | 453165 | S74727 | Hs.32042 | aspartacylase (aminocyclase 2, Canavan | 4.0 | 7.4 |
| | 456407 | AW968614 | | gb:EST380690 MAGE resequences, MAGJ Homo | 4.0 | 5.1 |
| 30 | 441869 | NM_003947 | Hs.8004 | huntinglin-associated protein interactin | 4.0 | 32.3 |
| | 429628 | H09604 | Hs.13268 | ESTs | 4.0 | 4.5 |
| | 410087 | F12079 | Hs.332579 | ESTs | 4.0 | 6.9 |
| | 419910 | AA662913 | Hs.190173 | ESTs, Weakly similar to A46010 X-linked | 4.0 | 2.6 |
| | 441005 | Z41305 | Hs.303172 | Homo sapiens mRNA: cDNA DKFZp547G133 (fr | 3.9 | 21.7 |
| 35 | 412677 | AW029608 | Hs.17384 | ESTs | 3.9 | 2.2 |
| | 453341 | AJ758912 | Hs.296341 | adenylyl cyclase-associated protein 2 | 3.9 | 7.2 |
| | 416854 | H40164 | Hs.80296 | Purkinje cell protein 4 | 3.9 | 2.2 |
| | 414666 | NM_004466 | Hs.76828 | glypican 5 | 3.8 | 6.2 |
| | 418217 | AJ910647 | Hs.13442 | ESTs | 3.8 | 3.2 |
| 40 | 421855 | F06504 | Hs.27384 | ESTs, Moderately similar to ALU4_HUMAN A | 3.8 | 2.2 |
| | 414764 | AW013887 | Hs.72047 | ESTs | 3.8 | 10.7 |
| | 433629 | R13140 | Hs.13359 | ESTs | 3.7 | 2.7 |
| | 424738 | AJ963740 | Hs.46826 | ESTs | 3.7 | 2.1 |
| | 407706 | AA191085 | Hs.26612 | ESTs, Moderately similar to S23650 retro | 3.7 | 5.3 |
| 45 | 437268 | AJ754847 | Hs.227571 | regulator of G-protein signalling 4 | 3.7 | 53.7 |
| | 423135 | N67655 | Hs.26411 | ESTs | 3.7 | 21.7 |
| | 446818 | AJ342668 | Hs.279765 | ESTs | 3.7 | 2.6 |
| | 427562 | R56424 | Hs.26534 | ESTs | 3.6 | 3.6 |
| | 439274 | AF086092 | Hs.48372 | ESTs | 3.6 | 34.5 |
| 50 | 452381 | H23329 | Hs.290880 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.6 | 6.0 |
| | 422897 | AA679784 | Hs.4290 | ESTs | 3.6 | 5.1 |
| | 429656 | X05608 | Hs.211584 | neurofilament, light polypeptide (68kD) | 3.6 | 24.6 |
| | 417154 | AJ674701 | Hs.21388 | ESTs | 3.6 | 5.8 |
| | 447176 | Z42549 | Hs.160893 | ESTs | 3.6 | 6.4 |
| 55 | 405977 | | | | 3.6 | 3.9 |
| | 423568 | NM_005256 | Hs.129818 | growth arrest-specific 2 | 3.6 | 2.5 |
| | 441235 | AJ884586 | Hs.135570 | Homo sapiens cDNA: FLJ21268 lis, clone C | 3.6 | 5.4 |
| | 426775 | AA384564 | Hs.108829 | ESTs | 3.6 | 3.4 |
| | 414831 | M31158 | Hs.77439 | protein kinase, cAMP-dependent, regulato | 3.6 | 2.8 |
| 60 | 425153 | AW023193 | Hs.27046 | ESTs | 3.6 | 4.9 |
| | 446495 | D60923 | Hs.153460 | ESTs | 3.5 | 9.8 |
| | 445898 | AF070623 | Hs.13423 | Homo sapiens clone 24468 mRNA sequence | 3.5 | 16.6 |
| | 418421 | AA134006 | Hs.79306 | eukaryotic translation initiation factor | 3.5 | 5.0 |
| | 418207 | C14685 | Hs.34772 | ESTs | 3.5 | 16.0 |
| 65 | 425383 | D83407 | Hs.156007 | Down syndrome critical region gene 1-lik | 3.5 | 6.2 |
| | 417027 | AA192306 | Hs.23926 | triadin | 3.5 | 2.5 |
| | 408367 | AK001178 | Hs.44424 | homolog of rat orphan transporter v7-3 | 3.5 | 5.3 |
| | 408776 | AA057365 | Hs.63356 | ESTs, Weakly similar to I38022 hypotheti | 3.5 | 5.5 |
| | 453220 | AB033089 | Hs.32452 | Homo sapiens mRNA for KIAA1263 protein, | 3.5 | 23.6 |
| 70 | 419347 | C15944 | Hs.90005 | superiorcervical ganglia, neural specifi | 3.5 | 42.3 |
| | 433803 | AJ823593 | Hs.27688 | ESTs | 3.4 | 3.6 |
| | 450715 | AJ266484 | Hs.31570 | ESTs, Weakly similar to KIAA1324 protein | 3.4 | 4.1 |
| | 415076 | NM_000857 | Hs.77890 | guanylate cyclase 1, soluble, beta 3 | 3.4 | 9.8 |
| | 423826 | U20325 | Hs.1707 | cocaine- and amphetamine-regulated trans | 3.4 | 4.7 |
| 75 | 427173 | BE255017 | Hs.97540 | ESTs | 3.4 | 2.4 |
| | 446092 | N33522 | Hs.145894 | ESTs | 3.4 | 3.5 |
| | 416868 | AJ656856 | Hs.292597 | ESTs | 3.4 | 4.5 |
| | 458234 | BE551408 | Hs.127196 | ESTs | 3.4 | 4.5 |
| | 434053 | AW445136 | Hs.134946 | ESTs | 3.4 | 3.9 |
| 80 | 428536 | AJ143139 | Hs.2288 | visinin-like 1 | 3.3 | 42.3 |
| | 410366 | AJ267589 | Hs.302689 | hypothetical protein | 3.3 | 14.4 |
| | 425785 | T27017 | Hs.159528 | Homo sapiens clone 24400 mRNA sequence | 3.3 | 4.6 |
| | 434998 | AW975157 | Hs.26037 | ESTs | 3.3 | 4.7 |
| | 456359 | AJ967991 | Hs.93574 | homeo box D3 | 3.3 | 4.4 |
| | 426527 | NM_001037 | Hs.170238 | sodium channel, voltage-gated, type I, b | 3.3 | 5.2 |
| | 400302 | N48056 | Hs.1915 | folate hydrolase (prostate-specific memb | 3.3 | 9.0 |
| | 419875 | AA853410 | Hs.93557 | proenkephalin | 3.3 | 3.6 |

| | | | | | | |
|----|--------|-----------|-----------|---|-----|------|
| 5 | 444612 | AW138111 | Hs.22902 | ESTs | 3.3 | 3.0 |
| | 415242 | R45986 | Hs.295014 | ESTs | 3.2 | 2.2 |
| | 421640 | AW966652 | | gb:EST378726 MAGC resequences, MAGI Homo | 3.2 | 3.8 |
| | 408806 | AW847814 | Hs.289005 | Homo sapiens cDNA: FLJ21532 fs, clone C | 3.2 | 2.4 |
| | 446015 | T30968 | Hs.13531 | hypothetical protein FLJ10971 | 3.2 | 3.2 |
| 10 | 425495 | AA358454 | Hs.78026 | ESTs, Weakly similar to similar to ankyr | 3.2 | 2.2 |
| | 403092 | | | | 3.2 | 2.9 |
| | 452971 | AI873878 | Hs.91789 | ESTs | 3.2 | 4.5 |
| | 454100 | AI693231 | Hs.126043 | chromosome 21 open reading frame 51 | 3.2 | 2.7 |
| | 448440 | AA173467 | Hs.62402 | p21/Cdc42/Rac1-activated kinase 1 (yeast | 3.2 | 2.8 |
| 15 | 421200 | AA284811 | Hs.264433 | ESTs | 3.2 | 2.7 |
| | 440827 | AI733110 | Hs.128128 | ESTs | 3.2 | 2.1 |
| | 429809 | AL162010 | Hs.223603 | Homo sapiens mRNA; cDNA DKFZp761D09121 (| 3.2 | 4.3 |
| | 420156 | AW449258 | Hs.6187 | ESTs | 3.2 | 19.0 |
| | 457535 | AA609685 | Hs.278672 | membrane component, chromosome 11, surfa | 3.2 | 2.0 |
| 20 | 419956 | AL137939 | Hs.40096 | ESTs | 3.1 | 8.7 |
| | 423930 | AA332697 | Hs.42721 | ESTs | 3.1 | 2.7 |
| | 417868 | AI078534 | Hs.122592 | ESTs | 3.1 | 12.6 |
| | 423346 | AI267677 | Hs.127416 | synaptotagmin 1 | 3.1 | 12.0 |
| | 441921 | AI733376 | Hs.164478 | hypothetical protein FLJ21939 similar to | 3.1 | 4.3 |
| 25 | 429470 | AI878901 | Hs.203862 | guanine nucleotide binding protein (G pr | 3.1 | 5.3 |
| | 408217 | AI433201 | Hs.279860 | tumor protein, translationally-controlled | 3.1 | 7.1 |
| | 427322 | AK002017 | Hs.176227 | hypothetical protein FLJ11155 | 3.1 | 6.3 |
| | 449078 | AK001256 | Hs.22975 | KIAA1576 protein | 3.1 | 30.1 |
| | 429608 | U49250 | Hs.210662 | T-box, brain, 1 | 3.1 | 2.2 |
| 30 | 442308 | AA899402 | Hs.111 | fibroblast growth factor 9 (glia-activat | 3.1 | 3.0 |
| | 411666 | AF106564 | Hs.71346 | neurofilament 3 (150kD medium) | 3.1 | 10.9 |
| | 427865 | AA416931 | Hs.126065 | ESTs | 3.1 | 7.5 |
| | 430708 | U78308 | Hs.278485 | olfactory receptor, family 1, subfamily | 3.1 | 3.4 |
| | 451829 | AW964081 | Hs.247377 | ESTs | 3.0 | 6.2 |
| 35 | 405911 | | | | 3.0 | 2.4 |
| | 418808 | AI821836 | Hs.10359 | ESTs | 3.0 | 6.2 |
| | 452893 | H18017 | Hs.22869 | ESTs, Moderately similar to KIAA1395 pro | 3.0 | 5.1 |
| | 423952 | AW877787 | Hs.136102 | KIAA0853 protein | 3.0 | 2.1 |
| | 412000 | AW576555 | Hs.15780 | ATP-binding cassette, sub-family A (ABC1 | 3.0 | 2.1 |
| 40 | 405793 | | | | 3.0 | 2.7 |
| | 410711 | AB002316 | Hs.65746 | KIAA0318 protein | 3.0 | 14.3 |
| | 427071 | AA397958 | Hs.192719 | ESTs | 3.0 | 2.1 |
| | 453534 | NM_014796 | Hs.33187 | KIAA0748 gene product | 3.0 | 14.5 |
| | 413903 | AA496493 | Hs.23136 | ESTs | 3.0 | 2.2 |
| 45 | 426866 | U02330 | Hs.172816 | neuregulin 1 | 3.0 | 11.3 |
| | 434945 | AB033065 | Hs.4280 | KIAA1239 protein | 3.0 | 3.5 |
| | 412639 | AW961284 | Hs.296235 | ESTs | 2.9 | 4.9 |
| | 453590 | AF150278 | Hs.33578 | KIAA0820 protein | 2.9 | 33.1 |
| | 414502 | AL133721 | Hs.224680 | ESTs | 2.9 | 2.3 |
| 50 | 434367 | AB020700 | Hs.3830 | KIAA0893 protein | 2.9 | 23.1 |
| | 425121 | AI797511 | Hs.154679 | synaptotagmin 1 | 2.9 | 8.1 |
| | 412494 | AL133900 | Hs.792 | ADP-ribosylation factor domain protein 1 | 2.9 | 20.8 |
| | 401213 | | | | 2.9 | 3.2 |
| | 401028 | AW673312 | Hs.50848 | hypothetical protein FLJ20331 | 2.9 | 3.4 |
| 55 | 415191 | AA190381 | Hs.120810 | ESTs | 2.9 | 3.0 |
| | 449275 | AW450848 | Hs.205457 | perlecan | 2.9 | 5.6 |
| | 419863 | AW952691 | Hs.93485 | Homo sapiens mRNA; cDNA DKFZp761D191 (fr | 2.9 | 35.0 |
| | 411421 | BE272110 | Hs.21177 | ESTs | 2.9 | 2.0 |
| | 430865 | AI073424 | Hs.5232 | HSPC125 protein | 2.9 | 11.4 |
| 60 | 437486 | AW952089 | Hs.5636 | RAB6A, member RAS oncogene family | 2.9 | 2.2 |
| | 442357 | AI458586 | Hs.135706 | ESTs | 2.9 | 6.0 |
| | 408274 | R17315 | | gb:yg12g11.1 Soares infant brain 1N1B H | 2.9 | 2.2 |
| | 444185 | AW298350 | Hs.66020 | ESTs | 2.8 | 5.0 |
| | 420173 | AA256151 | Hs.22999 | ESTs | 2.8 | 5.1 |
| 65 | 428358 | AA993222 | Hs.101915 | Stargardt disease 3 (autosomal dominant) | 2.8 | 7.0 |
| | 447252 | R90916 | Hs.12449 | Homo sapiens transmembrane protein HTMP1 | 2.8 | 4.4 |
| | 440260 | AI972867 | Hs.7130 | copine IV | 2.8 | 10.6 |
| | 417084 | H08370 | Hs.33067 | ESTs | 2.8 | 8.4 |
| | 438257 | AW474419 | Hs.224794 | ESTs | 2.8 | 2.8 |
| 70 | 441934 | T23939 | Hs.7344 | ESTs | 2.8 | 6.2 |
| | 447885 | F11528 | Hs.303172 | Homo sapiens mRNA; cDNA DKFZp547G133 (fr | 2.8 | 3.5 |
| | 423552 | AF107028 | Hs.129783 | sodium channel, voltage-gated, type II, | 2.8 | 3.4 |
| | 450940 | AI744943 | Hs.143209 | ESTs, Weakly similar to I38022 hypotheti | 2.8 | 14.4 |
| | 410011 | AB020641 | Hs.57856 | PFTAIRE protein kinase 1 | 2.8 | 21.7 |
| 75 | 445887 | AI263105 | Hs.145597 | ESTs | 2.8 | 5.1 |
| | 425494 | N55540 | Hs.78026 | ESTs, Weakly similar to similar to ankyr | 2.8 | 2.4 |
| | 438202 | AW169287 | Hs.22588 | ESTs | 2.8 | 11.9 |
| | 436199 | R38946 | Hs.127951 | hypothetical protein FLJ14503 | 2.8 | 6.0 |
| | 434826 | AF155661 | Hs.22265 | pyruvate dehydrogenase phosphatase | 2.8 | 2.4 |
| 80 | 415462 | R52692 | Hs.12698 | ESTs | 2.8 | 3.4 |
| | 418070 | NM_000844 | Hs.83407 | glutamate receptor, metabotropic 7 | 2.8 | 4.5 |
| | 432149 | AW614326 | Hs.157022 | ESTs, Weakly similar to T34549 probable | 2.8 | 9.5 |
| | 430371 | D87466 | Hs.240112 | KIAA0276 protein | 2.8 | 7.0 |
| | 437357 | AL359559 | Hs.331666 | Homo sapiens mRNA; cDNA DKFZp76202215 (f | 2.7 | 2.5 |
| | 415838 | R44336 | Hs.7093 | ESTs | 2.7 | 3.6 |
| | 438675 | AA813725 | Hs.213568 | ESTs | 2.7 | 2.5 |
| | 419558 | AW953679 | | gb:EST365749 MAGC resequences, MAGC Homo | 2.7 | 3.1 |

| | | | | | | |
|----|--------|-----------|-----------|--|-----|------|
| | 446318 | AI949389 | Hs.18067 | ESTs | 2.7 | 4.1 |
| | 445183 | AB007877 | Hs.12385 | KIAA0417 gene product | 2.7 | 5.3 |
| | 457012 | R41480 | Hs.127630 | ESTs | 2.7 | 19.0 |
| 5 | 431988 | AC002302 | Hs.77202 | protein kinase C, beta 1 | 2.7 | 7.2 |
| | 430223 | NM_002514 | Hs.235935 | nephroblastoma overexpressed gene | 2.7 | 2.8 |
| | 447932 | AA837474 | Hs.20021 | vesicle-associated membrane protein 1 (s | 2.7 | 3.8 |
| | 450214 | BE439763 | Hs.227571 | regulator of G-protein signalling 4 | 2.7 | 6.9 |
| | 434731 | AA648049 | Hs.121518 | ESTs | 2.7 | 5.0 |
| 10 | 428839 | AI767756 | Hs.82302 | Homo sapiens cDNA FLJ14814 fis, clone NT | 2.7 | 5.2 |
| | 407709 | AA456135 | Hs.23023 | ESTs | 2.7 | 2.5 |
| | 422420 | U03398 | Hs.1524 | tumor necrosis factor (ligand) superfam | 2.7 | 3.3 |
| | 443305 | AI050693 | Hs.133318 | ESTs | 2.7 | 5.9 |
| | 435648 | H24347 | Hs.27524 | ESTs | 2.7 | 15.0 |
| 15 | 418407 | AL044818 | Hs.84928 | nuclear transcription factor Y, beta | 2.7 | 2.7 |
| | 436771 | AW975687 | Hs.292979 | ESTs | 2.7 | 6.0 |
| | 428689 | NM_014351 | Hs.189810 | sulfotransferase family 4A, member 1 | 2.7 | 4.8 |
| | 440503 | NM_006539 | Hs.7235 | calcium channel, voltage-dependent, gamm | 2.7 | 4.4 |
| | 441006 | AW605267 | Hs.7627 | CGI-60 protein | 2.7 | 3.1 |
| 20 | 410330 | AW023630 | Hs.46786 | ESTs | 2.6 | 29.5 |
| | 434398 | AA121098 | Hs.3838 | serum-inducible kinase | 2.6 | 2.6 |
| | 438831 | BE263273 | Hs.6439 | synapsin II | 2.6 | 7.8 |
| | 419066 | Z98492 | Hs.6975 | PRO1073 protein | 2.6 | 3.4 |
| | 412643 | AW971239 | Hs.293982 | ESTs | 2.6 | 2.2 |
| 25 | 430456 | AA314998 | Hs.241503 | hypothetical protein | 2.6 | 17.9 |
| | 416498 | U33632 | Hs.79351 | potassium channel, subfamily K, member 1 | 2.6 | 2.9 |
| | 401421 | | | | 2.6 | 2.0 |
| | 419530 | X98330 | Hs.90821 | ryanodine receptor 2 (cardiac) | 2.6 | 4.2 |
| | 441817 | AW969706 | Hs.293332 | ESTs | 2.6 | 3.8 |
| 30 | 439203 | AA448930 | Hs.8453 | KIAA1587 protein | 2.6 | 4.2 |
| | 426054 | U12431 | Hs.166109 | ELAV (embryonic lethal, abnormal vision, | 2.6 | 5.1 |
| | 444583 | AW994403 | Hs.100851 | hypothetical protein FLJ14500 | 2.6 | 3.7 |
| | 417919 | AI928203 | Hs.86379 | ESTs | 2.6 | 3.0 |
| | 434293 | NM_004445 | Hs.3796 | EphB6 | 2.6 | 3.2 |
| 35 | 431716 | D89053 | Hs.268012 | fatty-acid-Coenzyme A ligase, long-chain | 2.6 | 6.4 |
| | 443037 | AW500305 | Hs.299166 | syntaxin 7 | 2.6 | 2.2 |
| | 440736 | D56919 | Hs.265848 | myomegalin | 2.6 | 7.1 |
| | 404648 | | | | 2.6 | 3.0 |
| | 429995 | AA463571 | | gb:zx72e09.r1 Soares_total_fetus_Nb2HF8_ | 2.6 | 3.5 |
| 40 | 436508 | AW604381 | Hs.121121 | ESTs, Weakly similar to S00755 pleckstri | 2.6 | 3.9 |
| | 441190 | H09073 | Hs.25046 | ESTs | 2.6 | 3.1 |
| | 432278 | AL137506 | Hs.274256 | hypothetical protein FLJ23563 | 2.6 | 2.9 |
| | 442731 | AI868167 | Hs.131044 | ESTs | 2.6 | 4.1 |
| | 416836 | D54745 | Hs.80247 | cholecystokinin | 2.6 | 14.9 |
| 45 | 449071 | NM_005872 | Hs.22960 | breast carcinoma amplified sequence 2 | 2.5 | 2.4 |
| | 436321 | AA709133 | Hs.180144 | ESTs | 2.5 | 2.8 |
| | 439693 | AI741816 | Hs.125897 | ESTs | 2.5 | 3.6 |
| | 443212 | AW269515 | Hs.102500 | hypothetical protein FLJ20481 | 2.5 | 2.8 |
| | 423981 | AL122104 | Hs.136664 | Homo sapiens mRNA; cDNA DKFZp434A1627 (f | 2.5 | 3.8 |
| 50 | 407868 | NM_000950 | Hs.40637 | proline-rich Gla (G-carboxyglutamic acid | 2.5 | 3.1 |
| | 443992 | AW022228 | Hs.322922 | ESTs | 2.5 | 27.9 |
| | 444124 | R43097 | Hs.6818 | ESTs | 2.5 | 5.3 |
| | 411379 | AI816344 | Hs.12554 | ESTs, Weakly similar to NPL4_HUMAN NUCLE | 2.5 | 38.0 |
| | 440474 | AI207936 | Hs.7195 | gamma-aminobutyric acid (GABA) A recepto | 2.5 | 3.8 |
| 55 | 446277 | AI284218 | Hs.159204 | ESTs | 2.5 | 2.2 |
| | 410111 | AI620206 | Hs.189647 | ESTs | 2.5 | 3.5 |
| | 445162 | AB011131 | Hs.12376 | piccolo (presynaptic cytomatrix protein) | 2.5 | 4.8 |
| | 410718 | AI920783 | Hs.191435 | ESTs | 2.5 | 4.5 |
| | 417201 | T60432 | Hs.269084 | ESTs, Moderately similar to AF097994 1 L | 2.5 | 2.9 |
| 60 | 426274 | AW968000 | Hs.143389 | ESTs, Weakly similar to T14318 ubiquitin | 2.5 | 2.8 |
| | 433496 | AF064254 | Hs.49765 | VLCS-H1 protein | 2.5 | 4.7 |
| | 437331 | AL353933 | Hs.21710 | hypothetical protein DKFZp761G0313 | 2.5 | 3.3 |
| | 437368 | AI471969 | Hs.182606 | ESTs | 2.5 | 3.0 |
| | 441985 | BE047625 | Hs.169815 | ESTs | 2.5 | 3.6 |
| 65 | 410025 | BE220489 | Hs.113592 | ESTs, Moderately similar to I54374 gene | 2.5 | 9.2 |
| | 414680 | AA743331 | Hs.272572 | hemoglobin, alpha 2 | 2.5 | 3.6 |
| | 429956 | AI374651 | Hs.22542 | ESTs | 2.5 | 23.9 |
| | 429028 | AA443439 | Hs.48797 | ESTs | 2.5 | 2.8 |
| | 438109 | AI076621 | Hs.71367 | ESTs, Moderately similar to ALU7_HUMAN A | 2.5 | 3.1 |
| 70 | 439780 | AL109688 | | gb:Homo sapiens mRNA full length insert | 2.5 | 2.3 |
| | 440888 | N45600 | Hs.326880 | ESTs | 2.5 | 3.9 |
| | 445246 | AI217713 | Hs.147586 | ESTs | 2.5 | 2.6 |
| | 440152 | AB002376 | Hs.7006 | KIAA0378 protein | 2.4 | 23.6 |
| | 432740 | AF061034 | Hs.278898 | tumor necrosis factor alpha-inducible ce | 2.4 | 2.1 |
| 75 | 415122 | D60708 | Hs.22245 | ESTs | 2.4 | 3.9 |
| | 432298 | AL118812 | Hs.274293 | Homo sapiens mRNA; cDNA DKFZp761G1111 (f | 2.4 | 9.8 |
| | 437948 | AA772920 | Hs.303527 | ESTs | 2.4 | 9.8 |
| | 421360 | AA297012 | Hs.103839 | erythrocyte membrane protein band 4.1-6 | 2.4 | 2.8 |
| | 427115 | AW972853 | Hs.112237 | ESTs | 2.4 | 2.2 |
| 80 | 452074 | BE299035 | Hs.27747 | G protein-coupled receptor 37 (endotheli | 2.4 | 10.0 |
| | 436639 | D14838 | Hs.111 | fibroblast growth factor 9 (glia-activat | 2.4 | 3.5 |
| | 434520 | AA205273 | Hs.177011 | hypothetical protein | 2.4 | 3.1 |
| | 411529 | AA430348 | Hs.317596 | Homo sapiens cDNA FLJ12927 fis, clone NT | 2.4 | 3.0 |
| | 442272 | AA988302 | Hs.129172 | ESTs | 2.4 | 2.1 |

| | | | | | | |
|----|--------|-----------|-----------|--|-----|------|
| | 422927 | AW247388 | Hs.301423 | calcium binding protein 1 (calbrain) | 2.4 | 2.7 |
| | 444547 | H14718 | Hs.11506 | Human clone Z3589 mRNA sequence | 2.4 | 2.8 |
| | 415827 | H17462 | Hs.23079 | ESTs | 2.4 | 15.0 |
| 5 | 451397 | AA017432 | Hs.84529 | ESTs, Weakly similar to Z202_HUMAN ZINC | 2.4 | 3.9 |
| | 445200 | AA084460 | Hs.12409 | somatostatin | 2.4 | 3.7 |
| | 451062 | AL110125 | Hs.25910 | Homo sapiens mRNA: cDNA DKFZp564C1416 (f | 2.4 | 2.4 |
| | 420328 | Y19062 | Hs.96870 | staufen (Drosophila, RNA-binding protein | 2.4 | 4.3 |
| | 432122 | AA526514 | | gb:nif0f02.s1 NCI_CGAP_Ov2 Homo sapiens | 2.4 | 4.3 |
| 10 | 444125 | AI124882 | Hs.118121 | ESTs | 2.4 | 3.5 |
| | 430538 | AB032435 | Hs.242821 | differentiation-associated Na-dependent | 2.4 | 10.8 |
| | 457519 | X69438 | Hs.3052 | early growth response 4 | 2.4 | 2.4 |
| | 409371 | R51736 | Hs.12381 | ESTs | 2.4 | 2.1 |
| | 456303 | AA224872 | Hs.115088 | ESTs | 2.4 | 3.2 |
| 15 | 440105 | AA694010 | Hs.6932 | Homo sapiens clone 23809 mRNA sequence | 2.4 | 23.4 |
| | 400979 | | | | 2.4 | 4.1 |
| | 435296 | R49685 | Hs.24980 | ESTs | 2.4 | 6.5 |
| | 408950 | AA707814 | Hs.14945 | long fatty acyl-CoA synthetase 2 gene | 2.4 | 18.5 |
| | 452032 | BE244005 | Hs.27610 | retinoic acid- and interferon-inducible | 2.4 | 2.2 |
| 20 | 432098 | AF252297 | Hs.91546 | cytochrome P450 retinoid metabolizing pr | 2.4 | 2.7 |
| | 408974 | AW015458 | Hs.297017 | ESTs | 2.4 | 2.5 |
| | 412177 | Z23091 | Hs.73734 | glycoprotein V (platelet) | 2.4 | 2.8 |
| | 413153 | N94205 | | gb:za27a08.r1 Soares fetal liver spleen | 2.4 | 2.5 |
| | 417583 | AA668782 | Hs.191284 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.4 | 2.6 |
| 25 | 452034 | F12234 | Hs.75893 | ankyrin 3, node of Ranvier (ankyrin G) | 2.3 | 3.0 |
| | 424940 | AA985308 | Hs.194327 | ESTs | 2.3 | 6.3 |
| | 431706 | AI816086 | Hs.296341 | adenylyl cyclase-associated protein 2 | 2.3 | 4.1 |
| | 419125 | AA642452 | Hs.130881 | B-cell CLL/lymphoma 11A (zinc finger pro | 2.3 | 2.9 |
| | 423641 | AL137256 | Hs.130489 | ATPase, aminophospholipid transporter-li | 2.3 | 8.7 |
| 30 | 436407 | T88803 | Hs.271507 | ESTs, Weakly similar to TIM_HUMAN PROBAB | 2.3 | 3.2 |
| | 448681 | AL109781 | Hs.21754 | Homo sapiens mRNA full length insert cDN | 2.3 | 5.2 |
| | 415669 | NM_005025 | Hs.78589 | serine (or cysteine) proteinase inhibito | 2.3 | 54.7 |
| | 410765 | AI694972 | Hs.66180 | nucleosome assembly protein 1-like 2 | 2.3 | 9.1 |
| | 422386 | AF105374 | Hs.115830 | heparan sulfate (glucosamine) 3-O-sulfot | 2.3 | 5.0 |
| 35 | 414828 | AA156651 | | gb:z105h05.r1 Soares_pregnant_uterus_NbH | 2.3 | 2.4 |
| | 445556 | AI910241 | Hs.12887 | actin-related protein 3-beta | 2.3 | 8.5 |
| | 426968 | U07616 | Hs.173034 | amphiphysin (Süß-Mann syndrome with br | 2.3 | 26.3 |
| | 444562 | AA186715 | Hs.336429 | RIKEN cDNA 9130422N19 gene | 2.3 | 2.5 |
| | 423420 | AI571364 | Hs.128382 | Homo sapiens mRNA: cDNA DKFZp7111224 (f | 2.3 | 7.6 |
| 40 | 439450 | R51613 | Hs.125304 | ESTs | 2.3 | 26.3 |
| | 427127 | AW802282 | Hs.22265 | pyruvate dehydrogenase phosphatase | 2.3 | 2.2 |
| | 447179 | AW015633 | Hs.157299 | ESTs | 2.3 | 3.8 |
| | 414711 | AI310440 | Hs.288735 | Homo sapiens cDNA FLJ13522 fis, clone PL | 2.3 | 2.3 |
| | 433449 | AW772282 | | gb:hn71b05.x1 NCI_CGAP_Kd11 Homo sapien | 2.3 | 3.8 |
| 45 | 414320 | U13616 | Hs.75893 | ankyrin 3, node of Ranvier (ankyrin G) | 2.3 | 2.5 |
| | 416778 | M16505 | Hs.79876 | steroid sulfatase (microsomal), arylsulf | 2.3 | 7.8 |
| | 425130 | AA448208 | Hs.99163 | ESTs | 2.3 | 4.1 |
| | 456664 | AW963354 | Hs.334409 | metallothionein 1G | 2.3 | 2.5 |
| | 438283 | AI458931 | Hs.37282 | ESTs | 2.3 | 4.2 |
| 50 | 417455 | AW007066 | Hs.18949 | ESTs, Weakly similar to CA2B_HUMAN COLLA | 2.3 | 3.0 |
| | 412100 | AW892731 | | gb:CM0-NN0005-100300-279-c02 NN0005 Homo | 2.3 | 3.7 |
| | 448981 | AI968719 | Hs.195387 | ESTs | 2.3 | 3.2 |
| | 416101 | R24854 | Hs.268806 | ESTs | 2.3 | 6.5 |
| | 439731 | AI953135 | Hs.45140 | hypothetical protein FLJ14084 | 2.3 | 17.8 |
| 55 | 415734 | NM_014747 | Hs.78748 | KIAA0237 gene product | 2.3 | 40.1 |
| | 424596 | AB020639 | Hs.151017 | estrogen-related receptor gamma | 2.3 | 2.9 |
| | 420230 | AL034344 | Hs.284186 | forkhead box C1 | 2.3 | 2.4 |
| | 451559 | AL119980 | Hs.20935 | hypothetical protein DKFZp761D221 | 2.3 | 5.7 |
| | 404835 | | | | 2.3 | 2.1 |
| 60 | 456755 | AI497900 | Hs.33067 | ESTs | 2.3 | 4.1 |
| | 455517 | AW984068 | | gb:RCO-HN0006-160300-011-e06 HN0006 Homo | 2.3 | 2.4 |
| | 408206 | AF041853 | Hs.43670 | kinesin family member 3A | 2.2 | 18.5 |
| | 411770 | NM_014278 | Hs.71992 | heat shock protein (hsp110 family) | 2.2 | 3.9 |
| | 430105 | X70297 | Hs.2540 | cholinergic receptor, nicotinic, alpha p | 2.2 | 2.6 |
| 65 | 458694 | F12832 | Hs.13298 | ESTs | 2.2 | 4.9 |
| | 415091 | AL044872 | Hs.77910 | 3-hydroxy-3-methylglutaryl-Coenzyme A sy | 2.2 | 4.4 |
| | 439642 | W81441 | Hs.153967 | ESTs | 2.2 | 2.4 |
| | 450138 | AW152104 | Hs.200879 | ESTs | 2.2 | 4.9 |
| | 454222 | BE144344 | Hs.7589 | ESTs, Weakly similar to A45010 X-linked | 2.2 | 3.7 |
| 70 | 405326 | | | | 2.2 | 2.7 |
| | 431342 | AW971018 | Hs.21659 | ESTs | 2.2 | 5.2 |
| | 453101 | AW952776 | Hs.94943 | ESTs | 2.2 | 3.3 |
| | 408897 | N50204 | Hs.283709 | lipopolysaccharide specific response-7 p | 2.2 | 2.8 |
| | 451398 | AI793124 | Hs.144479 | ESTs | 2.2 | 4.6 |
| 75 | 438208 | AL041224 | Hs.65379 | ESTs | 2.2 | 10.4 |
| | 408449 | NM_004408 | Hs.166161 | dynamitin 1 | 2.2 | 6.1 |
| | 414130 | AI570831 | Hs.71592 | Homo sapiens cDNA: FLJ21893 fis, clone H | 2.2 | 3.1 |
| | 445016 | U79716 | Hs.12246 | refin | 2.2 | 3.9 |
| | 424375 | AF070547 | Hs.146312 | Homo sapiens clone 24820 mRNA sequence | 2.2 | 2.3 |
| 80 | 424645 | NM_014682 | Hs.151449 | KIAA0535 gene product | 2.2 | 11.7 |
| | 409729 | D51315 | Hs.106289 | ESTs | 2.2 | 4.9 |
| | 432809 | AA565509 | Hs.131703 | ESTs | 2.2 | 19.9 |
| | 422890 | Z43784 | Hs.75893 | ankyrin 3, node of Ranvier (ankyrin G) | 2.2 | 10.4 |
| | 428532 | AF157326 | Hs.184786 | TBP-interacting protein | 2.2 | 6.5 |

| | | | | | | |
|----|--------|-----------|-----------|--|-----|------|
| 5 | 413074 | AJ871368 | Hs.8417 | hypothetical protein DKFZp761M0423 | 2.2 | 3.4 |
| | 414442 | AA156238 | Hs.32501 | ESTs | 2.2 | 3.2 |
| | 452768 | AW069459 | Hs.61539 | ESTs | 2.2 | 2.0 |
| | 450440 | AB024334 | Hs.25001 | tyrosine 3-monooxygenase/tryptophan 5-mo | 2.2 | 3.2 |
| | 426281 | AK000987 | Hs.169111 | oxidation resistance 1 | 2.2 | 2.3 |
| 10 | 428411 | AW291464 | Hs.10338 | ESTs | 2.2 | 2.3 |
| | 413787 | AJ352558 | Hs.75544 | tyrosine 3-monooxygenase/tryptophan 5-mo | 2.2 | 3.1 |
| | 451734 | NM_006176 | Hs.26944 | neurogranin (protein kinase C substrate, | 2.2 | 8.5 |
| | 439108 | AW163034 | Hs.6467 | synaptogyrin 3 | 2.2 | 7.9 |
| | 405385 | | | | 2.2 | 2.4 |
| 15 | 447285 | AJ371849 | Hs.200696 | ATPase, Class VI, type 11C | 2.2 | 2.2 |
| | 452667 | T87219 | Hs.13219 | ESTs | 2.2 | 3.1 |
| | 422234 | AF119818 | Hs.113287 | discs, large (Drosophila) homolog-associ | 2.1 | 8.3 |
| | 410339 | AJ916499 | Hs.298258 | ESTs | 2.1 | 3.2 |
| | 413231 | D87461 | Hs.75244 | BCL2-like 2 | 2.1 | 4.5 |
| 20 | 447104 | R19085 | Hs.210706 | Homo sapiens cDNA FLJ13182 fis, clone NT | 2.1 | 2.2 |
| | 451952 | AL120173 | Hs.301663 | ESTs | 2.1 | 36.5 |
| | 415841 | Z45637 | Hs.7093 | ESTs | 2.1 | 2.4 |
| | 441086 | AJ928489 | Hs.213490 | ESTs, Weakly similar to N33_HUMAN N33 PR | 2.1 | 2.2 |
| | 450407 | NM_000810 | Hs.24969 | gamma-aminobutyric acid (GABA) A recepto | 2.1 | 6.6 |
| 25 | 427627 | R87582 | Hs.179915 | guanine nucleotide binding protein (G pr | 2.1 | 5.3 |
| | 449712 | R56545 | Hs.6100 | ESTs | 2.1 | 4.5 |
| | 409660 | AW452065 | Hs.258905 | ESTs | 2.1 | 2.1 |
| | 430434 | AL049548 | Hs.241420 | Homo sapiens mRNA for KIAA1756 protein, | 2.1 | 5.4 |
| | 434138 | AA625804 | | gb:zu88h01.s1 Soares_testis_NHT Homo sap | 2.1 | 3.0 |
| 30 | 448610 | NM_006157 | Hs.21602 | nel (chicken)-like 1 | 2.1 | 4.8 |
| | 418948 | AJ217097 | | gb:qd43h07.x1 Soares_fetal_heart_NbHH19W | 2.1 | 2.9 |
| | 414876 | AW950925 | Hs.924 | crystallin, mu | 2.1 | 3.4 |
| | 440426 | AJ159800 | Hs.7181 | Homo sapiens cDNA FLJ13663 fis, clone PL | 2.1 | 3.7 |
| | 451249 | AA016227 | Hs.27280 | ESTs | 2.1 | 4.1 |
| 35 | 451475 | T19093 | Hs.26450 | KIAA0725 protein | 2.1 | 2.1 |
| | 448743 | AB032962 | Hs.21896 | KIAA1136 protein | 2.1 | 29.7 |
| | 430814 | U89336 | Hs.247993 | NGS protein | 2.1 | 2.7 |
| | 426990 | AL044315 | Hs.173094 | Homo sapiens mRNA for KIAA1750 protein, | 2.1 | 2.3 |
| | 426642 | AW068223 | Hs.171581 | ubiquitin C-terminal hydrolase UCH37 | 2.1 | 4.5 |
| 40 | 427335 | AA448542 | Hs.251677 | G antigen 7B | 2.1 | 2.2 |
| | 459089 | F13036 | Hs.27373 | Homo sapiens mRNA; cDNA DKFZp564O1763 (f | 2.1 | 2.3 |
| | 435832 | AA425688 | Hs.41641 | Bruno (Drosophila)-like 4, RNA binding | 2.1 | 5.9 |
| | 446383 | T05816 | Hs.92511 | ESTs | 2.1 | 2.9 |
| | 412768 | AW996044 | Hs.26239 | Human DNA sequence from clone RP11-43882 | 2.1 | 2.1 |
| 45 | 453976 | BE463830 | Hs.163714 | ESTs | 2.1 | 4.2 |
| | 415111 | R39039 | Hs.328455 | EST | 2.1 | 3.3 |
| | 452238 | F01811 | Hs.187931 | ESTs | 2.1 | 4.9 |
| | 445279 | R41900 | Hs.22245 | ESTs | 2.1 | 9.8 |
| | 448799 | AJ937094 | Hs.179080 | ESTs | 2.1 | 3.1 |
| 50 | 418338 | NM_002522 | Hs.84154 | neuronal pentraxin I | 2.1 | 8.3 |
| | 445725 | AK000956 | Hs.13209 | hypothetical protein FLJ10094 | 2.1 | 5.4 |
| | 443537 | D13305 | Hs.203 | cholecystokinin B receptor | 2.1 | 4.1 |
| | 454066 | X00356 | Hs.37058 | calcitonin/calcitonin-related polypeptid | 2.1 | 6.4 |
| | 429954 | AJ918130 | Hs.21374 | ESTs | 2.1 | 7.2 |
| 55 | 415292 | H29016 | Hs.200576 | ESTs | 2.1 | 3.9 |
| | 423563 | R34734 | Hs.75209 | protein kinase (cAMP-dependent, catalyti | 2.1 | 3.1 |
| | 424906 | AI566086 | Hs.153716 | Homo sapiens mRNA for Hmob33 protein, 3' | 2.1 | 4.7 |
| | 459309 | AA040620 | Hs.5672 | hypothetical protein AF140225 | 2.1 | 2.2 |
| | 439340 | AB032436 | Hs.6535 | brain-specific Na-dependent inorganic ph | 2.1 | 4.7 |
| 60 | 402598 | BE314624 | Hs.3128 | polymerase (RNA) II (DNA directed) polyp | 2.1 | 5.4 |
| | 435406 | F26698 | Hs.4884 | calcium/calmodulin-dependent protein kin | 2.1 | 6.6 |
| | 448792 | R42550 | Hs.12826 | ESTs | 2.1 | 4.1 |
| | 449500 | AW956345 | Hs.12926 | ESTs | 2.1 | 2.4 |
| | 441134 | W29092 | Hs.7678 | cellular retinoic acid-binding protein 1 | 2.1 | 5.8 |
| 65 | 433361 | AW469373 | Hs.300141 | ribosomal protein L39 | 2.1 | 2.7 |
| | 452946 | X95425 | Hs.31092 | EphA5 | 2.1 | 5.0 |
| | 426167 | AF039023 | Hs.167496 | RAN binding protein 6 | 2.0 | 2.2 |
| | 453666 | AW015681 | Hs.135229 | ESTs, Weakly similar to A2BP_HUMAN ATAX1 | 2.0 | 3.1 |
| | 424632 | AB014523 | Hs.151406 | KIAA0623 gene product | 2.0 | 3.5 |
| 70 | 448589 | AF017090 | Hs.21554 | KIAA1107 protein | 2.0 | 4.1 |
| | 430416 | AC005531 | Hs.57806 | Homo sapiens PAC clone RP4-701016 from 7 | 2.0 | 2.3 |
| | 445627 | AW818475 | Hs.7363 | ESTs | 2.0 | 2.1 |
| | 417092 | H97508 | Hs.181165 | eukaryotic translation elongation factor | 2.0 | 2.5 |
| | 453653 | AW505554 | Hs.144559 | ESTs | 2.0 | 4.7 |
| 75 | 435850 | AF250847 | Hs.283514 | mitochondrial ceramidase | 2.0 | 3.7 |
| | 435086 | AW975243 | Hs.122596 | ESTs | 2.0 | 2.1 |
| | 423191 | D61506 | Hs.8417 | hypothetical protein DKFZp761M0423 | 2.0 | 2.1 |
| | 411562 | AL050201 | Hs.70769 | hypothetical protein DKFZp586E1923 | 2.0 | 2.8 |
| | 431645 | AF078849 | Hs.266483 | dynein light chain-A | 2.0 | 2.5 |
| 80 | 429834 | AJ929645 | Hs.225936 | synapsin I | 2.0 | 3.6 |
| | 439607 | BE540565 | Hs.159460 | ESTs | 2.0 | 17.5 |
| | 408033 | AW138045 | Hs.242256 | ESTs | 2.0 | 4.0 |
| | 430317 | AB020645 | Hs.239189 | glutaminase | 2.0 | 2.7 |
| | 419631 | AW188117 | Hs.303154 | poppey protein 3 | 2.0 | 2.6 |
| | 432660 | AI288430 | Hs.64004 | ESTs | 2.0 | 2.3 |
| | 454048 | H05626 | Hs.6921 | ESTs | 2.0 | 15.9 |
| | 426917 | AA913814 | Hs.172854 | DKFZP586B0923 protein | 2.0 | 3.1 |

| | | | | | | |
|---|--------|----------|-----------|---|-----|------|
| 5 | 423246 | AL119114 | Hs.77196 | spectrin, alpha, non-erythrocytic 1 (atp) | 2.0 | 2.9 |
| | 415898 | AI267700 | Hs.317584 | ESTs | 2.0 | 4.8 |
| | 420276 | AA290938 | Hs.190561 | ESTs, Highly similar to SORL_HUMAN SORT1 | 2.0 | 5.1 |
| | 424983 | AI742434 | Hs.169911 | ESTs | 2.0 | 15.9 |
| | 446296 | AA985662 | Hs.63131 | Homo sapiens cDNA FLJ13155 fis, clone NT | 2.0 | 2.7 |
| | 450006 | AI241555 | Hs.60171 | ESTs | 2.0 | 3.5 |

TABLE 27B:

| | |
|-------------|---------------------------------------|
| Pkey: | Unique Eos probeset identifier number |
| CAT number: | Gene cluster number |
| Accession: | Genbank accession numbers |

| | | | |
|----|--------|------------|--|
| 15 | Pkey | CAT Number | Accession |
| | 408274 | 104999_1 | R17315 Z43964 AA053547 |
| | 412100 | 1277224_1 | AW892731 H08502 Z45826 |
| | 412112 | 1277883_1 | BE180342 BE180347 AW901900 BE180222 BE180218 BE180226 BE180413 BE180416 AW901899 BE180228 AW901897 BE180224 AW901898 BE180223 BE180219 BE180346 BE180343 BE180418 BE180225 BE180221 BE180341 AW901894 BE180217 BE180227 AW901891 BE180345 AW893614 AW893615 H85799 H83501 BE180220 |
| 20 | 413153 | 1350849_1 | N94205 BE067565 BE067556 |
| | 413510 | 1374377_1 | F13044 T77009 BE145525 BE145493 |
| | 414828 | 149563_1 | AA156651 AA156622 R14472 |
| | 418948 | 180808_1 | AI217097 AW886090 W38035 W38792 AA232835 AW936043 |
| 25 | 419558 | 185904_1 | AW953679 AW953680 AA244436 H82527 AA361046 AA244483 H82526 |
| | 421249 | 200649_1 | AA285362 AW752386 AW847156 AA285373 AW879575 AW879558 |
| | 421640 | 204833_1 | AW966652 AW966653 AA294989 AA385977 |
| | 429995 | 311738_1 | AA463571 AI277645 AL118763 |
| 30 | 430212 | 314437_1 | AA469153 AI718503 AA469225 |
| | 432122 | 341756_1 | AA526514 AW973343 AA554293 |
| | 433449 | 366532_1 | AW772282 AA592974 |
| | 434138 | 380572_1 | AA625804 AW418787 AW074833 AI675642 AI393368 |
| 35 | 437483 | 43756_1 | AL390174 AW898817 |
| | 439780 | 47673_1 | AL109688 R23665 R26578 |
| | 452502 | 919733_1 | AI904296 BE007223 R30687 |
| | 455517 | 1321782_1 | AW984068 AW984072 AW984077 |
| | 456407 | 184986_1 | AW968614 AA243209 AA281411 |

TABLE 27C:

| | |
|--------------|---|
| Pkey: | Unique number corresponding to an Eos probeset |
| Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. |
| Strand: | Indicates DNA strand from which exons were predicted. |
| NT_position: | Indicates nucleotide positions of predicted exons. |

| | | | | |
|----|--------|---------|--------|---|
| 45 | Pkey | Ref | Strand | NT_position |
| | 400979 | 8072554 | Plus | 160842-161028 |
| | 401213 | 9858408 | Plus | 98243-98380,98489-98619 |
| | 401421 | 7452889 | Minus | 142291-142461 |
| 50 | 403092 | 8954241 | Plus | 174720-175016,175104-175406,175508-175813 |
| | 404648 | 9796894 | Minus | 115334-116020 |
| | 404793 | 7232206 | Minus | 61087-61590 |
| | 404835 | 6970743 | Plus | 85462-85684,88139-88287,90338-91018,94827-94990 |
| 55 | 405326 | 4375975 | Plus | 10633-10709,30805-30893,38078-38253,55112-55327,57718-57818,66696-66841 |
| | 405385 | 6552772 | Plus | 48332-48454 |
| | 405793 | 1405887 | Minus | 89197-89453 |
| | 405911 | 6758795 | Plus | 101008-101643 |
| | 405977 | 8247789 | Minus | 135548-136177 |

TABLE 28A: About 139 genes up-regulated in glioma compared to normal adult tissues
 Table 28A lists about 139 genes up-regulated in glioma compared to normal adult tissues. In order to identify new genes that are associated with glioma, a non-redundant set of 6614 genes that have been previously identified were removed from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array. Genes associated with glioma value was greater than or equal to 50 units (this selects for the most abundant of the up-regulated genes). The "average" glioma level was set to the 94th percentile value amongst various glioblastoma, astrocytoma, and oligodendroglioma specimens; the "average" normal adult tissue level was set to the 85th percentile value amongst various non-malignant organs and tissues and other non-malignant brain tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated. Predicted protein domains are noted.

| | |
|----------------|---|
| Pkey: | Unique Eos probeset identifier number |
| ExAccn: | Exemplar Accession number, Genbank accession number |
| UnigeneID: | Unigene number |
| Unigene Title: | Unigene gene title |
| Prot. Doms: | Predicted Protein Domains |
| R1: | glioma vs normal adult tissues |

| | | | | | | |
|----|--------|-----------|------------|-------------------------------------|--------------------------|-----|
| 75 | Pkey | ExAccn | UniGene ID | Unigene Title | Protein Domains | R1 |
| | 443902 | W28470 | Hs.12600 | N-ethylmaleimide-sensitive factor a | | 4.0 |
| | 441476 | R44566 | Hs.173134 | ESTs | | 4.0 |
| | 446048 | AI272364 | Hs.182081 | KIAA1811 protein | | 3.8 |
| 80 | 407061 | X97748 | | gb:H.sapiens PTX3 gene promoter reg | | 3.7 |
| | 414323 | NM_014759 | Hs.334688 | KIAA0273 gene product | fn3;TM; | 3.6 |
| | 439769 | AA448828 | Hs.30596 | Homo sapiens mRNA full length inser | lactamase_B,Rhomboid,TPR | 3.6 |
| | 429319 | AL023754 | Hs.199068 | similar to calcium/calmodulin depen | pkinese;TM;SS | 3.6 |
| | 443412 | W84893 | Hs.9305 | angiotensin receptor-like 1 | | 3.5 |
| | 425533 | T47802 | Hs.9305 | angiotensin receptor-like 1 | | 3.5 |

| | | | | | | |
|----|--------|-----------|-----------|-------------------------------------|-----------------------------|-----|
| 5 | 408610 | AW026692 | Hs.285050 | ESTs | ion_trans_K_tetra,Kv2chan | 3.4 |
| | 450678 | AL109703 | Hs.25314 | Homo sapiens mRNA full length inser | | 3.4 |
| | 419171 | NM_002846 | Hs.89655 | protein tyrosine phosphatase, recep | Y_phosphatase,ART;TM;SS | 3.4 |
| | 445875 | AF070524 | Hs.13410 | Homo sapiens clone 24453 mRNA seque | | 3.4 |
| | 412581 | AA224244 | Hs.182704 | ESTs, Moderately similar to alterna | | 3.3 |
| | 424911 | AA984364 | Hs.7913 | ESTs | | 3.3 |
| | 452753 | AA028049 | Hs.277728 | SEC14 (S. cerevisiae)-like 2 | CRAL_TRIO | 3.3 |
| | 436648 | R18556 | Hs.352385 | ESTs | pkinese, pkinese_C, PMP22_C | 3.2 |
| 10 | 452130 | AW248349 | Hs.28088 | SGC32445 protein | TB2_DP1_HVA22;TM;SS | 3.2 |
| | 448848 | AF131851 | Hs.22241 | hypothetical protein | | 3.2 |
| | 426470 | AA528794 | Hs.128644 | ESTs | | 3.2 |
| | 419344 | U94905 | Hs.277445 | diacylglycerol kinase, zeta (104kd) | ank_DAGKa,DAGKc,DAG_PE-bi | 3.2 |
| | 439783 | AI125760 | Hs.24835 | hypothetical protein FLJ14594 | ig_LRR,LRRNT,LRRCT;TM;S | 3.2 |
| | 411358 | R47479 | Hs.94761 | KIAA1691 protein | TM;SS | 3.2 |
| 15 | 409433 | AA074382 | Hs.135255 | ADAMTS14 | | 3.2 |
| | 456940 | H46986 | Hs.31861 | ESTs | | 3.1 |
| | 423744 | D26158 | Hs.1701 | ELAV (embryonic lethal, abnormal vi | rm, Gene66; | 3.1 |
| | 432227 | U28389 | Hs.274122 | erythrocyte membrane protein band 4 | VHP;TM; | 3.1 |
| | 449181 | X96783 | Hs.23179 | synaptotagmin V | C2;TM;SS | 3.1 |
| 20 | 422274 | NM_015564 | Hs.114169 | KIAA0416 protein | LRR,LRRNT,LRRCT;TM;SS | 3.1 |
| | 424607 | NM_016848 | Hs.151123 | neuronal Shc | PID,SH2; | 3.1 |
| | 416898 | BE219510 | Hs.234074 | Homo sapiens mRNA; cDNA DKFZp761G02 | EGF,Rhabd_glycop;TM;SS= | 3.1 |
| | 438162 | NM_014618 | Hs.6090 | deleted in bladder cancer chromosom | TM;SS | 3.1 |
| | 439892 | AL043463 | Hs.6755 | RaP2 interacting protein 8 | RUN;SS | 3.1 |
| 25 | 445330 | R52656 | Hs.21691 | ESTs | 7tm_1 | 3.0 |
| | 451766 | NM_001406 | Hs.26988 | ephrin-B3 | Ephrin;TM;SS | 3.0 |
| | 444457 | AI204146 | Hs.92556 | ESTs | Fork_head | 3.0 |
| | 458247 | R14439 | Hs.209194 | ESTs | | 3.0 |
| 30 | 424616 | U72671 | Hs.151250 | intercellular adhesion molecule 5, | ig_ICAM_N;TM;SS | 3.0 |
| | 408971 | R38990 | Hs.13485 | ESTs | | 3.0 |
| | 423940 | NM_012429 | Hs.277728 | SEC14 (S. cerevisiae)-like 2 | CRAL_TRIO;TM; | 3.0 |
| | 458124 | AW005548 | Hs.124590 | ESTs | | 3.0 |
| | 410491 | AA465131 | Hs.64001 | Homo sapiens clone 25218 mRNA seque | | 3.0 |
| 35 | 444808 | H20019 | Hs.286084 | ESTs | ank_ras,PH,ArfGap,HCO3_co | 3.0 |
| | 437696 | Z83844 | Hs.5790 | hypothetical protein dJ37E16.5 | Hydrolase;TM; | 2.9 |
| | 424016 | AW163729 | Hs.6140 | hypothetical protein MGC15730 | ig;SS | 2.9 |
| | 421680 | AL031186 | Hs.289106 | Human DNA sequence from clone CTA-9 | Collagen;TM;SS | 2.9 |
| | 418055 | R18516 | Hs.351299 | ESTs, Weakly similar to 138022 hypo | ZZ_ZZ | 2.9 |
| 40 | 444819 | AI697836 | Hs.148433 | ESTs | | 2.9 |
| | 420524 | AB010575 | Hs.98547 | amiloride-sensitive cation channel | ASC;TM; | 2.9 |
| | 416237 | H30684 | Hs.159863 | ESTs | | 2.9 |
| | 432270 | AK001008 | Hs.274233 | Homo sapiens cDNA FLJ10146 fis, clo | | 2.9 |
| | 405569 | | | NM_031481::Homo sapiens soluble car | mito_carr;TM;SS | 2.9 |
| 45 | 428950 | BE311879 | Hs.194673 | phosphoprotein enriched in astrocyt | DED;TM; | 2.9 |
| | 426128 | NM_001471 | Hs.167017 | gamma-aminobutyric acid (GABA) B re | 7tm_3,sushi,ANF_receptor; | 2.9 |
| | 447758 | H17302 | Hs.93967 | ESTs, Weakly similar to NBHUC8 deco | LRR,LRRNT,LRRCT;TM;SS | 2.9 |
| | 445331 | H04489 | Hs.12520 | Homo sapiens clone 23568, 23621, 23 | PC_rep | 2.9 |
| | 431010 | BE251246 | Hs.248214 | complexin 1 | TM; | 2.9 |
| 50 | 433065 | N62902 | Hs.343660 | Homo sapiens PAC clone RP4-651K2 fr | :SS | 2.9 |
| | 426845 | AB025186 | Hs.172740 | microtubule-associated protein, RP1 | EB1,CH;TM; | 2.9 |
| | 454360 | L78207 | Hs.54470 | ATP-binding cassette, sub-family C | ABC_tran,ABC_membrane,PRK | 2.9 |
| | 438859 | AJ559626 | Hs.93522 | Homo sapiens mRNA for KIAA1647 prot | bZIP,K-box,7tm_2,EGF,cdh | 2.9 |
| | 410515 | F12086 | Hs.4257 | ESTs | PID,SH2,PID,SH2 | 2.8 |
| | 434022 | R18374 | Hs.117956 | ESTs | hormone_rec,zf-C4 | 2.8 |
| 55 | 428960 | AF052224 | Hs.194684 | bassoon (presynaptic cytomatrix pro | Carla_C4,RPH3A_effector;T | 2.8 |
| | 426290 | AB007918 | Hs.169182 | KIAA0449 protein | WD40;TM; | 2.8 |
| | 417287 | AI831678 | Hs.285714 | KIAA1599 protein | C2;TM; | 2.8 |
| | 422575 | AK000546 | Hs.118552 | hypothetical protein FLJ20539 | PT2;TM;SS | 2.8 |
| 60 | 417941 | AI056049 | Hs.96297 | ESTs | Band_41,ERM | 2.8 |
| | 452707 | AI093823 | Hs.45070 | ESTs | | 2.8 |
| | 424873 | AB018294 | Hs.153610 | KIAA0751 gene product | C2,PDZ;TM; | 2.8 |
| | 408209 | NM_004454 | Hs.43697 | ets variant gene 5 (ets-related mol | Ets;TM; | 2.8 |
| | 415935 | H09663 | Hs.106490 | ESTs | PID | 2.8 |
| 65 | 437999 | AW905038 | Hs.90242 | ESTs | ion_trans | 2.8 |
| | 428248 | AJ126772 | Hs.40479 | ESTs | | 2.8 |
| | 414001 | AJ610347 | Hs.103812 | ESTs, Moderately similar to ALU1_HU | Gelsolin,VHP,p450 | 2.8 |
| | 406634 | AA386235 | Hs.74576 | GDP dissociation inhibitor 1 | GDI;TM; | 2.8 |
| | 453439 | AI572438 | Hs.32976 | guanine nucleotide binding protein | G-gamma;TM; | 2.8 |
| 70 | 433320 | D60647 | Hs.250879 | ESTs, Highly similar to CTXN RAT CO | rm | 2.8 |
| | 420888 | AB006713 | Hs.100058 | dihydropyrimidinase-like 4 | Dihydroorotase;TM; | 2.7 |
| | 440001 | AJ740721 | Hs.128292 | ESTs | | 2.7 |
| | 417622 | AW298163 | Hs.82318 | WAS protein family, member 3 | WH2;TM; | 2.7 |
| | 438626 | AI198059 | Hs.26370 | ESTs | | 2.7 |
| 75 | 404439 | | | ENSP00000067222::Mitochondrial 28S | OLF;SS | 2.7 |
| | 448375 | NM_004644 | Hs.21022 | adaptor-related protein complex 3, | Adaptin_N;TM; | 2.7 |
| | 420989 | AB002372 | Hs.323833 | syntaphilin | TM; | 2.7 |
| | 419651 | NM_007023 | Hs.91971 | cAMP-regulated guanine nucleotide e | cnMP_binding,DEP,RasGEF,R | 2.7 |
| | 414562 | AW955734 | Hs.112195 | ESTs, Weakly similar to 2108402A ca | | 2.7 |
| 80 | 410865 | T16342 | Hs.66727 | ESTs, Weakly similar to T31613 hypo | IRK | 2.7 |
| | 421146 | AI082215 | Hs.97993 | ESTs, Moderately similar to SERP1 | | 2.7 |
| | 419087 | AI671245 | Hs.24835 | hypothetical protein FLJ14594 | ig_LRR,LRRNT,LRRCT;TM;S | 2.7 |
| | 421499 | AI271438 | Hs.236131 | homeodomain-interacting protein kin | pkinese,Peptidase_M1;TM | 2.7 |
| | 425014 | AI251449 | Hs.171939 | ESTs | PID,PDZ | 2.7 |

| | | | | | | |
|----|---|--|------------|-------------------------------------|----------------------------|------|
| 5 | 448655 | AL035289 | Hs.21708 | hypothetical protein from clone 248 | TM;SS | 2.7 |
| | 424410 | W79027 | Hs.271762 | ESTs | | 2.7 |
| | 447117 | AI362798 | Hs.40183 | ESTs | | 2.7 |
| | 447478 | BE618843 | Hs.28144 | fibronectin type 3 and SPRY domain- | fn3,SPRY;TM; | 2.7 |
| | 437645 | R20728 | Hs.21164 | ESTs | | 2.7 |
| | 433698 | H24201 | Hs.247423 | adducin 2 (beta) | Aldolase-II;TM; | 2.7 |
| | 419701 | AA248999 | Hs.7913 | ESTs | | 2.7 |
| 10 | 410510 | AW294625 | Hs.64064 | potassium voltage-gated channel, su | cNMP_binding,ion_trans,PA | 2.7 |
| | 452869 | AB014534 | Hs.30898 | KIAA0634 protein | fn3;SS | 2.7 |
| | 428045 | T15465 | Hs.182231 | thyrotropin-releasing hormone | ;SS | 2.7 |
| | 425218 | NM_014909 | Hs.155182 | KIAA1036 protein | TM; | 2.7 |
| | 425558 | AF040723 | Hs.158300 | huntingtin-associated protein 1 (ne | TM; | 2.6 |
| | 440789 | AB007857 | Hs.7416 | KIAA0397 gene product | TBC,RUN;TM; | 2.6 |
| 15 | 418423 | NM_014732 | Hs.301658 | KIAA0513 gene product | TM; | 2.6 |
| | 450400 | AI694722 | Hs.279744 | ESTs | lectin_c | 2.6 |
| | 413566 | AW604451 | Hs.285814 | sprouty (Drosophila) homolog 4 | SH2,SH3;TM;SS | 2.6 |
| | 443759 | BE390832 | Hs.134729 | FXD domain-containing ion transpor | ATP1G1,PLM_MAT8;TM;SS | 2.6 |
| | 425069 | AA687465 | Hs.298184 | potassium voltage-gated channel, sh | aldo_ket_red | 2.6 |
| | 429291 | AI933057 | Hs.349189 | mannosyl (alpha-1,3)-glycoprotein | | 2.6 |
| 20 | 424798 | AW016523 | Hs.182850 | ESTs | | 2.6 |
| | 447455 | H36335 | Hs.6750 | Homo sapiens mRNA for FLJ00058 prot | TM;SS | 2.6 |
| | 417212 | AW952823 | Hs.351547 | NS1-binding protein | E2_N,E2_C,DNA_mis_repair, | 2.6 |
| | 432265 | BE382679 | Hs.285753 | SCG10-like-protein | Stathmin;TM;SS | 2.6 |
| 25 | 417005 | C21115 | Hs.26612 | ESTs, Moderately similar to S23650 | | 2.6 |
| | 421091 | W22821 | Hs.351612 | ribosomal protein L26 | TM; | 2.6 |
| | 445472 | AB006631 | Hs.12784 | Homo sapiens mRNA for KIAA0293 gene | homeobox,CUT;TM; | 2.6 |
| | 431967 | AJ243653 | Hs.373498 | organic cation transporter | sugar_tr;TM;SS | 2.6 |
| | 439151 | AW135066 | Hs.283110 | carbonic anhydrase X | carb_anhydrase;TM;SS | 2.6 |
| 30 | 424134 | AF070637 | Hs.140950 | hypothetical protein | DUF176;SS | 2.6 |
| | 430213 | AW993446 | Hs.235445 | hypothetical protein FLJ21313 | GRAM;TM; | 2.6 |
| | 445954 | AA148926 | Hs.27836 | hypothetical protein FLJ22362 | fn3;TM; | 2.6 |
| | 445084 | H38914 | Hs.250848 | hypothetical protein FLJ14761 | TM;SS | 2.6 |
| | 446236 | NM_006293 | Hs.301 | TYRO3 protein tyrosine kinase | fn3,ig,ptkinase;TM; | 2.6 |
| 35 | 433706 | AW947250 | Hs.283645 | ESTs | PH,RhoGAP | 2.6 |
| | 423606 | AB011094 | Hs.129892 | KIAA0522 protein | PH,bZIP,JQ,Sec7;TM; | 2.5 |
| | 438915 | AA280174 | Hs.285681 | Williams-Beuren syndrome chromosome | | 2.5 |
| | 448923 | AL034562 | Hs.22584 | prodynorphin | Opioids_neuropep;SS | 2.5 |
| | 408115 | AB033107 | Hs.42796 | KIAA1281 protein | | 2.5 |
| 40 | 446772 | AW294404 | Hs.144515 | Homo sapiens cDNA FLJ11672 fis, clo | | 2.5 |
| | 427989 | H85525 | Hs.40479 | gb:yv88h06.r1 Soares melanocyte 2Nb | TM;SS | 2.5 |
| | 435833 | BE259178 | Hs.41641 | Bruno (Drosophila)-like 4, RNA bin | nm;TM; | 2.5 |
| | 423797 | BE259364 | Hs.132898 | fatty acid desaturase 1 | heme_1,FA_desaturase;TM | 2.5 |
| | 448277 | BE622827 | Hs.99486 | hypothetical protein FLJ13044 | mito_carr;TM;SS | 2.5 |
| 45 | 417298 | AW665639 | Hs.37958 | ESTs | | 2.5 |
| | 415577 | AF257770 | Hs.20930 | poly(rC)-binding protein 4 | KH-domain;TM; | 2.5 |
| | 420742 | U79251 | Hs.99902 | opioid-binding protein/cell adhesio | ig;TM;SS | 2.5 |
| | 419109 | BE169157 | Hs.172717 | ESTs | ptkinase,LRRCT,ig,LRR,LRRN | 2.5 |
| 50 | TABLE 28C: | | | | | |
| | Pkey: | Unique number corresponding to an Eos probeset | | | | |
| | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. | | | | |
| | Strand: | Indicates DNA strand from which exons were predicted. | | | | |
| 55 | NL_position: | Indicates nucleotide positions of predicted exons. | | | | |
| | Pkey | Ref | Strand | NL_position | | |
| | 405569 | 6006906 | Plus | 99719-99873 | | |
| | 404439 | 7139680 | Plus | 55316-55585 | | |
| 60 | TABLE 29A: ABOUT 362 GENES UP-REGULATED IN GLIOMA COMPARED TO NON-MALIGNANT ADULT BRAIN TISSUE | | | | | |
| | Table 29A lists about 362 genes up-regulated in glioma compared to non-malignant adult brain tissue. These were selected as for Table 28A, except that the ratio of "average" glioma to "average" normal brain was greater than or equal to 3.0, the "average" glioma level was set to the 99th percentile value amongst various glioma specimens, the "average" normal adult tissue level was set to the 90th percentile value amongst various non-malignant adult brain specimens, the "average" glioma value was greater than or equal to 50 units. Predicted protein domains are noted. | | | | | |
| 65 | Pkey: | Unique Eos probeset identifier number | | | | |
| | ExAccn: | Exemplar Accession number, Genbank accession number | | | | |
| | UnigeneID: | Unigene number | | | | |
| | Unigene Title: | Unigene gene title | | | | |
| 70 | Protein Domains: | Predicted Protein Domains | | | | |
| | R1: | glioma vs non-malignant adult brain tissue | | | | |
| | Pkey | ExAccn | Unigene ID | Unigene Title | Protein Domains | R1 |
| | 414477 | U41635 | Hs.76228 | amplified in osteosarcoma | ptkinase,LRR,TM;SS | 11.2 |
| | 407241 | M34516 | | gb:Human omega light chain protein | TM; | 10.9 |
| 75 | 408972 | AL050100 | Hs.49378 | DKFZP585D0919 protein | TM; | 7.0 |
| | 417512 | X76534 | Hs.82226 | glycoprotein (transmembrane) numb | PKD;TM;SS | 6.9 |
| | 414001 | AI610347 | Hs.103812 | ESTs, Moderately similar to ALU1_HU | Gelsolin,VHP,p450 | 6.3 |
| | 428847 | AI954833 | Hs.98881 | ESTs | | 6.2 |
| 80 | 407061 | X97748 | | gb:H.sapiens PTX3 gene promotor reg | | 5.4 |
| | 440020 | AI480204 | Hs.177131 | ESTs | | 5.4 |
| | 408832 | AW085690 | Hs.63428 | ESTs, Weakly similar to Z195_HUMAN | | 5.3 |
| | 406837 | R70292 | Hs.156110 | immunoglobulin kappa constant | | 5.2 |
| | 407607 | NM_001887 | Hs.37135 | crystallin, beta B1 | crystallin;TM; | 5.1 |

| | | | | | |
|----|--------|-----------|-----------|-------------------------------------|-----|
| 5 | 435013 | H91923 | Hs.110024 | NM_020142:Homo sapiens NADH:ubiquin | 5.1 |
| | 424916 | AW867440 | Hs.23096 | ESTs | 5.1 |
| | 409659 | AW970843 | Hs.55682 | eukaryotic translation initiation f | 5.1 |
| | 432576 | AW157424 | Hs.165954 | ESTs, Weakly similar to I38022 hypo | 5.1 |
| | 406621 | X57809 | Hs.181125 | immunoglobulin lambda locus | 5.1 |
| | 430418 | R98852 | Hs.36029 | heart and neural crest derivatives | 5.1 |
| | 441633 | AW958544 | Hs.112242 | normal mucosa of esophagus specific | 5.0 |
| | 429707 | W76631 | Hs.211819 | matrix metalloproteinase 238 | 5.0 |
| 10 | 438915 | AA280174 | Hs.285681 | Williams-Beuren syndrome chromosome | 5.0 |
| | 441321 | H17182 | Hs.7771 | B-cell associated protein | 5.0 |
| | 406848 | AJ264844 | Hs.275865 | ribosomal protein S18 | 4.9 |
| | 423505 | AF064090 | Hs.129708 | tumor necrosis factor (ligand) supe | 4.8 |
| | 433848 | AF095719 | Hs.93764 | carboxypeptidase A4 | 4.8 |
| 15 | 431882 | NM_001426 | Hs.271977 | engrailed homolog 1 | 4.8 |
| | 446295 | AJ355029 | Hs.101660 | ESTs, Weakly similar to T14171 atax | 4.8 |
| | 409170 | W91994 | Hs.16145 | ESTs | 4.8 |
| | 421155 | H87879 | Hs.102267 | lysyl oxidase | 4.7 |
| | 409202 | AA236881 | Hs.51043 | hexosaminidase B (beta polypeptide) | 4.7 |
| 20 | 412115 | AK001763 | Hs.73239 | hypothetical protein FLJ10901 | 4.7 |
| | 450463 | AW952018 | Hs.201398 | G protein coupled receptor interact | 4.7 |
| | 445980 | AJ268399 | Hs.140489 | ESTs, Weakly similar to LIN1_HUMAN | 4.7 |
| | 406807 | AA057605 | Hs.180920 | ribosomal protein S9 | 4.6 |
| | 409190 | AU076536 | Hs.50984 | sarcoma amplified sequence | 4.6 |
| 25 | 401699 | | | Target Exon | 4.6 |
| | 408901 | AK001330 | Hs.48855 | hypothetical protein FLJ10468 | 4.6 |
| | 441669 | R78195 | Hs.29692 | Homo sapiens cDNA FLJ11436 fis, clo | 4.6 |
| | 406858 | AA505445 | Hs.300697 | immunoglobulin heavy constant gamma | 4.6 |
| | 406699 | L06505 | Hs.182979 | ribosomal protein L12 | 4.6 |
| 30 | 406663 | U24683 | | immunoglobulin heavy constant mu | 4.6 |
| | 427714 | AF119850 | Hs.2186 | eukaryotic translation elongation f | 4.6 |
| | 407260 | L09095 | | gb:Homo sapiens mRNA fragment | 4.5 |
| | 406803 | H42321 | Hs.163593 | ribosomal protein L18a | 4.5 |
| | 430397 | AF924533 | Hs.105607 | bicarbonate transporter related pro | 4.5 |
| 35 | 414044 | BE614194 | Hs.75721 | profilin 1 | 4.5 |
| | 424238 | AA337401 | Hs.137635 | ESTs | 4.5 |
| | 421532 | AW138207 | Hs.146170 | hypothetical protein FLJ22969 | 4.4 |
| | 421241 | X91817 | Hs.102866 | transketolase-like 1 | 4.4 |
| | 436398 | H87136 | Hs.5174 | ribosomal protein S17 | 4.4 |
| 40 | 428479 | Y00272 | Hs.334562 | cell division cycle 2, G1 to S and | 4.4 |
| | 446921 | AB012113 | Hs.16530 | small inducible cytokine subfamily | 4.3 |
| | 433271 | BE621697 | Hs.14317 | nucleolar protein family A, member | 4.3 |
| | 406964 | M21305 | | FGENES predicted novel secreted pro | 4.3 |
| | 432191 | AA043193 | Hs.273186 | hypothetical protein, clone Teletho | 4.3 |
| 45 | 420890 | AA434058 | Hs.100071 | 6-phosphogluconolactonase | 4.3 |
| | 413053 | AW963263 | Hs.65377 | ESTs, Moderately similar to KIAA139 | 4.2 |
| | 406687 | M31126 | Hs.352054 | matrix metalloproteinase 11 (stroma | 4.2 |
| | 425157 | NM_006227 | Hs.283007 | phospholipid transfer protein | 4.2 |
| | 426386 | AA748850 | Hs.125830 | bladder cancer overexpressed protei | 4.2 |
| 50 | 446490 | AK000706 | Hs.15125 | hypothetical protein FLJ20699 | 4.2 |
| | 431750 | AA514986 | Hs.283705 | ESTs | 4.2 |
| | 428327 | AW206236 | Hs.28773 | ESTs | 4.2 |
| | 417342 | W40277 | Hs.81994 | glycophorin C (Gerbich blood group) | 4.1 |
| | 433688 | AA628467 | Hs.112572 | Homo sapiens cDNA FLJ14130 fis, clo | 4.1 |
| 55 | 433170 | AB037816 | Hs.8982 | KIAA1395 | 4.1 |
| | 423084 | AU076474 | Hs.123178 | translocase of inner mitochondrial | 4.1 |
| | 407926 | AW956382 | Hs.59771 | ESTs | 4.1 |
| | 445636 | AW105401 | Hs.350068 | ribosomal protein L29 | 4.1 |
| | 418689 | AJ360883 | Hs.375584 | hypothetical protein FLJ11029 | 4.1 |
| 60 | 450690 | AA296696 | Hs.333418 | FXD domain-containing ion transpor | 4.1 |
| | 419092 | J05581 | Hs.89603 | mucin 1, transmembrane | 4.0 |
| | 447813 | AJ394345 | Hs.238513 | hypothetical protein MGCS442 | 4.0 |
| | 436419 | AJ948626 | Hs.171356 | ESTs | 4.0 |
| | 458147 | AW752597 | | gb:IL3-CT0214-161299-045-B06 CT0214 | 4.0 |
| 65 | 443402 | U77846 | Hs.356316 | elastin (supraaortic aortic steno | 4.0 |
| | 433435 | BE545277 | Hs.340959 | Ts translation elongation factor, m | 4.0 |
| | 413595 | AW235215 | Hs.16145 | ESTs | 4.0 |
| | 412607 | Z33642 | Hs.74115 | immunoglobulin superfamily, member | 4.0 |
| | 419913 | AW270040 | Hs.34455 | ESTs | 4.0 |
| 70 | 415209 | F00183 | Hs.172004 | titin | 4.0 |
| | 439310 | AF086120 | Hs.102793 | ESTs | 3.9 |
| | 421777 | BE562088 | Hs.108196 | HSPC037 protein | 3.9 |
| | 409485 | S80990 | Hs.252136 | ficolin (collagen/fibrinogen domain | 3.9 |
| | 402241 | | | Target Exon | 3.9 |
| 75 | 432716 | AJ762964 | Hs.205180 | ESTs | 3.9 |
| | 418140 | BE613836 | Hs.83551 | microfibrillar-associated protein 2 | 3.9 |
| | 434214 | AF119871 | Hs.155860 | hypothetical protein PRO2268 | 3.9 |
| | 406855 | AA902829 | | gb:ok72e06.s1 NCI_CGAP_GCA Homo sap | 3.9 |
| | 421567 | AJ272137 | Hs.198265 | matrix metalloproteinase 25 | 3.9 |
| 80 | 403364 | | | Target Exon | 3.9 |
| | 412339 | BE151267 | Hs.314466 | ESTs | 3.8 |
| | 423007 | AA320134 | Hs.195029 | Homo sapiens mRNA for KIAA1657 prot | 3.8 |
| | 427600 | AW630918 | Hs.179774 | proteasome (prosome, macropain) act | 3.8 |
| | 405201 | | | Target Exon | 3.8 |
| | | | | nm | 5.1 |
| | | | | ;SS | 5.1 |
| | | | | nm | 5.1 |
| | | | | ig,HSP70,Ppx-GppA;TM;SS | 5.1 |
| | | | | HLH | 5.1 |
| | | | | TM;SS | 5.0 |
| | | | | ig,Peptidase_M10;TM;SS= | 5.0 |
| | | | | Band_7;TM; | 5.0 |
| | | | | Ribosomal_S13; | 4.9 |
| | | | | TNF;TM;SS | 4.8 |
| | | | | Zn_carbOpept,Propep_M14;T | 4.8 |
| | | | | homeobox;TM; | 4.8 |
| | | | | LJM | 4.8 |
| | | | | nm | 4.8 |
| | | | | Lysyl_oxidase,Aldose_epim | 4.7 |
| | | | | Glyco_hydro_20,Glyco_hydr | 4.7 |
| | | | | ;SS | 4.7 |
| | | | | C1q,Collagen;TM;SS | 4.7 |
| | | | | zf-C2H2,bZIP | 4.7 |
| | | | | Ribosomal_S4,S4,tRNA_inL | 4.6 |
| | | | | transmembrane4;TM;SS | 4.6 |
| | | | | TM; | 4.6 |
| | | | | TM; | 4.6 |
| | | | | ig;TM; | 4.6 |
| | | | | Ribosomal_L11;TM; | 4.6 |
| | | | | ;SS | 4.6 |
| | | | | COX8,SHMT,MIF,GST_C,EF1G_ | 4.6 |
| | | | | Ribosomal_L18ae;TM; | 4.5 |
| | | | | HCO3_cotransp;TM; | 4.5 |
| | | | | profilin;TM; | 4.5 |
| | | | | TM;SS | 4.5 |
| | | | | Armadillo_seg,HEAT;TM;S | 4.4 |
| | | | | transketolase,transket_py | 4.4 |
| | | | | Ribosomal_S17e,PolYA_pol; | 4.4 |
| | | | | pkinase,ICE_p10,ICE_p20;T | 4.4 |
| | | | | IL8;SS | 4.3 |
| | | | | ; | 4.3 |
| | | | | ABC1;TM; | 4.3 |
| | | | | Glucosamine_iso;TM; | 4.3 |
| | | | | TM; | 4.3 |
| | | | | hemopexin,Peptidase_M10;T | 4.2 |
| | | | | LBP_BPI_CETP,LBP_BPI_CETP | 4.2 |
| | | | | TM; | 4.2 |
| | | | | cpn60_TCP1 | 4.2 |
| | | | | cystatin,Coprogen_oxidase, | 4.2 |
| | | | | TM; | 4.1 |
| | | | | TM; | 4.1 |
| | | | | nm | 4.1 |
| | | | | TYA;SS | 4.1 |
| | | | | filament,GTP_EFTU,EF6_C,G | 4.1 |
| | | | | ATP1G1_PLM_MAT8;TM;SS | 4.1 |
| | | | | SEA;TM;SS | 4.0 |
| | | | | ubiquitin;TM;SS | 4.0 |
| | | | | AT_hook,ATHILA | 4.0 |
| | | | | PMM | 4.0 |
| | | | | PDZ,LIM,pkinase | 4.0 |
| | | | | EF_TS,UBA; | 4.0 |
| | | | | nm | 4.0 |
| | | | | ig;TM;SS | 4.0 |
| | | | | EPH_lbd,ln3,pkinase, | 4.0 |
| | | | | | 4.0 |
| | | | | casein_kappa,pkinase,ig,n | 3.9 |
| | | | | TM; | 3.9 |
| | | | | Collagen,fibrinogen_C;TM= | 3.9 |
| | | | | p450;TM;SS | 3.9 |
| | | | | LRR,UPAR_LY6;TM; | 3.9 |
| | | | | TM;SS | 3.9 |
| | | | | ;SS | 3.9 |
| | | | | hemopexin,Peptidase_M10;T | 3.9 |
| | | | | SH2_Y_phosphatase | 3.9 |
| | | | | tubulin | 3.8 |
| | | | | TIMP | 3.8 |
| | | | | PA28_alpha,PA28_beta; | 3.8 |
| | | | | mito_carr,SH2,SH3,Alpha_a | 3.8 |

| | | | | | | |
|----|--------|-----------|-----------|-------------------------------------|---------------------------|-----|
| 5 | 436906 | H95990 | Hs.181244 | major histocompatibility complex, c | ig,MHC_I;TM;SS | 3.8 |
| | 407319 | A1743332 | Hs.257729 | ESTs, Moderately similar to ALU7_HU | nm,Lipoprotein_2 | 3.8 |
| | 400290 | H18836 | Hs.31608 | hypothetical protein FLJ20041 | Cys_knot | 3.8 |
| | 430240 | BE303038 | Hs.236547 | Homo sapiens, clone IMAGE:2905978, | HEAT_PBS;TM; | 3.8 |
| | 442487 | AF191019 | Hs.8361 | hypothetical protein, estradiol-ind | LRR,LRRNT;TM;SS | 3.8 |
| | 408135 | AA317248 | Hs.42957 | methyltransferase-like 1 | Methyltransf_4;TM; | 3.8 |
| | 419942 | U25138 | Hs.93841 | potassium large conductance calcium | CaKb;TM;SS | 3.8 |
| | 410584 | AB011112 | Hs.64742 | KIAA0540 protein | | 3.8 |
| 10 | 440676 | NM_004987 | Hs.112378 | LIM and senescent cell antigen-like | LIM;SS | 3.8 |
| | 406874 | AW161706 | Hs.180842 | ribosomal protein L13 | Ribosomal_L13e;SS | 3.7 |
| | 429249 | X81479 | Hs.2375 | egl-like module containing, mucin-1 | 7tm_2EGF_GPS,S_locus_gly | 3.7 |
| | 430799 | C19035 | Hs.164259 | ESTs | FKBP,TPR | 3.7 |
| | 453099 | H62087 | Hs.31659 | thyroid hormone receptor-associated | WD40;TM; | 3.7 |
| 15 | 421794 | X86096 | Hs.108371 | E2F transcription factor 4, p107/p1 | E2F_TDP,KOW,Ribosomal_L14 | 3.7 |
| | 444795 | A193356 | Hs.160316 | ESTs | Tropomyosin,ACOX | 3.7 |
| | 443834 | A1741510 | Hs.173548 | ESTs | CUB,MAM,F5_F8_type_C | 3.7 |
| | 429731 | AK001592 | Hs.212172 | beta-carotene 15,15'-dioxygenase | RPE65;SS | 3.7 |
| | 426433 | L38969 | Hs.169875 | thrombospondin 3 | TSPN,tsp_3,EGF,toxin;TM | 3.7 |
| 20 | 426395 | BE151985 | Hs.355669 | hypothetical protein FLJ23316 | pkinase | 3.7 |
| | 406704 | M21665 | Hs.929 | myosin, heavy polypeptide 7, cardia | myosin_head,IQ,Myosin_tai | 3.7 |
| | 447860 | AF193807 | Hs.131835 | Rhesus blood group, B glycoprotein | Ammonium_transp,FacCD;TM= | 3.7 |
| | 430281 | A1878842 | Hs.237924 | CGI-69 protein | mito_carr,homeobox;TM;S | 3.7 |
| | 448360 | AL117560 | Hs.306352 | Homo sapiens mRNA: cDNA DKFZp566P23 | | 3.7 |
| 25 | 446057 | A1420227 | Hs.366053 | Trp-p8 transient receptor potential | | 3.7 |
| | 432078 | BE314877 | Hs.24553 | hypothetical protein FLJ12541 simil | | 3.7 |
| | 406854 | AA613705 | Hs.252259 | ribosomal protein S3 | TM;SS | 3.7 |
| | 422532 | AL008726 | Hs.118126 | protective protein for beta-galacto | KH-domain,Ribosomal_S3_C; | 3.7 |
| | 428171 | AA489323 | Hs.182825 | ribosomal protein L35 | serine_carbpepl,GalP_UDP_ | 3.7 |
| 30 | 442285 | W28729 | Hs.356072 | uncharacterized hypothalamus protei | Ribosomal_L29; | 3.6 |
| | 411281 | BE392792 | Hs.4786 | Homo sapiens cDNA: FLJ22849 fis, cl | cadherin | 3.6 |
| | 457657 | AW411509 | Hs.352567 | hypothetical protein PRO2121 | UQ_con;TM; | 3.6 |
| | 414624 | BE389320 | Hs.23628 | 3 beta-hydroxy-delta 5-C27-steroid | | 3.6 |
| | 451564 | AU076698 | Hs.132760 | hypothetical protein MGC15729 | sugar_tr,Condensation;TM= | 3.6 |
| 35 | 445411 | ALJ37255 | Hs.12646 | hypothetical protein FLJ22693 | hormone_rec,zf-CCCH;TM; | 3.6 |
| | 400785 | | | C11000861:gil9938016[ref]NP_064687. | TM;SS | 3.6 |
| | 413343 | BE392026 | Hs.334346 | hypothetical protein MGC13045 | TM; | 3.6 |
| | 427380 | NM_005534 | Hs.177559 | interferon gamma receptor 2 (interf | fn3;TM;SS | 3.6 |
| | 427818 | AW511222 | Hs.193765 | ESTs | | 3.6 |
| 40 | 449957 | D31365 | Hs.24220 | hypothetical protein | TM; | 3.6 |
| | 451529 | A1917901 | Hs.208641 | ESTs | actin | 3.6 |
| | 446528 | AU076640 | Hs.15243 | nucleolar protein 1 (120kD) | Nol1_Nop2_Sun;TM; | 3.6 |
| | 431659 | AA031875 | Hs.266940 | I-complex-associated-testis-express | Tclx-1;TM; | 3.6 |
| | 433350 | BE563152 | Hs.10362 | Homo sapiens cDNA: FLJ20944 fis, cl | zf-C3HC4,SPRY | 3.6 |
| 45 | 412896 | AW804157 | Hs.375570 | major histocompatibility complex, c | ig,MHC_II_beta;TM;SS | 3.6 |
| | 441748 | R14439 | Hs.209194 | ESTs | | 3.6 |
| | 406853 | AA614553 | Hs.252259 | hypothetical protein FLJ23059 | KH-domain,Ribosomal_S3_C; | 3.5 |
| | 457464 | AW972234 | Hs.126680 | ESTs | | 3.5 |
| | 429619 | AL120751 | Hs.211568 | eukaryotic translation initiation f | | 3.5 |
| 50 | 423309 | BE008775 | Hs.126782 | sushi-repeat protein | sushi,HYR;SS | 3.5 |
| | 438682 | AA354489 | Hs.375594 | EBP50-PDZ interactor of 64 kD | | 3.5 |
| | 453022 | AA031499 | Hs.118489 | ESTs | Amino_oxidase | 3.5 |
| | 434042 | A1589941 | Hs.8254 | Homo sapiens, Similar to tumor diff | | 3.5 |
| | 424867 | A1024860 | Hs.153591 | Not56 (D. melanogaster)-like protei | TM;SS | 3.5 |
| 55 | 417298 | AW665639 | Hs.37958 | ESTs | | 3.5 |
| | 403943 | | | C5000355:gil4503225[ref]NP_000765.1 | | 3.5 |
| | 429497 | AB028953 | Hs.204121 | KIAA1030 protein | fn3;TM; | 3.5 |
| | 426613 | U96132 | Hs.171280 | hydroxyacyl-Coenzyme A dehydrogenas | adh_short;TM;SS | 3.5 |
| 60 | 428343 | AL043021 | Hs.12705 | ESTs | WD40;SS | 3.5 |
| | 456376 | AA663904 | Hs.89862 | TNFRSF1A-associated via death domai | death;TM; | 3.5 |
| | 400348 | AJ251708 | Hs.352588 | Target | | 3.5 |
| | 404854 | | | Target Exon | :SS | 3.5 |
| | 427930 | AA417696 | Hs.372121 | ESTs | | 3.5 |
| 65 | 453143 | AA382234 | Hs.356289 | protein tyrosine phosphatase, recep | serpin;SS | 3.5 |
| | 406806 | AW088535 | Hs.350108 | ribosomal protein, large, P0 | TM; | 3.5 |
| | 406793 | AW264291 | Hs.5662 | guanine nucleotide binding protein | WD40;TM; | 3.5 |
| | 414525 | C14904 | Hs.45184 | Homo sapiens cDNA FLJ12284 fis, clo | | 3.5 |
| | 419950 | AK001645 | Hs.93871 | hypothetical protein FLJ10783 | Glyco_hydro_47;TM;SS | 3.5 |
| 70 | 404243 | | | NM_006778:Homo sapiens ring finger | zf-C3HC4,zf-B_box;TM;SS | 3.4 |
| | 424611 | NM_001421 | Hs.151139 | E74-like factor 4 (ets domain trans | Ets;SS | 3.4 |
| | 432831 | A1821702 | Hs.115959 | ESTs, Weakly similar to I38022 hypo | | 3.4 |
| | 413943 | AW294416 | Hs.144687 | Homo sapiens cDNA FLJ12581 fis, clo | TM; | 3.4 |
| | 418558 | AW082266 | Hs.85131 | Fas (TNFRSF6)-associated via death | death,DED;SS | 3.4 |
| | 408930 | AA146721 | Hs.334686 | hypothetical protein FLJ21588 | CUE;TM; | 3.4 |
| 75 | 403246 | | | Target Exon | HMG_box;SS | 3.4 |
| | 416330 | AU077101 | Hs.79222 | galactosidase, beta 1 | Glyco_hydro_35;TM;SS | 3.4 |
| | 404864 | | | NM_025204:Homo sapiens hypothetica | | 3.4 |
| | 441384 | AA447849 | Hs.288660 | Homo sapiens cDNA: FLJ22182 fis, cl | 7tm_3 | 3.4 |
| | 430284 | A1693534 | Hs.293196 | ESTs | | 3.4 |
| 80 | 433669 | AL047879 | Hs.194251 | ESTs, Weakly similar to ALU2_HUMAN | RNA_pol_LRNA_pol_L,RasGA | 3.4 |
| | 456050 | R79445 | Hs.76230 | ribosomal protein S10 | S10_plectin;TM; | 3.4 |
| | 422311 | AF073515 | Hs.114948 | cytokine receptor-like factor 1 | fn3;TM; | 3.4 |
| | 408909 | AW502034 | Hs.287379 | ESTs, Weakly similar to T26022 hypo | | 3.4 |
| | 428028 | US2112 | Hs.182018 | interleukin-1 receptor-associated k | death,pkinase;TM; | 3.4 |

| | | | | | | |
|----|--------|-----------|-----------|--|--------------------------------|-----|
| | 424213 | BE390125 | Hs.143187 | hypothetical protein | DEAD, helicase_C; TM; | 3.4 |
| | 416432 | BE391767 | Hs.79322 | glutamyl-IRNA synthetase | | 3.4 |
| | 400233 | | | Eos Control | Ribosomal_S9; | 3.4 |
| | 403252 | | | Target Exon | TM; SS | 3.4 |
| 5 | 409433 | AA074382 | Hs.135255 | ADAMTS14 | | 3.4 |
| | 426053 | U68105 | Hs.172182 | poly(A)-binding protein, cytoplasmic | rm, PABP; TM; | 3.4 |
| | 448222 | AI648587 | Hs.20725 | Mov10 (Moloney leukemia virus 10, m | TM; | 3.4 |
| | 432982 | AA531058 | Hs.182248 | truncated calcium binding protein | OPR_ZZ; TM; | 3.4 |
| 10 | 453914 | NM_000507 | Hs.574 | fructose-1,6-bisphosphatase 1 | FBPase; TM; | 3.4 |
| | 444626 | AA320893 | Hs.117062 | hypothetical protein FLJ14497 | pyr_redox; TM; SS | 3.4 |
| | 427751 | AF000152 | Hs.355816 | conserved gene amplified in osteosarcoma | NIF; TM; | 3.4 |
| | 416971 | R34657 | Hs.80658 | uncoupling protein 2 (mitochondrial | mito_carr; TM; | 3.4 |
| | 428046 | AW812795 | Hs.337534 | ESTs, Moderately similar to I38022 | ank | 3.4 |
| 15 | 456575 | AW063659 | Hs.191649 | ESTs | Myosin_tail | 3.4 |
| | 407366 | AF026942 | Hs.17518 | gb:Homo sapiens cig33 mRNA, partial | IBR | 3.4 |
| | 414738 | L24038 | Hs.77183 | v-rat murine sarcoma 3611 viral onc | pk kinase, DAG_PE-bind, RBD; T | 3.4 |
| | 456356 | M74715 | Hs.89560 | iduronidase, alpha-L- | Glyco_hydro_39; SS | 3.3 |
| | 429668 | AA626142 | Hs.179991 | ESTs, Weakly similar to S28942 prot | | 3.3 |
| 20 | 404913 | | | NM_024408: Homo sapiens Notch (Dros | EGF, ank, notch, metalthio, E | 3.3 |
| | 426059 | BE292842 | Hs.166120 | interferon regulatory factor 7 | IRF; SS | 3.3 |
| | 451619 | AA018854 | Hs.353196 | glutathione peroxidase 3 (plasma) | Ph; SS | 3.3 |
| | 410225 | AW608964 | Hs.12030 | ESTs | | 3.3 |
| | 402534 | | | Target Exon | | 3.3 |
| 25 | 433750 | H15448 | Hs.31330 | Homo sapiens clone HQ0319 | GLFV_dehydrog, GLFV_dehydr | 3.3 |
| | 421712 | AK000140 | Hs.107139 | hypothetical protein | TM; SS | 3.3 |
| | 433333 | AI016521 | Hs.71816 | v-akt murine thymoma viral oncogene | pk kinase, PH, pk kinase_C | 3.3 |
| | 424915 | R42755 | Hs.23096 | ESTs | rm | 3.3 |
| | 408494 | AA554714 | Hs.187578 | Homo sapiens cDNA FLJ11639 fis, cdo | | 3.3 |
| 30 | 445084 | H38914 | Hs.250848 | hypothetical protein FLJ14761 | TM; SS | 3.3 |
| | 446478 | AI950021 | Hs.370306 | ESTs | TM; | 3.3 |
| | 425274 | BE281191 | Hs.155462 | minichromosome maintenance deficien | MCM; TM; | 3.3 |
| | 456655 | AI376736 | Hs.111779 | secreted protein, acidic, cysteine- | kazat; SS | 3.3 |
| | 438912 | AF085843 | | gb:Homo sapiens full length insert | | 3.3 |
| 35 | 428396 | U70539 | Hs.184161 | exostosins (multiple) 1 | Exostosin; TM; SS | 3.3 |
| | 437546 | AW074836 | Hs.173984 | T-box 1 | T-box, WD40; TM; | 3.3 |
| | 410693 | BE044206 | | gb:ho40c08.x1 Soares_NFL_T_GBC_S1 H | C1q, Collagen, cystati | 3.3 |
| | 414961 | U27266 | Hs.927 | myosin-binding protein H | tn3; ig; TM; | 3.3 |
| | 422766 | AA334108 | Hs.159572 | heparan sulfate (glucosamine) 3-O-s | | 3.3 |
| 40 | 426120 | AA325243 | Hs.166887 | copine 1 | C2, rm; TM; | 3.3 |
| | 452383 | T70900 | Hs.27189 | ESTs | zf-C2H2, PRK | 3.3 |
| | 456799 | AC004923 | Hs.135187 | unc93 (C.elegans) homolog B | TM; | 3.3 |
| | 409227 | AA806165 | Hs.130323 | Homo sapiens, clone IMAGE:3960432, | NA; NA | 3.3 |
| | 432659 | AA281633 | Hs.278586 | KIAA1108 protein | TBC; TM; | 3.3 |
| | 448997 | AA130390 | Hs.25549 | hypothetical protein FLJ20898 | TM; SS | 3.3 |
| 45 | 446990 | AI354717 | Hs.223908 | ESTs | transmembrane4 | 3.3 |
| | 437259 | AI377755 | Hs.120695 | ESTs | MHC_II_alpha, ig | 3.3 |
| | 423461 | AB020527 | Hs.128827 | solute carrier family 17 (sodium ph | sugar_tr; TM; | 3.3 |
| | 421563 | NM_006433 | Hs.105806 | granulysin | ; SS | 3.3 |
| 50 | 453804 | AA300204 | Hs.35276 | KIAA0852 protein | TM; | 3.3 |
| | 428810 | AF068236 | Hs.193788 | nitric oxide synthase 2A (inducible | NAD_binding, flavodoxin, FA | 3.3 |
| | 453933 | AI452933 | Hs.65377 | ESTs | EF_TS, UBA, transmembr | 3.3 |
| | 449267 | AI638640 | Hs.220624 | ESTs | | 3.3 |
| | 418165 | R45959 | Hs.6637 | ESTs | mito_carr | 3.3 |
| 55 | 446673 | NM_016361 | Hs.15871 | LPAP for lysophosphatidic acid phos | acid_phosphat; TM; SS | 3.3 |
| | 402475 | | | ubiquitin specific protease 18 | : | 3.2 |
| | 404233 | | | Target Exon | HIT | 3.2 |
| | 406655 | M21533 | Hs.277477 | major histocompatibility complex, c | ig, MHC_I; TM; SS | 3.2 |
| 60 | 414556 | AW975063 | Hs.343443 | ribosomal protein L36 | Ribosomal_L36e; | 3.2 |
| | 450191 | AW137243 | Hs.248074 | ESTs | homeobox; TM; | 3.2 |
| | 435906 | AI686379 | Hs.110796 | SAR1 protein | arf, ras; TM; | 3.2 |
| | 412540 | C18341 | Hs.73999 | thyroid hormone receptor interactor | SH3, FCH; SS | 3.2 |
| | 422562 | AI962060 | Hs.118397 | AE-binding protein 1 | Zn_carbOpept, F5_F8_type_C | 3.2 |
| | 431051 | AA491143 | Hs.283374 | ESTs, Weakly similar to CA15_HUMAN | TM; | 3.2 |
| 65 | 407984 | AW134708 | Hs.243569 | ESTs | | 3.2 |
| | 441494 | AW452344 | Hs.129977 | ESTs | | 3.2 |
| | 423114 | AU076497 | Hs.1614 | cholinergic receptor, nicotinic, al | Neur_chan_LBD, Neur_chan_m | 3.2 |
| | 419833 | AA251131 | Hs.220697 | ESTs | WHEP-TRS, IRNA-synt_1b, non | 3.2 |
| | 419036 | T80957 | Hs.372603 | gb:yd23112.s1 Soares fetal liver sp | | 3.2 |
| 70 | 431222 | X56777 | Hs.273790 | zona pellucida glycoprotein 3A (spe | zona_pellucida; TM; SS | 3.2 |
| | 453094 | AA740928 | Hs.27356 | ESTs | | 3.2 |
| | 426989 | AI815206 | Hs.367644 | ESTs | BAG, ubiquitin | 3.2 |
| | 445033 | AV652402 | Hs.72901 | cyclin-dependent kinase inhibitor 2 | ank; | 3.2 |
| | 446272 | BE268912 | Hs.14601 | hematopoietic cell-specific Lyn sub | SH3, HS1_rep; TM; | 3.2 |
| 75 | 438930 | AW843633 | Hs.343261 | hypothetical protein AL110115 | HLH | 3.2 |
| | 438183 | BE263252 | Hs.6101 | hypothetical protein MGC3178 | thioredox; TM; | 3.2 |
| | 421310 | AW630087 | Hs.103315 | trinucleotide repeat containing 1 | PHD | 3.2 |
| | 409293 | R02673 | Hs.110156 | ESTs | | 3.2 |
| 80 | 407115 | AA084921 | Hs.76230 | ribosomal protein S10 | S10_plectin; TM; | 3.2 |
| | 401174 | | | Target Exon | transmembrane4, EF_TS, UBA | 3.2 |
| | 400217 | | | Eos Control | ras; SS | 3.2 |
| | 408676 | AI815189 | Hs.57475 | sex comb on midleg homolog 1 | | 3.2 |
| | 418245 | AA088767 | Hs.83883 | transmembrane, prostate androgen in | TM; SS | 3.2 |
| | 403694 | | | Target Exon | UDPGT | 3.2 |

| | | | | | | |
|----|--------|-----------|-----------|-------------------------------------|-------------------------------|-----|
| 5 | 414265 | BE410411 | Hs.75864 | endoplasmic reticulum glycoprotein | | |
| | 451118 | AJ862096 | Hs.60640 | ESTs | EGF, vwc, TIL;SS | 3.2 |
| | 422624 | BE516678 | Hs.76152 | KDEL (Lys-Asp-Glu-Leu) endoplasmic | ER_lumen_recept | 3.2 |
| | 437388 | AL359586 | Hs.14478 | Homo sapiens mRNA; cDNA DKFZp762H18 | | 3.2 |
| | 429150 | AF120103 | Hs.197366 | smoothed (Drosophila) homolog | COX8, SHMT, MIF, GST_C, EF1G, | 3.2 |
| | 430379 | AF134149 | Hs.240395 | potassium channel, subfamily K, mem | ion, trans;TM;SS | 3.2 |
| | 434956 | BE266566 | Hs.4268 | hypothetical protein DKFZp434K046 | Cullin;TM; | 3.2 |
| | 422166 | W72424 | Hs.112405 | S100 calcium-binding protein A9 (ca | efhand, S_100;TM; | 3.2 |
| 10 | 452493 | A1904031 | Hs.106826 | KIAA1696 protein | PHD, Myc-LZ, DC1, AT_hook;TM | 3.2 |
| | 413100 | BE065208 | | gb:RC1-BT0314-310300-015-b09 BT0314 | | 3.2 |
| | 420764 | BE250676 | Hs.19928 | hypothetical protein SP329 | F-box;TM; | 3.2 |
| | 421680 | AL031186 | Hs.289106 | Human DNA sequence from clone CTA-9 | Collagen;TM;SS | 3.2 |
| | 406738 | AA587983 | | gb:nj30b09.s1 NCI_CGAP_AA1 Homo sap | TM, Ribosomal_S5;TM;SS= | 3.2 |
| 15 | 434288 | AW189075 | Hs.116265 | fibrillin3 | EGF, granulin, TB, EB, TIL;TM | 3.1 |
| | 438264 | T86773 | Hs.6133 | calpain 5 | Calpain_III, Peptidase_C2, | 3.1 |
| | 436819 | AA731746 | Hs.120232 | ESTs | mm | 3.1 |
| | 459298 | R86701 | | gb:ym86d09.r1 Soares adult brain N2 | TM; | 3.1 |
| 20 | 452127 | BE562126 | Hs.28081 | eukaryotic translation initiation f | mm, 7tm_1, SNF;TM; | 3.1 |
| | 422305 | A1928242 | Hs.293438 | ESTs, Highly similar to AF198488 1 | | 3.1 |
| | 414393 | AA146855 | | gb:zo41h10.r1 Stratagene endothelia | | 3.1 |
| | 423369 | BE219099 | Hs.279513 | ESTs | | 3.1 |
| | 429457 | BE243065 | Hs.202955 | hypothetical protein FLJ20507 | Cys-protease-3C;TM; | 3.1 |
| | 409124 | AW292809 | Hs.50727 | N-acetylglucosaminidase, alpha- (Sa | TM;SS | 3.1 |
| 25 | 429615 | AF258627 | Hs.211562 | ATP-binding cassette, sub-family A | ABC_tran;TM;SS | 3.1 |
| | 445519 | A1635202 | Hs.170132 | hypothetical protein FLJ22494 | TM; | 3.1 |
| | 410007 | AW950887 | Hs.57813 | zinc ribbon domain containing, 1 | TFIIS;TM; | 3.1 |
| | 407228 | M25079 | Hs.155376 | hemoglobin, beta | globin;TM; | 3.1 |
| | 411573 | AB029000 | Hs.70823 | KIAA1077 protein | Sulfatase;TM; | 3.1 |
| 30 | 406654 | M90686 | Hs.73885 | HLA-G histocompatibility antigen, c | ig, MHC_1;TM;SS | 3.1 |
| | 435072 | AW592176 | Hs.116932 | ESTs | zf-RanBP, MDM2 | 3.1 |
| | 456642 | AW451623 | Hs.109752 | putative c-Myc-responsive | :SS | 3.1 |
| | 445457 | AF168793 | Hs.12743 | camitine O-octanoyltransferase | Car_n_acyltransf;TM; | 3.1 |
| | 448389 | AW188950 | Hs.345838 | ESTs | ZOG-Fel1_Oxy, mm, SH3, ras | 3.1 |
| 35 | 458248 | BE407379 | Hs.108082 | ESTs, Weakly similar to T31636 hypo | C1q, Collagen;TM;SS | 3.1 |
| | 451310 | AW250651 | Hs.26213 | Human DNA sequence from clone RP3-4 | TM; | 3.1 |
| | 414688 | A1750246 | Hs.76901 | for protein disulfide isomerase-rel | thiorel;SS | 3.1 |
| | 428797 | AA496205 | Hs.193700 | Homo sapiens mRNA; cDNA DKFZp586I03 | UM, Ran_BP1, GRIP, TPR, pro_ | 3.1 |
| | 425067 | BE223071 | Hs.169142 | ESTs | | 3.1 |
| 40 | 410639 | BE269047 | Hs.65234 | hypothetical protein FLJ20596 | DEAD, helicase_C, PRK, AIP3; | 3.1 |
| | 413011 | AW068115 | Hs.821 | biglycan | LRR, LRRNT;SS | 3.1 |
| | 421502 | AF111856 | Hs.105039 | solute carrier family 34 (sodium ph | Ribosomal_L20, Na_Pi, cotra | 3.1 |
| | 447164 | AF026941 | Hs.17518 | viprin; similar to inflammatory r | MoaA, NifB_PqqE;TM; | 3.1 |
| | 414907 | X90725 | Hs.77597 | polo (Drosophila)-like kinase | Ribosomal_L37ae, kinase, P | 3.1 |
| 45 | 418613 | AA744529 | Hs.86575 | mitogen-activated protein kinase ki | pkase, CNH;TM; | 3.1 |
| | 406734 | A1565616 | | gb:to16h12.x1 NCI_CGAP_U12 Homo sap | | 3.1 |
| | 410188 | AL096739 | Hs.107260 | hypothetical protein DKFZp586H0623 | Ricin_B_lectin, Glycos_tra | 3.1 |
| | 437959 | AA72068 | Hs.375604 | KIAA1856 protein | elf5, elf2B, W2;TM; | 3.1 |
| | 406764 | AA429825 | Hs.343443 | ribosomal protein L36 | Ribosomal_L36e; | 3.1 |
| 50 | 406637 | U14966 | Hs.180946 | ribosomal protein L5 | Ribosomal_L18p; | 3.1 |
| | 451080 | H41082 | Hs.271783 | ESTs | ig, MHC_II_alpha;TM;SS | 3.1 |
| | 414875 | H42679 | Hs.77522 | major histocompatibility complex, c | DENN, dDENN, uDENN;TM;SS= | 3.1 |
| | 416365 | U15131 | Hs.79265 | suppression of tumorigenicity 5 | ig, MHC_II_beta;TM;SS | 3.1 |
| | 400261 | | | Eos Control | G-alpha, arf;TM; | 3.1 |
| 55 | 412270 | AC005262 | Hs.73797 | guanine nucleotide binding protein | | 3.1 |
| | 456843 | BE301883 | Hs.152707 | glioblastoma amplified sequence | C1q, Collagen;SS | 3.1 |
| | 443071 | AL080021 | Hs.8986 | complement component 1, q subcomp | efhand;SS | 3.1 |
| | 426196 | BE272095 | Hs.167791 | reticulocalbin 1, EF-hand calcium b | cadherin;TM;SS | 3.1 |
| 60 | 424010 | AL080188 | Hs.137556 | Homo sapiens mRNA; cDNA DKFZp434A13 | Ham1p_like;TM; | 3.1 |
| | 439975 | AW328081 | Hs.6817 | inosine triphosphatase (nucleoside | | 3.1 |
| | 450761 | R75930 | Hs.174838 | Homo sapiens cDNA FLJ14192 fs, clo | Y_phosphatase, DSPc;TM;S | 3.1 |
| | 418322 | AA284166 | Hs.84113 | cyclin-dependent kinase inhibitor 3 | Xlink, zf-CCCH, G_patch, non | 3.1 |
| | 432396 | AW295956 | Hs.11900 | hypothetical protein FLJ14972 | | 3.1 |
| | 407904 | W44735 | Hs.107260 | Homo sapiens cDNA: FLJ21278 fs, d | WD40 | 3.1 |
| 65 | 452500 | AW373011 | Hs.54558 | hypothetical protein FLJ22222 | lectin_c;TM;SS | 3.1 |
| | 432171 | A1202503 | Hs.343661 | ESTs, Weakly similar to ALUB_HUMAN | Ribosomal_L14; | 3.0 |
| | 416768 | AA363733 | Hs.1032 | regenerating islet-derived 1 alpha | TM;SS | 3.0 |
| | 442492 | AA528489 | Hs.234518 | ribosomal protein L23 | RA, Band_7, MBOAT | 3.0 |
| | 421210 | U80016 | Hs.102598 | mucosal vascular addressin cell adh | Acyl-CoA_hydro;TM; | 3.0 |
| 70 | 439429 | AF150286 | | gb:AF150286 Human mRNA from cd34 st | AlpC-TSA, SET, MBD;TM;SS= | 3.0 |
| | 447463 | AW378685 | Hs.18625 | Mitochondrial Acyl-CoA Thioesterase | | 3.0 |
| | 448352 | AA337951 | Hs.20991 | SET domain, bifurcated 1 | Pep_M12B_propep, tsp_1, Rep | 3.0 |
| | 428291 | AA534009 | Hs.183487 | interferon stimulated gene (20kD) | SPRY, zf-B_box, zf-C3HC4;TM | 3.0 |
| | 445669 | A1570830 | Hs.174870 | ESTs | | 3.0 |
| | 452862 | AW378065 | Hs.8687 | ADAMTS2 (a disintegrin-like and me | Ribosomal_L4;TM; | 3.0 |
| 75 | 430069 | A1219293 | Hs.293660 | Homo sapiens, clone IMAGE:3535476, | WD40, DUF6; | 3.0 |
| | 451028 | AA021258 | Hs.123073 | ESTs | crystalin;TM; | 3.0 |
| | 446021 | BE389213 | Hs.286 | ribosomal protein L4 | Rhodanese;SS | 3.0 |
| | 434652 | AF148713 | Hs.125830 | bladder cancer overexpressed protei | G_glu_transpept;TM;SS | 3.0 |
| 80 | 425829 | AL133079 | Hs.134126 | crystallin, gamma S | WD40;TM; | 3.0 |
| | 424909 | S78187 | Hs.153752 | cell division cycle 25B | CUB, MAM, F5, F8_type_C | 3.0 |
| | 423579 | NM_004121 | Hs.1675 | gamma-glutamyltransferase-like acti | | 3.0 |
| | 444652 | BE513613 | Hs.11538 | actin related protein 2/3 complex, | | 3.0 |
| | 441283 | AA927670 | Hs.131704 | ESTs | | 3.0 |

| | | | | | | |
|------------|--------------|--|---|--|---------------------------|-----|
| 5 | 437415 | AL137400 | Hs.306456 | pre-mRNA processing factor 18 | Band_41,hormone2,Prp18;TM | 3.0 |
| | 444542 | AI161293 | Hs.280380 | aminopeptidase | NAD_binding,flavodoxin,FA | 3.0 |
| | 442426 | AI373062 | Hs.332938 | hypothetical protein MGC5370 | zf-RanBP,MDM2 | 3.0 |
| | 447910 | AL137679 | Hs.20000 | Homo sapiens mRNA; cDNA DKFZp434D24 | Exonuclease,SS | 3.0 |
| | 426858 | NM_004182 | Hs.172791 | ubiquitously-expressed transcript | DUF232,SS | 3.0 |
| | 445417 | AK001058 | Hs.12680 | a disintegrin-like and metalloprote | tsf_1,Reprolysin,Pep_M12B | 3.0 |
| | 430482 | AF131810 | Hs.241545 | hypothetical protein | TM;SS | 3.0 |
| | 427661 | AA410292 | Hs.104761 | ESTs | wnt1 | 3.0 |
| | 451876 | T63141 | | gby:b99a12.s1 Stratagene lung (9372 | SH3 | 3.0 |
| 10 | 453852 | AL137493 | Hs.35945 | Homo sapiens mRNA; cDNA DKFZp434B12 | ig;TM; | 3.0 |
| | 452965 | AI904779 | Hs.247525 | Human DNA sequence from clone RP11- | C2,PHD,RPH3A_effector,zf- | 3.0 |
| | 441455 | AJ271671 | Hs.7854 | zinc/ferron regulated transporter-like | Zip;TM;SS | 3.0 |
| | 452600 | AI910842 | Hs.103381 | ESTs | Exo_endo_phos | 3.0 |
| | 450775 | AA902384 | Hs.73853 | bone morphogenetic protein 2 | TGFb_propeptide,TGF-beta, | 3.0 |
| 15 | 417634 | WZ7202 | Hs.82327 | glutathione synthetase | GSH_synthase;TM; | 3.0 |
| | 415152 | WZ2644 | Hs.278712 | Homo sapiens cDNA FLJ11074 fis, clo | | 3.0 |
| | 410093 | AW589558 | Hs.295883 | ESTs, Weakly similar to KIAA0970 pr | | 3.0 |
| | 412404 | AW075995 | Hs.86228 | TRIAD3 protein | | 3.0 |
| 20 | 443466 | BE243123 | Hs.321045 | IKK-related kinase epsilon; inducib | pkinese,RIO1;TM; | 3.0 |
| TABLE 29B: | | | | | | |
| | Pkey: | Unique Eos probeset identifier number | | | | |
| | CAT number: | Gene cluster number | | | | |
| | Accession: | Genbank accession numbers | | | | |
| 25 | Pkey | CAT Number | Accession | | | |
| | 458147 | 1030220_1 | AW848781 AW848490 AW849062 AW752597 AW752699 | | | |
| | 406855 | 0_0 | AA902829 | | | |
| 30 | 400233 | 11259_1 | BC004324 NM_001020 BC007977 M60854 BM050628 BG829809 BE385504 BG744451 BI826914 BE440007 BI260656 BE395117 BE389334 | | | |
| | | | BE255792 BI194169 BI668218 BI194376 BG716213 BG714408 BE392513 AV722219 AW328077 BM424171 BI828267 AW958606 BG831252 | | | |
| | | | BE392943 BE394033 BI858915 BI668334 BE621019 BG706995 BE791985 BF967484 BI193635 BG761859 BM466537 BG747165 BG827488 AI133550 | | | |
| | | | BM011511 BI227282 BG489212 BG478388 BE727789 BI160880 BG831707 BG324692 BM470427 BI083899 BG831605 BG754114 BG420536 | | | |
| | | | BF308210 BE384213 BG832271 BG828032 BG481641 BF205675 BE899041 BE271558 BI193807 BI159866 BG473786 BG397178 BI194428 BI117210 | | | |
| 35 | | | BG768326 BG759507 BF975645 BF343657 BM020598 BG831082 BG829943 BG829501 BF306557 BE562511 BM050145 BM017978 BI193934 | | | |
| | | | BI160764 BI160371 BG754991 BF973348 BF663234 BF032537 BE388168 BM009051 BI192794 BG831002 BG830459 BG764737 BG761808 | | | |
| | | | BG481705 BG104314 BM464565 BI261500 BG831857 BG831684 BG829852 BG765030 BG760419 BG760268 BG749762 BG480900 BG419627 | | | |
| | | | BG248771 BF975542 BM042233 BI161149 BG831302 BG830033 BG829626 BM050064 BI193014 BI161360 BG822729 BG110091 BG106500 | | | |
| 40 | | | BI258369 BG831982 BM458301 BM019513 BI161350 BI114178 BG481969 BG474870 BF974048 BF971122 BE741405 BE395269 BG832027 | | | |
| | | | BG831469 BG490895 BM413638 BG943529 BG831012 BG829471 BG686284 BG337575 BG336551 BF206677 BI258301 BI160946 BG105893 | | | |
| | | | BF183072 BM459542 BI193881 BG832043 BG831323 BI194545 BI160968 BG755930 BG706018 BE743865 BM465145 BG831227 BG774290 | | | |
| | | | BF683451 BE907161 BM045391 BI194396 BI161269 BG747091 BG546643 BF984863 BI160206 BI226402 BI226336 AW328236 BG339458 BF972634 | | | |
| | | | BE909808 BI160988 BI160251 BG828764 BG826860 BG758360 BF568228 BI182822 BI457127 BG831491 BG759864 AI830010 BF568381 BE907238 | | | |
| 45 | | | BI161172 BI116773 BG827153 BG825088 BG335419 BG109404 AI929068 BE906354 BE408564 BM045000 BG339617 BG282794 BG335767 | | | |
| | | | BE907263 BF568921 BG829961 BG479305 BG260397 AI922228 BE301975 AW516055 BG480919 BG480626 AW196817 BG336261 BE906157 | | | |
| | | | BE395717 BE391427 BI192954 BG829757 BG476379 BE301536 BE394727 BE257695 BE905344 AI433577 BE894416 BE886992 BE409223 | | | |
| | | | BF034756 BE904077 BG830886 BE909153 BE907998 BE395767 AI871751 BE744523 BI192663 BG831669 AI000225 BE743836 BE272515 AA628078 | | | |
| | | | BM463802 BE393375 BE393033 AW170187 BE730961 BE395410 BE744572 BE392297 BE391448 BE390780 BE388821 BE258477 BE905970 | | | |
| 50 | | | BE901567 BE898833 BE880326 BF726889 BE910504 BE390753 BE390131 AA650542 BE744156 BE394125 BE742207 BE395265 BE392942 | | | |
| | | | BE894336 BE378222 BE906926 BE904650 BE393704 BE620999 BE515162 BE378753 BE272370 BE907458 BE612801 BE392484 BE907636 | | | |
| | | | BE907353 BE910491 BE909796 BE905331 AW248173 AI683576 BE908826 BE620180 BF037570 BE908312 BE615015 BE256977 BE746875 | | | |
| | | | BE394133 BE391478 BE910068 BE907185 BE742109 AA995746 BE561195 BE908825 BE906472 BE906509 BE906017 BE910442 BE514657 | | | |
| | | | BI261969 BE741707 BE392216 BM042793 BF570283 BI262119 BE395707 BE378298 AW327827 BE394422 BF569178 BE263240 AI700512 | | | |
| 55 | | | BG830290 BF569308 BF569156 BI194587 BE390831 BG745096 AI681675 BE395674 AA136372 BE279892 AA442822 BE384898 AA313519 AI878866 | | | |
| | | | AA305904 F33366 BE394852 F29153 F33618 AI133637 AA300009 F34063 F29455 AU099691 AI905085 AI906656 AA343249 BE388691 AW404280 | | | |
| | | | AA379888 F29022 BF089981 F31013 F24305 | | | |
| | 438912 | 4071_1 | AF085843 R70623 R70523 | | | |
| | 410693 | 1054267_1 | BE044206 AW797320 BE161676 AW797356 AW797352 | | | |
| | 413100 | 1490226_1 | BE065224 BE065168 BE065313 BE065208 | | | |
| 60 | 406738 | 0_0 | AA587983 | | | |
| | 459298 | 90831_2 | AL157655 BF802216 R86701 BF802224 R84600 BF356151 BG982935 | | | |
| | 414393 | 15833_3 | AL532972 BI092731 AI765546 AA393801 AI129669 AI393538 AW519008 AI432598 AW295856 AI650941 AI470541 AL550388 AA146856 AI074762 | | | |
| | | | BE895187 AA393867 BI052082 | | | |
| | 406734 | 0_0 | AI565616 AI190141 | | | |
| 65 | 400261 | 23110_1 | BC006097 X03066 NM_002120 M26040 AW469119 AW469127 AI299772 AW518149 AI144456 AW628070 AI629032 AI358810 AI880433 AI440472 | | | |
| | | | AI357070 AI865365 AW014799 AI767973 AW518041 AA909398 AW768606 | | | |
| | 439429 | 452694_1 | AF150286 AV739062 AA835857 | | | |
| | 451876 | 2328579_1 | T63141 AI821021 BF370092 BF370127 BF370060 T62998 | | | |
| TABLE 29C: | | | | | | |
| 70 | Pkey: | Unique number corresponding to an Eos probeset | | | | |
| | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. | | | | |
| | Strand: | Indicates DNA strand from which exons were predicted. | | | | |
| 75 | Nt_position: | Indicates nucleotide positions of predicted exons. | | | | |
| | Pkey | Ref | Strand | Nt_position | | |
| | 401699 | 3176654 | Minus | 33285-34084 | | |
| | 402241 | 7690131 | Minus | 125073-125206,130996-131125 | | |
| | 403364 | 8571785 | Plus | 120351-120465 | | |
| 80 | 405201 | 7230116 | Plus | 36934-37314 | | |
| | 400785 | 8131682 | Plus | 43113-43967 | | |
| | 403943 | 7711864 | Plus | 100742-100904,101322-101503 | | |
| | 404854 | 7143420 | Plus | 14260-14537 | | |

| | | | | |
|----|--------|---------|-------|--|
| 5 | 404243 | 5672609 | Plus | 74695-75123 |
| | 403246 | 7637831 | Minus | 143547-143654,143741-143900 |
| | 404864 | 5263010 | Plus | 94495-94661,95055-95195,97396-97506,9760 |
| | 403252 | 7677983 | Plus | 102214-102692 |
| | 404913 | 7341740 | Plus | 97717-97976 |
| | 402534 | 9801061 | Plus | 58989-59457 |
| | 402475 | 7547191 | Plus | 65363-65725 |
| | 404233 | 8218045 | Minus | 84791-85123 |
| 10 | 401174 | 9438414 | Minus | 132847-133917 |
| | 403694 | 7107765 | Plus | 142925-143080,165505-166186,167486-16763 |

TABLE 30A: ABOUT 282 GENES UP-REGULATED IN GLIOMA COMPARED TO NON-MALIGNANT ADULT BRAIN TISSUES THAT ARE LIKELY TO ENCODE EXTRACELLULAR OR CELL-SURFACE PROTEINS

Table 30A lists about 282 genes up-regulated in glioma compared to non-malignant adult brain tissues that are likely to encode extracellular or cell-surface proteins. These were selected as for Table 28A, except that the ratio of "average" glioma to "average" normal adult tissues was greater than or equal to 4.0, the "average" glioma level was set to the 99th percentile value amongst various glioma specimens, the "average" normal adult brain tissue level was set to the 75th percentile value amongst various non-malignant brain tissues, the "average" glioma value was greater than or equal to 50 units (this selects for the most abundant of the up-regulated genes), and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig, fn3, efg, 7tm domains, signal sequences, transmembrane domains). Predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenID: Unigene number
 Unigene Title: Unigene gene title
 Protein Domains: Predicted Protein Domains
 R1: glioma vs. non-malignant adult brain tissues likely to encode extracellular or cell-surface proteins

| | | | | | | |
|----|--------|-----------|------------|--------------------------------------|---------------------------|------|
| | Pkey | Accession | UniGene ID | Unigene Title | Protein Domains | R1 |
| | 406868 | AA505445 | Hs.300697 | immunoglobulin heavy constant gamma | ig;TM; | 37.6 |
| | 407241 | M34516 | | gb:Human omega light chain protein | TM; | 22.7 |
| 30 | 414477 | U41635 | Hs.76228 | amplified in osteosarcoma | kinase,LRR;TM;SS | 22.7 |
| | 417512 | X76534 | Hs.82226 | glycoprotein (transmembrane) nmb | PKD;TM;SS | 15.4 |
| | 406803 | H42321 | Hs.163593 | ribosomal protein L18a | Ribosomal_L18a;TM; | 14.2 |
| | 429707 | W76631 | Hs.211819 | matrix metalloproteinase 23B | ig,Peptidase_M10;TM;SS= | 12.8 |
| 35 | 419092 | J05581 | Hs.89603 | mucin 1, transmembrane | SEA;TM;SS | 12.8 |
| | 414738 | L24038 | Hs.77183 | v-rat murine sarcoma 3611 viral onc | kinase,DAG_PE-bind,RBD;T | 12.4 |
| | 441384 | AA447849 | Hs.288660 | Homo sapiens cDNA: FLJ22182 ts, cl | 7tm_3;none | 11.6 |
| | 406621 | X57809 | Hs.181125 | immunoglobulin lambda locus | ig,HSP70,Ppx-GppA;TM;SS | 11.0 |
| | 410584 | AB011112 | Hs.64742 | KIAA0540 protein | none | 11.0 |
| 40 | 426395 | BE151985 | Hs.355669 | hypothetical protein FLJ23316 | kinase,none | 10.7 |
| | 425184 | BE278288 | Hs.155048 | Lutheran blood group (Aubergier b an | ig;TM;SS | 10.7 |
| | 430379 | AF134149 | Hs.240395 | potassium channel, subfamily K, mem | ion_trans;TM;SS | 10.3 |
| | 408972 | AL050100 | Hs.49378 | DKFZP586D0919 protein | TM; | 9.9 |
| | 446921 | AB012113 | Hs.16530 | small inducible cytokine subfamily | IL8;SS | 9.9 |
| 45 | 452862 | AW378065 | Hs.8687 | ADAMTS2 (a disintegrin-like and me | Pep_M12B_propep,isp_1,Rep | 9.7 |
| | 418101 | AL047476 | Hs.296310 | gap junction protein, alpha 4, 37kD | connexin;TM;SS | 8.5 |
| | 400290 | H18836 | Hs.31608 | hypothetical protein FLJ20041 | Cys_knot | 8.4 |
| | 401699 | | | Target Exon | TM; | 8.1 |
| | 423309 | BE006775 | Hs.126782 | sushi-repeat protein | sushi,HYR;SS | 8.1 |
| 50 | 427600 | AW630918 | Hs.179774 | proteasome (prosome, macropain) act | PA28_alpha,PA28_beta; | 7.9 |
| | 436906 | H95990 | Hs.181244 | major histocompatibility complex, c | ig,MHC_I;TM;SS | 7.8 |
| | 425335 | BE394327 | Hs.296267 | folistatin-like 1 | efhand,kazal,arf,ras,7tm_ | 7.7 |
| | 413011 | AW068115 | Hs.821 | biglycan | LRR,LRRNT;SS | 7.7 |
| | 446295 | AI355029 | Hs.101660 | ESTs, Weakly similar to T14171 atax | LIM | 7.7 |
| 55 | 436398 | H87136 | Hs.5174 | ribosomal protein S17 | Ribosomal_S17e,PolyA_pol; | 7.6 |
| | 435013 | H91923 | Hs.110024 | NM_020142:Homo sapiens NADH:tubiquin | none | 7.4 |
| | 431809 | AI623488 | Hs.333488 | Homo sapiens, clone IMAGE:3603998, | TM;SS | 7.4 |
| | 424608 | X80695 | Hs.151134 | oxidase (cytochrome c) assembly 1-1 | 60KD_IMP;TM; | 7.3 |
| | 438560 | AA481690 | Hs.300697 | immunoglobulin heavy constant gamma | ig | 7.3 |
| 60 | 429297 | X82494 | Hs.198862 | fibulin 2 | EGF_ANATO,TIL,spidertoxin | 7.3 |
| | 450463 | AW952018 | Hs.201398 | G protein coupled receptor interact | C1q,Collagen;TM;SS | 7.2 |
| | 417342 | W40277 | Hs.81994 | glycophorin C (Gerbich blood group) | TM; | 7.2 |
| | 414688 | AI750246 | Hs.76901 | for protein disulfide isomerase-rel | thiorel;SS | 7.2 |
| | 414044 | BE614194 | Hs.75721 | profilin 1 | profilin;TM; | 7.1 |
| 65 | 404864 | | | NM_025204:Homo sapiens hypothetica | ; | 7.1 |
| | 452127 | BE562126 | Hs.28081 | eukaryotic translation initiation I | rm,7tm_1,SNF;TM; | 7.0 |
| | 412115 | AK001763 | Hs.73239 | hypothetical protein FLJ10901 | SS | 7.0 |
| | 409826 | AW501112 | Hs.353013 | hypothetical protein FLJ23412 | none | 6.9 |
| | 434343 | AW955705 | Hs.3804 | DKFZP564C1940 protein | Idl_recept_a;TM; | 6.9 |
| 70 | 427714 | AF119850 | Hs.2186 | eukaryotic translation elongation I | COX8,SHMT,MIF,GST_C,EF1G_ | 6.9 |
| | 437259 | AI377755 | Hs.120695 | ESTs | MHC_II_alpha,ig,none | 6.9 |
| | 429212 | NM_001504 | Hs.198252 | G protein-coupled receptor 9 | 7tm_1;TM; | 6.8 |
| | 448988 | Y09763 | Hs.22785 | gamma-aminobutyric acid (GABA) A re | Neur_chan_LBD,Neur_chan_m | 6.8 |
| | 423505 | AF064090 | Hs.129708 | tumor necrosis factor (ligand) supe | TNF;TM;SS | 6.8 |
| 75 | 413053 | AW963263 | Hs.65377 | ESTs, Moderately similar to KIAA139 | TM; | 6.7 |
| | 430542 | AI557486 | Hs.119122 | ribosomal protein L13a | Ribosomal_L13,LACT,arf,ra | 6.7 |
| | 435906 | AI686379 | Hs.110796 | SAR1 protein | arf,ras;TM; | 6.6 |
| | 429307 | AU076592 | Hs.198951 | jun B proto-oncogene | bZIP;TM; | 6.4 |
| | 437388 | AL359586 | Hs.14478 | Homo sapiens mRNA: cDNA DKFZp762H18 | none | 6.4 |
| 80 | 415714 | NM_002290 | Hs.78672 | laminin, alpha 4 | laminin_EGF,laminin_G,Tro | 6.3 |
| | 406733 | AA976565 | Hs.297753 | vimentin | filamentbZIP_Apofipoprot | 6.3 |
| | 411296 | BE207307 | Hs.10114 | growth suppressor 1 | ZOG-Fell_Oxy;TM;SS | 6.3 |
| | 441321 | H17182 | Hs.7771 | B-cell associated protein | Band_7;TM; | 6.3 |
| | 444637 | T19101 | Hs.11494 | fibulin 5 | EGF,TIL,SS | 6.3 |

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|----|--------|-----------|-----------|--------------------------------------|
| 5 | 413731 | BE243845 | Hs.75511 | connective tissue growth factor |
| | 422901 | R81936 | Hs.374568 | ribosomal protein L44 |
| | 430397 | AJ924533 | Hs.105607 | bicarbonate transporter related pro |
| | 429630 | M85289 | Hs.211573 | heparan sulfate proteoglycan 2 (per |
| | 434867 | AF159442 | Hs.103382 | phospholipid scramblase 3 |
| | 431449 | M55994 | Hs.256278 | tumor necrosis factor receptor supe |
| | 440676 | NM_004987 | Hs.112378 | LM and senescent cell antigen-like |
| | 424658 | NM_002406 | Hs.151513 | mannosyl (alpha-1,3)-glycoprotein |
| 10 | 439310 | AF086120 | Hs.102793 | ESTs |
| | 410169 | AI373741 | Hs.59384 | hypothetical protein MGC3047 |
| | 423007 | AA320134 | Hs.196029 | Homo sapiens mRNA for KIAA1657 prot |
| | 414265 | BE410411 | Hs.75864 | endoplasmic reticulum glycoprotein |
| | 427715 | BE245274 | Hs.180428 | KIAA1181 protein |
| 15 | 409220 | BE243323 | Hs.51233 | tumor necrosis factor receptor supe |
| | 450690 | AA296696 | Hs.333418 | FXD domain-containing ion transpor |
| | 433848 | AF095719 | Hs.93764 | carboxypeptidase A4 |
| | 446404 | AA019961 | Hs.26216 | LOC50627 |
| | 441641 | AIG50417 | Hs.247068 | ESTs, Moderately similar to ALU8_HU |
| 20 | 418875 | W19971 | Hs.233459 | ESTs |
| | 424748 | AA346257 | Hs.134933 | ESTs |
| | 439737 | AJ751438 | Hs.41271 | Homo sapiens collagen, type VIII, a |
| | 448950 | AF288687 | Hs.9275 | CGI-152 protein |
| | 406654 | M90686 | Hs.73885 | HLA-G histocompatibility antigen, c |
| 25 | 423084 | ALU076474 | Hs.123178 | translocase of inner mitochondrial |
| | 402241 | | | Target Exon |
| | 425157 | NM_006227 | Hs.283007 | phospholipid transfer protein |
| | 428343 | ALD43021 | Hs.12705 | ESTs |
| | 447990 | BE048821 | Hs.20144 | small inducible cytokine subfamily |
| 30 | 412607 | Z33642 | Hs.74115 | immunoglobulin superfamily, member |
| | 447625 | AW505364 | Hs.19074 | LATS (large tumor suppressor, Dros |
| | 408056 | AA312329 | Hs.42331 | ephrin-A4 |
| | 445960 | A268399 | Hs.140489 | ESTs, Weakly similar to LINC1_HUMAN |
| | 406874 | AW161706 | Hs.180842 | ribosomal protein L13 |
| 35 | 418558 | AW082266 | Hs.86131 | Fas (TNFRSF6)-associated via death |
| | 414638 | W03516 | Hs.76698 | stress-associated endoplasmic retic |
| | 409190 | AU076536 | Hs.50984 | sarcoma amplified sequence |
| | 429150 | AF120103 | Hs.197366 | smoothed (Drosophila) homolog |
| | 453099 | H62087 | Hs.31659 | thyroid hormone receptor-associated |
| 40 | 414443 | ALU077268 | Hs.76144 | platelet-derived growth factor rece |
| | 441283 | AA927670 | Hs.131704 | ESTs |
| | 414249 | AI797994 | Hs.279929 | gp25L2 protein |
| | 451154 | AA015879 | Hs.33536 | ESTs |
| | 406655 | M21533 | Hs.277477 | major histocompatibility complex, c |
| 45 | 406656 | M16714 | Hs.89643 | major histocompatibility complex, c |
| | 449224 | AW995911 | Hs.295883 | hypothetical protein FLJ23399 |
| | 422562 | AI962060 | Hs.118397 | AE-binding protein 1 |
| | 436127 | W94824 | Hs.11565 | RIKEN cDNA 2010100012 gene |
| 50 | 428327 | AW206236 | Hs.28773 | ESTs |
| | 427080 | AW068287 | Hs.301175 | ras-related C3 botulinum toxin subs |
| | 414624 | BE389320 | Hs.23628 | 3 beta-hydroxy-delta 5-C27-steroid |
| | 430281 | AI878842 | Hs.237924 | CGI-69 protein |
| | 426433 | L38969 | Hs.169875 | thrombospondin 3 |
| | 432716 | AI762964 | Hs.205180 | ESTs |
| 55 | 451564 | AU076698 | Hs.132760 | hypothetical protein MGC15729 |
| | 409340 | BE174629 | Hs.321130 | hypothetical protein MGC2771 |
| | 432680 | T47364 | Hs.278613 | interferon, alpha-inducible protein |
| | 404913 | | | NM_024408: Homo sapiens Notch (Dros |
| 60 | 409485 | S80990 | Hs.252136 | ficollin (collagen/fibrinogen domain |
| | 432078 | BE314877 | Hs.24553 | hypothetical protein FLJ12541 simil |
| | 406687 | M31126 | Hs.352054 | matrix metalloproteinase 11 (stroma |
| | 423712 | W46802 | Hs.81988 | disabled (Drosophila) homolog 2 (mi |
| | 441595 | AW206035 | Hs.356457 | ESTs |
| | 450435 | AI695975 | Hs.201805 | ESTs |
| 65 | 443177 | BE268461 | Hs.202 | benzodiazepine receptor (peripheral |
| | 433435 | BE545277 | Hs.340959 | Ts translation elongation factor, m |
| | 426386 | AA748850 | Hs.125830 | bladder cancer overexpressed protei |
| | 419913 | AW270040 | Hs.34455 | ESTs |
| | 446696 | AF279265 | Hs.298476 | solute carrier family 26, member 6 |
| 70 | 448997 | AA130390 | Hs.25549 | hypothetical protein FLJ20898 |
| | 413891 | BE271020 | Hs.355753 | tumor suppressor deleted in oral ca |
| | 453143 | AA382234 | Hs.356289 | protein tyrosine phosphatase, recep |
| | 448249 | AW855331 | Hs.337124 | ESTs |
| | 412819 | T25829 | Hs.24048 | FK506 binding protein precursor |
| 75 | 426059 | BE292842 | Hs.166120 | interferon regulatory factor 7 |
| | 432295 | BE091049 | Hs.343655 | ribosomal protein S15a |
| | 412540 | C18341 | Hs.73999 | thyroid hormone receptor interactor |
| | 414455 | AW270645 | Hs.76194 | ribosomal protein S5 |
| | 456655 | AI376736 | Hs.111779 | secreted protein, acidic, cysteine- |
| 80 | 421794 | X86096 | Hs.108371 | E2F transcription factor 4, p107/p1 |
| | 444824 | AA843575 | Hs.12056 | asialoglycoprotein receptor 1 |
| | 438278 | BE409248 | Hs.57988 | hypothetical protein FLJ22357 simil |
| | 418140 | BE613836 | Hs.83551 | microfibrillar-associated protein 2 |
| | 429457 | BE243065 | Hs.202955 | hypothetical protein FLJ20507 |

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|-------------------------------|-----|
| Cys_knot, tsp_1, vwc, IGFBP; | 6.2 |
| sushi, none | 6.2 |
| HCO3_cotransp; TM; | 6.1 |
| EGF, ig, laminin_B, laminin_ | 6.1 |
| SAPA, Scramblase; TM; SS | 6.1 |
| TNFR_c6; TM; SS | 6.1 |
| UIM; SS | 6.0 |
| GNT-1, Glycos_transf_2; TM= | 5.9 |
| casein_kappa, kinase, ig, n | 5.9 |
| ig; TM; | 5.8 |
| TIMP, none | 5.8 |
| none | 5.8 |
| TM; | 5.8 |
| TNFR_c6, death, Lipoprotein | 5.8 |
| ATP1G1_PLM_MAT8; TM; SS | 5.8 |
| Zn_carbOpept, Propep_M14; T | 5.7 |
| none | 5.7 |
| Pterin_4a, fibrinogen_C, Co | 5.7 |
| Xlink, none | 5.7 |
| none | 5.7 |
| C1q, Collagen, none | 5.7 |
| E1-E2_ATPase, Hydrolase; TM | 5.6 |
| ig, MHC_1; TM; SS | 5.6 |
| rm | 5.6 |
| p450; TM; SS | 5.6 |
| LBP_BPI_CETP, LBP_BPI_CETP | 5.6 |
| WD40; SS | 5.6 |
| IL8; SS | 5.6 |
| ig; TM; SS | 5.5 |
| kinase, kinase_C, UBA, Pol | 5.5 |
| Ephrin; TM; SS | 5.5 |
| zf-C2H2, bZIP, none | 5.5 |
| Ribosomal_L13e; SS | 5.4 |
| death, DED; SS | 5.4 |
| TM; SS | 5.4 |
| transmembrane4; TM; SS | 5.4 |
| COX8, SHMT, MIF, GST_C, EF1G_ | 5.3 |
| WD40; TM; | 5.3 |
| ig, kinase; TM; | 5.3 |
| CUB, MAM, F5_F8_type_C, none | 5.3 |
| Sulfoiransfer, EMP24_GP25L | 5.3 |
| TIMP, none | 5.2 |
| ig, MHC_1; TM; SS | 5.2 |
| transketolase, transket_py | 5.2 |
| fn3; TM; | 5.2 |
| Zn_carbOpept, F5_F8_type_C | 5.2 |
| TM; SS | 5.2 |
| cystatin, Coprogen_oxidase, | 5.2 |
| ras; TM; | 5.2 |
| none | 5.2 |
| mito_carr, homeobox; TM; S | 5.2 |
| TSPN, tsp_3, EGF, toxin; TM | 5.1 |
| LRP, UPAR_LY6; TM; | 5.1 |
| sugar_tr, Condensation; TM= | 5.1 |
| aa_permeases, pyridoxal_de | 5.1 |
| TM; SS | 5.1 |
| EGF, ank, notch, metalthio, E | 5.1 |
| Collagen, fibrinogen_C; TM= | 5.1 |
| TM; SS | 5.1 |
| hemopexin, Peptidase_M10; T | 5.1 |
| PID, MACPF, Jdl_recept_a, ts | 5.0 |
| sugar_tr, none | 5.0 |
| EGF, laminin_B, laminin_EGF | 5.0 |
| TspO_MBR; TM; SS | 5.0 |
| EF_TS, UBA; | 5.0 |
| none | 5.0 |
| EPH_Ibd, fn3, kinase, | 5.0 |
| Sulfate_transp, STAS, xan_u | 5.0 |
| TM; SS | 5.0 |
| none | 5.0 |
| serpin; SS | 5.0 |
| carb_anhydrase, UCH-1, UCH- | 5.0 |
| FKBP; TM; SS | 5.0 |
| IRF; SS | 5.0 |
| Ribosomal_S8, RNase_PH, KH- | 5.0 |
| SH3, FCH; SS | 5.0 |
| Ribosomal_S7; | 5.0 |
| kazal; SS | 5.0 |
| E2F_TDP, KOW, Ribosomal_L14 | 4.9 |
| lectin_c, Tropomyosin; TM | 4.9 |
| TFIIS, RNA_POL_M_15KD, UPF0 | 4.9 |
| TM; SS | 4.9 |
| Cys-protease-3C; TM; | 4.9 |

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|----|--------|-----------|-----------|--------------------------------------|---------------------------|-----|
| 5 | 449475 | A1348027 | Hs.108557 | hypothetical protein PP1057 | transmembrane4;TM;SS | 4.9 |
| | 425274 | BE281191 | Hs.155462 | minichromosome maintenance deficien | MCM;TM; | 4.9 |
| | 442110 | AF113008 | Hs.8102 | ribosomal protein S20 | Ribosomal_S10;TM; | 4.9 |
| | 415209 | F00183 | Hs.172004 | titin | none | 4.9 |
| | 451849 | A199261 | Hs.27191 | hypothetical protein from clone 247 | TM; | 4.9 |
| | 421567 | AJ272137 | Hs.198265 | matrix metalloproteinase 25 | hemopexin;Peptidase_M10;T | 4.9 |
| | 427380 | NM_005534 | Hs.177559 | interferon gamma receptor 2 (interl | fn3;TM;SS | 4.9 |
| | 431303 | AW241605 | Hs.253928 | ESTs | none | 4.9 |
| 10 | 432396 | AW295956 | Hs.11900 | hypothetical protein FLJ14972 | Xlink,zf-CCCH,G-patch,non | 4.9 |
| | 415021 | R54409 | Hs.301693 | Homo sapiens, clone IMAGE:3638994, | none | 4.8 |
| | 430498 | X02910 | Hs.241570 | tumor necrosis factor (TNF) superfam | TNF;TM;SS | 4.8 |
| | 449957 | D31365 | Hs.24220 | hypothetical protein | TM; | 4.8 |
| | 419603 | BE262579 | Hs.91566 | PL6 protein | OMPdecase;TM;SS | 4.8 |
| 15 | 427588 | L25081 | Hs.179735 | ras homolog gene family, member C | ras,none | 4.8 |
| | 421502 | AF111856 | Hs.105039 | solute carrier family 34 (sodium ph | Ribosomal_L20,Na_Pi_cotra | 4.8 |
| | 404854 | | | Target Exon | :SS | 4.7 |
| | 411281 | BE392792 | Hs.4786 | Homo sapiens cDNA: FLJ22849 fis, c | cadherin | 4.7 |
| | 414045 | NM_002951 | Hs.75722 | ribophorin II | gpdh,gpdh_C,pili_assembly | 4.7 |
| 20 | 431830 | Y15645 | Hs.271387 | small inducible cytokine subfamily | IL8;SS | 4.7 |
| | 412896 | AW804157 | Hs.375570 | major histocompatibility complex, c | ig,MHC_II_beta;TM;SS | 4.7 |
| | 429305 | AF095727 | Hs.287832 | myelin protein zero-like 1 | ig,transmembrane4;TM;SS | 4.7 |
| | 451698 | Y16187 | Hs.26880 | endothelin converting enzyme-like 1 | Peptidase_M13;TM; | 4.7 |
| | 422687 | AW068823 | Hs.119206 | insulin-like growth factor binding | zf-C2H2,ig,none | 4.7 |
| 25 | 444542 | AJ161293 | Hs.280380 | aminopeptidase | NAD_binding,flavodoxin,FA | 4.7 |
| | 429833 | NM_012079 | Hs.288627 | diacylglycerol O-acyltransferase (m | ACAT;TM; | 4.7 |
| | 456376 | AA663904 | Hs.89862 | TNFRSF1A-associated via death domai | death;TM; | 4.7 |
| | 438568 | R88865 | Hs.11135 | major histocompatibility complex, c | MHC_II_alpha,ig,none | 4.7 |
| | 456356 | M74715 | Hs.89560 | iduronidase, alpha-L- | Glyco_hydro_39;SS | 4.7 |
| 30 | 420486 | AF036365 | Hs.98303 | caveolin 3 | Caveolin;TM; | 4.6 |
| | 425123 | AW205274 | Hs.154695 | phosphomannomutase 2 | PMM;SS | 4.6 |
| | 439512 | AA418287 | Hs.58093 | Homo sapiens, clone IMAGE:3163559, | laminin_EGF;TM; | 4.6 |
| | 418424 | Y13622 | Hs.85087 | latent transforming growth factor b | EGF,TB,spideroxin,granul | 4.6 |
| 35 | 433350 | BE563152 | Hs.10362 | Homo sapiens cDNA: FLJ20944 fis, c | zf-C3HC4,SPRY,none | 4.6 |
| | 432659 | AA281633 | Hs.278586 | KIAA1108 protein | TBC;TM; | 4.6 |
| | 445417 | AK001058 | Hs.12680 | a disintegrin-like and metalloprote | tsp_1,Reprolysin,Pep_M12B | 4.6 |
| | 437408 | AL359598 | Hs.36606 | Homo sapiens mRNA; cDNA DKFZp547B08 | none | 4.6 |
| | 427349 | AA360154 | Hs.177415 | Finkel-Biskis-Reilly murine sarcoma | ubiquitin;TM; | 4.6 |
| 40 | 418918 | X07871 | Hs.89476 | CD2 antigen (p50), sheep red blood | ig;TM;SS | 4.6 |
| | 421310 | AW630087 | Hs.103315 | trinucleotide repeat containing 1 | PHD | 4.6 |
| | 427969 | NM_001963 | Hs.2230 | epidermal growth factor (beta-uroga | EGF,ldl_recept_b,EB;TM; | 4.6 |
| | 447860 | AF193807 | Hs.131835 | Rhesus blood group, B glycoprotein | Ammonium_transp,FecCD;TM= | 4.6 |
| | 418916 | BE392781 | Hs.89474 | ADP-ribosylation factor 6 | arf,ras;TM; | 4.6 |
| | 425720 | AA362394 | Hs.293984 | hypothetical protein MGC13102 | TM;SS | 4.6 |
| 45 | 419942 | U25138 | Hs.93841 | potassium large conductance calcium | CaKB;TM;SS | 4.6 |
| | 403105 | | | Target Exon | ISK_Channel;TM;SS | 4.6 |
| | 418067 | AI127958 | Hs.83393 | cystatin E/M | cystatin;SS | 4.6 |
| | 427863 | AF189712 | Hs.181002 | MLL septin-like fusion | GTP_CDC;TM; | 4.5 |
| 50 | 458147 | AW752597 | | gb:IL3-CT0214-161299-045-B06 CT0214 | PMM,none | 4.5 |
| | 456799 | AC004923 | Hs.135187 | unc93 (C.elegans) homolog B | TM; | 4.5 |
| | 427136 | AL117415 | Hs.173716 | a disintegrin and metalloproteinase | ig | 4.5 |
| | 458766 | AW183618 | Hs.55610 | solute carrier family 30 (zinc tran | Cation_efflux;TM;SS | 4.5 |
| | 445033 | AV652402 | Hs.72901 | cyclin-dependent kinase inhibitor 2 | ank; | 4.5 |
| | 441281 | BE501247 | Hs.144084 | ESTs | Collagen,C4,none | 4.5 |
| 55 | 439720 | AI935202 | Hs.31181 | Homo sapiens cDNA: FLJ23230 fis, c | SDF_sugar_tr | 4.5 |
| | 410184 | AW503667 | Hs.59545 | ring finger protein 15 | SPRY,zf-B_box,zf-C3HC4;TM | 4.5 |
| | 431760 | NM_005317 | Hs.268531 | granzyme M (lymphocyte met-ase 1) | trypsin;TM;SS | 4.5 |
| | 446990 | AJ354717 | Hs.223908 | ESTs | transmembrane4 | 4.5 |
| | 407366 | AF026942 | Hs.17518 | gb:Homo sapiens cig33 mRNA, partial | IBR | 4.5 |
| 60 | 426156 | BE244537 | Hs.167382 | natriuretic peptide receptor A/guan | ANF_receptor,guanylate_cy | 4.5 |
| | 442941 | AU076728 | Hs.8867 | cysteine-rich, angiogenic inducer, | Cys_knot,tsp_1,vwc,IGFBP; | 4.5 |
| | 451118 | AI862096 | Hs.60640 | ESTs | EGF,vwc,TIL;SS | 4.5 |
| | 457657 | AW411509 | Hs.352567 | hypothetical protein PRO2121 | UQ_con;TM; | 4.4 |
| | 437016 | AU076916 | Hs.5398 | guanine monophosphate synthetase | PHD,SET,zf-CXXC,EGF,ank,n | 4.4 |
| 65 | 429497 | AB028953 | Hs.204121 | KIAA1030 protein | fn3;TM; | 4.4 |
| | 444090 | S69115 | Hs.10306 | natural killer cell group 7 sequenc | PMP22_Claudin;TM;SS | 4.4 |
| | 454005 | AF039237 | Hs.288600 | hypothetical protein MGC3123 | TM;SS | 4.4 |
| | 412270 | AC005262 | Hs.73797 | guanine nucleotide binding protein | G-alpha,arf;TM; | 4.4 |
| | 406729 | AA069711 | | gb:zm52b11.s1 Stratagene fibroblast | filamenLbZIP,Apolipoprot | 4.4 |
| 70 | 404610 | | | Homo sapiens cDNA FLJ11027 fis, clo | EGF,laminin_B,laminin_EGF | 4.4 |
| | 422311 | AF073515 | Hs.114948 | cytokine receptor-like factor 1 | fn3;TM; | 4.4 |
| | 406973 | M34996 | Hs.198253 | major histocompatibility complex, c | ig,MHC_II_alpha;TM;SS | 4.4 |
| | 407196 | D11747 | Hs.177415 | Finkel-Biskis-Reilly murine sarcoma | ERGA_ERG24,none | 4.4 |
| | 404243 | | | NM_006778:Homo sapiens ring finger | zf-C3HC4,zf-B_box;TM;SS | 4.4 |
| 75 | 443834 | AI741510 | Hs.173548 | ESTs | CUB,MAM,F5_F8_type_C,none | 4.4 |
| | 446057 | AI420227 | Hs.366053 | Trp-p8 transient receptor potential | none | 4.4 |
| | 413661 | AA071146 | Hs.343354 | ribosomal protein L18 | Ribosomal_L18e,L15;TM;S | 4.4 |
| | 414875 | HA2679 | Hs.77522 | major histocompatibility complex, c | ig,MHC_II_alpha;TM;SS | 4.4 |
| | 439730 | AF035292 | Hs.6654 | KIAA0657 protein | fn3;ig; | 4.3 |
| 80 | 406257 | | | Target Exon | 7tm_1,none | 4.3 |
| | 434025 | AF114264 | Hs.216381 | Homo sapiens clone HH409 unknown mR | ig;TM; | 4.3 |
| | 414961 | U27266 | Hs.927 | myosin-binding protein H | fn3;ig;TM; | 4.3 |
| | 430265 | L36033 | Hs.237356 | stromal cell-derived factor 1 | IL8;SS | 4.3 |
| | 429249 | XB1479 | Hs.2375 | egf-like module containing, mucin-I | 7tm_2,EGF,GPS,S_locus_gly | 4.3 |

| | | | | | |
|--------|-----------|-----------|--------------------------------------|---------------------------|-----|
| 433541 | AW081538 | Hs.220324 | hypothetical protein FLJ13052 | NAD_kinase;TM; | 4.3 |
| 400575 | | | NM_022146:Homo sapiens neuropeptide | 7tm_1;TM;SS | 4.3 |
| 427661 | AA410292 | Hs.104761 | ESTs | wnt:none | 4.3 |
| 452056 | AW955065 | Hs.101150 | Homo sapiens, clone IMAGE:4054156, | TM; | 4.3 |
| 433669 | AL047879 | Hs.194251 | ESTs, Weakly similar to ALU2_HUMAN | RNA_pol_L,RNA_pol_L,RasGA | 4.3 |
| 422624 | BE616678 | Hs.76152 | KDEL (Lys-Asp-Glu-Leu) endoplasmic | ER_lumen_recept:none | 4.3 |
| 421680 | AL031186 | Hs.289106 | Human DNA sequence from clone CTA-9 | Collagen;TM;SS | 4.3 |
| 422766 | AA334108 | Hs.159572 | heparan sulfate (glucosamine) 3-O-s | none | 4.3 |
| 437596 | AA761490 | Hs.351250 | ESTs, Moderately similar to S65657 | kinase,WD40 | 4.3 |
| 419285 | D31887 | Hs.89868 | KIAA0062 protein | Zip;TM;SS | 4.3 |
| 453082 | H18835 | Hs.31608 | hypothetical protein FLJ20041 | ion_trans;TM;SS | 4.2 |
| 410693 | BE044206 | | gb:hp040c08.x1 Soares_NFL_T_GBC_S1 H | C1q,Collagen,cystati | 4.2 |
| 413100 | BE065208 | | gb:RC1-BT0314-310300-015-b09 BT0314 | none | 4.2 |
| 432497 | AA551104 | | ESTs, Moderately similar to ALUC_HU | none | 4.2 |
| 423041 | BE170842 | Hs.123059 | chloride channel Kb | CBS,voltage_CLC;TM;SS | 4.2 |
| 449799 | AI143466 | Hs.125060 | ESTs | none | 4.2 |
| 438472 | AW974907 | Hs.86228 | TRIAD3 protein | none | 4.2 |
| 432179 | X75208 | Hs.2913 | EphB3 | EPH_lbd,fn3,kinase,SAM;T | 4.2 |
| 424488 | AK000413 | Hs.149227 | hypothetical protein FLJ20406 | Xlink_xf-CCCH,G_patch;TM= | 4.2 |
| 406809 | AF000574 | Hs.22405 | leukocyte immunoglobulin-like recep | ig,Gemini_mov;TM;SS | 4.2 |
| 407586 | Z37544 | Hs.37121 | phospholipase C, beta 3 (phosphatid | C2,PI-PLC-Y,PI-PLC-X;TM | 4.2 |
| 407228 | M25079 | Hs.155376 | hemoglobin, beta | globin;TM; | 4.2 |
| 450900 | H61005 | Hs.37902 | ESTs | none | 4.2 |
| 410188 | AL096739 | Hs.107260 | hypothetical protein DKFZp586H0623 | Ricin_B_lectin,Glycos_tra | 4.2 |
| 458248 | BE407379 | Hs.108082 | ESTs, Weakly similar to T31636 hypo | C1q,Collagen;TM;SS | 4.2 |
| 403138 | | | NM_006056:Homo sapiens G protein-co | 7tm_1,HECT;TM;SS | 4.2 |
| 432074 | AA525248 | Hs.149723 | ESTs | Y_phosphatase:none | 4.2 |
| 438682 | AA354489 | Hs.375594 | EBP50-PDZ interactor of 64 kD | none | 4.2 |
| 401908 | | | C17000154:gi12003980 gb AAAG43830.1 | TM;SS | 4.2 |
| 451287 | AK002158 | Hs.26194 | likely homolog of mouse immunity-as | TM; | 4.2 |
| 407904 | W44735 | Hs.107260 | Homo sapiens cDNA: FLJ21278 fis, cl | none | 4.1 |
| 403694 | | | Target Exon | UDPGT- | 4.1 |
| 423461 | AB020527 | Hs.128827 | solute carrier family 17 (sodium ph | sugar_tr;TM; | 4.1 |
| 425603 | U52219 | Hs.158329 | G protein-coupled receptor 50 | 7tm_1;TM;SS | 4.1 |
| 421485 | AA243499 | Hs.104800 | hypothetical protein FLJ10134 | TM;SS | 4.1 |
| 414509 | AW161311 | Hs.76294 | CD63 antigen (melanoma 1 antigen) | transmembrane4;TM;SS | 4.1 |
| 423313 | NM_014269 | Hs.126838 | a disintegrin and metalloproteinase | disintegrin,Reprolysin,Pe | 4.1 |
| 432171 | AI202503 | Hs.343661 | ESTs, Weakly similar to ALUB_HUMAN | WD40 | 4.1 |
| 434552 | AF148713 | Hs.125830 | bladder cancer overexpressed protei | WD40,DUF6; | 4.1 |
| 429592 | AB029041 | Hs.209646 | KIAA1118 protein | Troponin,Exo_endo_phos,IQ | 4.1 |
| 432982 | AA531058 | Hs.182248 | truncated calcium binding protein | OPR,ZZ;TM; | 4.1 |
| 424867 | AI024860 | Hs.153591 | Not56 (D. melanogaster)-like protei | TM;SS | 4.1 |
| 441455 | AJ271671 | Hs.7854 | zincron regulated transporter-lik | Zip;TM;SS | 4.1 |
| 400785 | | | C11000861:gi19938016 ref NP_064687. | TM;SS | 4.1 |
| 447232 | AW499834 | Hs.327 | interleukin 10 receptor, alpha | TM;SS | 4.1 |
| 450785 | AA852713 | Hs.108885 | Homo sapiens, alpha-1 (VI) collagen | vwa,Collagen;TM;SS | 4.1 |
| 424027 | AW337575 | Hs.201591 | ESTs | 7tm_2,HRM:none | 4.1 |
| 435857 | AF253468 | Hs.3736 | delta-like 4 homolog (Drosophila) | EGF,DSLEB;TM;SS | 4.1 |
| 437118 | AB037857 | Hs.300591 | CD9 partner 1 | none | 4.1 |
| 411410 | R20693 | Hs.69954 | laminin, gamma 3 | laminin_B,laminin_EGF,lam | 4.1 |
| 413902 | AU076743 | Hs.75613 | CD36 antigen (collagen type I recep | E2F_TDP,CD36;SS | 4.1 |
| 428938 | AC002425 | Hs.194660 | ceroid-lipofuscinosis, neuronal 3, | CLN3;TM;SS | 4.1 |
| 453094 | AA740928 | Hs.27356 | ESTs | none | 4.1 |
| 440811 | BE384713 | Hs.74655 | ESTs, Weakly similar to T34482 hypo | hormone_rec,zf-C4:none | 4.0 |
| 407287 | AI678812 | Hs.345139 | gb:tu59d08.x1 NCI_CGAP_Gas4 Homo sa | ras,cadherin | 4.0 |
| 428028 | U52112 | Hs.182018 | interleukin-1 receptor-associated k | death,kinase;TM; | 4.0 |
| 428469 | BE549205 | Hs.184488 | flotillin 2 | none | 4.0 |
| 423114 | AU076497 | Hs.1614 | cholinergic receptor, nicotinic, al | Neur_chan_LBD,Neur_chan_m | 4.0 |
| 426858 | NM_004182 | Hs.172791 | ubiquitously-expressed transcript | DUF232;SS | 4.0 |
| 444626 | AA320893 | Hs.117062 | hypothetical protein FLJ14497 | pyr_redox;TM;SS | 4.0 |

TABLE 30B:

| | |
|-------------|---------------------------------------|
| Pkey: | Unique Eos probeset identifier number |
| CAT number: | Gene cluster number |
| Accession: | Genbank accession numbers |

| Pkey | CAT Number | Accession |
|--------|------------|---|
| 458147 | 1030220_1 | AW848781 AW848490 AW849062 AW752597 AW752699 |
| 406729 | 0_0 | AA069711 |
| 410693 | 1054267_1 | BE044206 AW797320 BE161676 AW797356 AW797352 |
| 413100 | 1490226_1 | BE065224 BE065168 BE065313 BE065208 |
| 432497 | 852_71 | AW874688 R94134 AA551104 AA777322 A1033094 BE247143 |

TABLE 30C:

| | |
|--------------|---|
| Pkey: | Unique number corresponding to an Eos probeset |
| Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. |
| Strand: | Indicates DNA strand from which exons were predicted. |
| Nt_position: | Indicates nucleotide positions of predicted exons. |

| Pkey | Ref | Strand | Nt_position |
|--------|---------|--------|--|
| 401699 | 3176654 | Minus | 33285-34084 |
| 404864 | 5263010 | Plus | 94495-94661,95055-95195,97396-97506,9760 |

| | | | |
|--------|---------|-------|--|
| 402241 | 7690131 | Minus | 125073-125206,130996-131125 |
| 404913 | 7341740 | Plus | 97717-97976 |
| 404854 | 7143420 | Plus | 14260-14537 |
| 403105 | 8980016 | Minus | 145287-145744 |
| 404610 | 9588566 | Minus | 89583-89725,90402-90555,91428-91673 |
| 404243 | 5672609 | Plus | 74695-75123 |
| 406257 | 7417784 | Plus | 55821-56037 |
| 400575 | 9886575 | Plus | 131603-132095 |
| 403138 | 9211494 | Minus | 164684-165066,167757-168651 |
| 401908 | 8698760 | Minus | 126888-127024 |
| 403694 | 7107765 | Plus | 142925-143080,165505-166186,167486-16763 |
| 400785 | 8131682 | Plus | 43113-43967 |

TABLE 31A: ABOUT 189 GENES DOWN-REGULATED IN GLIOMA COMPARED TO NON-MALIGNANT ADULT BRAIN TISSUE
 Table 31A lists about 189 genes down-regulated in glioma compared to non-malignant adult brain tissue. These were selected as for Table 30A, except that the numerator was set to the 90th percentile amongst various non-malignant brain specimens, the denominator was set to the 90th percentile value amongst various gliomas, the numerator was greater than or equal to 50 units, and the ratio was greater than or equal to 2.5 (i.e. 2½-fold downregulation in brain tumor vs. normal brain).

PKey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 Protein Domains: Predicted Protein Domains
 R1: non-malignant adult brain tissue vs. glioma

| PKey | ExAccn | UniGene ID | Unigene Title | Protein Domains | R1 |
|--------|-----------|------------|-------------------------------------|---------------------------|------|
| 412524 | AA417813 | Hs.44208 | hypothetical protein FLJ23153 | F420_oxidored;TM;SS | 14.5 |
| 432874 | W94322 | Hs.279651 | melanoma inhibitory activity | SH3;TM;SS | 8.3 |
| 452669 | AA216363 | Hs.262958 | hypothetical protein DKFZp434B044 | SCP;LCCL;TM;SS | 8.2 |
| 426300 | U15979 | Hs.169228 | delta-like homolog (Drosophila) | EGF;laminin_EGF;TM;SS | 8.2 |
| 447990 | BE048821 | Hs.20144 | small inducible cytokine subfamily | IL8;SS | 7.3 |
| 439477 | W69813 | Hs.58042 | ESTs, Moderately similar to GFR3_HU | GDNF;TPR | 7.1 |
| 411602 | L01406 | Hs.767 | growth hormone releasing hormone re | 7tm_2;HRM;TM;SS | 6.1 |
| 417067 | AJ001417 | Hs.81086 | solute carrier family 22 (extraneur | sugar_tr;TM;SS | 6.0 |
| 426488 | X03350 | Hs.4 | alcohol dehydrogenase 1B (class I), | adh_zinc;TM; | 5.9 |
| 447656 | NM_003726 | Hs.19126 | src kinase-associated phosphoprotei | SH3;PH;TM; | 5.3 |
| 436950 | L05779 | Hs.113 | epoxide hydrolase 2, cytoplasmic | abhydrolase,Hydrolase;TM= | 5.2 |
| 406837 | R70292 | Hs.156110 | immunoglobulin kappa constant | | 4.9 |
| 410387 | A127367 | Hs.47094 | ESTs | | 4.8 |
| 432855 | AF017988 | Hs.279565 | secreted frizzled-related protein 5 | Fz;NTR;TM;SS | 4.7 |
| 441499 | AW298235 | Hs.101689 | ESTs | | 4.6 |
| 421481 | AW391972 | Hs.104696 | KIAA1324 protein | TM;SS | 4.5 |
| 420255 | NM_007289 | Hs.1298 | membrane metallo-endopeptidase (neu | Peptidase_M13;TM;SS | 4.5 |
| 407230 | AA157857 | Hs.182265 | keratin 19 | filament_bZIP;SS | 4.4 |
| 412445 | X51362 | Hs.73893 | dopamine receptor D2 | 7tm_1;TM;SS | 4.3 |
| 413966 | AA133935 | Hs.173704 | ESTs, Moderately similar to A53959 | | 4.2 |
| 415165 | AW887604 | Hs.78065 | complement component 7 | kd1_recept_a_sushi;isp_1, | 4.2 |
| 420103 | AA382259 | Hs.95197 | aldehyde dehydrogenase 1 family, me | aldedh;TM; | 4.2 |
| 426723 | AW003069 | Hs.183860 | ESTs | GN1-4;TM;SS | 4.1 |
| 409081 | AJ010277 | Hs.50403 | T-box 19 | T-box;TM; | 4.0 |
| 407142 | AA12535 | | gb:zt99b10.s1 Soares_testis_NHT Hom | Na_sulph_symp;TM; | 4.0 |
| 414449 | AA557660 | Hs.76152 | decorin | LRRNT,LRR,LRR,LRRNT | 4.0 |
| 444784 | D12485 | Hs.11951 | ectonucleotide pyrophosphatase/phos | Somatomedin_B,Endonucleas | 3.9 |
| 420321 | D78761 | Hs.96657 | hypothetical protein | isp_1;SS | 3.8 |
| 401700 | | | Target Exon | TM; | 3.8 |
| 418807 | NM_004944 | Hs.88646 | deoxyribonuclease I-like 3 | Exo_endo_phos;TM;SS | 3.8 |
| 406746 | AA580395 | Hs.279860 | tumor protein, translationally-cont | TCTP;TM; | 3.7 |
| 449077 | AW262836 | Hs.252844 | ESTs | | 3.7 |
| 415718 | F30631 | Hs.200237 | ESTs | isoamylase_N | 3.7 |
| 402449 | | | Target Exon | pkinaase,LRR,LRRCT;TM;SS | 3.6 |
| 457489 | AI693815 | Hs.127179 | cryptic gene | TM;SS | 3.6 |
| 406743 | AA911568 | Hs.279860 | tumor protein, translationally-cont | TCTP;TM; | 3.6 |
| 416950 | AL049798 | Hs.80552 | dermatopontin | | 3.6 |
| 451554 | AI474866 | Hs.193237 | ESTs | | 3.6 |
| 440708 | AF038962 | Hs.7381 | voltage-dependent anion channel 3 | Euk_porin,Enterotoxin_A,P | 3.5 |
| 426095 | AI278023 | Hs.89986 | ESTs | WD40_none | 3.5 |
| 406742 | AI468091 | Hs.279860 | tumor protein, translationally-cont | TCTP;TM; | 3.5 |
| 429343 | AK000785 | Hs.199480 | Homo sapiens, Similar to epsin 3, c | VHS,ENTH,UIM;SS | 3.4 |
| 439457 | AF086274 | | gb:Homo sapiens full length insert | | 3.4 |
| 408796 | AA688292 | Hs.170345 | ESTs | hormone_rec,zf-C4 | 3.4 |
| 440659 | AF134160 | Hs.7327 | claudin 1 | PMP22_Claudin;TM;SS | 3.4 |
| 415042 | NM_006759 | Hs.77837 | UDP-glucose pyrophosphorylase 2 | UDPGP;SS | 3.4 |
| 417967 | BE244373 | Hs.1119 | nuclear receptor subfamily 4, group | hormone_rec,zf-C4_none | 3.3 |
| 445234 | AW137636 | Hs.146059 | ESTs | 14-3-3_none | 3.3 |
| 430511 | BE018156 | Hs.2575 | calpain 1, (mu/f) large subunit | ehand,Peptidase_C2,Calpa | 3.3 |
| 420485 | AF218586 | Hs.288835 | cell death-inducing DFFA-like effec | 7tm_1,CIDE-N;TM;SS | 3.3 |
| 413687 | AI522318 | Hs.103819 | ESTs | TM;SS | 3.3 |
| 428928 | BE409838 | Hs.194657 | cadherin 1, type 1, E-cadherin (epi | cadherin,Cadherin_C_term, | 3.3 |
| 409738 | BE222975 | Hs.56205 | insulin induced gene 1 | | 3.3 |
| 442046 | AA974575 | Hs.287385 | ESTs | zf-C2H2,SET;TM; | 3.2 |
| 413127 | BE066529 | | gb:RC3-BT0333-300300-017-a12 BT0333 | | 3.2 |
| 429350 | AI754634 | Hs.131987 | ESTs | MAM;TM; | 3.2 |
| 427980 | AA418305 | Hs.303205 | EST | LRR_none | 3.2 |

| | | | | | | |
|----|--------|-----------|-----------|-------------------------------------|---------------------------|-----|
| | 424498 | AB033043 | Hs.149377 | hypothetical protein DKFZp761L0424 | AIP3;TM;SS | 3.2 |
| | 435684 | NM_001290 | Hs.4980 | LIM domain binding 2 | LIM_bind;TM; | 3.2 |
| | 402632 | | | Target Exon | ig;TM;SS | 3.1 |
| 5 | 431130 | NM_006103 | Hs.2719 | HE4; epididymis-specific, whey-acid | wap;TM;SS | 3.1 |
| | 410636 | AA088177 | Hs.172870 | ESTs | TM;SS | 3.1 |
| | 452658 | N88604 | Hs.30212 | thyroid receptor interacting protei | PC1;TM; | 3.1 |
| | 453180 | N45243 | Hs.110373 | ESTs, Highly similar to T42626 secr | laminin_G,LRRCCT,none | 3.1 |
| | 430319 | AI480214 | Hs.356075 | ninjurin 2 | TM;SS | 3.1 |
| 10 | 438424 | AI912498 | Hs.25895 | hypothetical protein FLJ14996 | C2;TM; | 3.1 |
| | 456063 | NM_006744 | Hs.76461 | retinol-binding protein 4, intersti | lipocalin,TGF-beta,TGFb_p | 3.1 |
| | 429798 | AL117578 | Hs.222909 | DKFZP434C128 protein | TM; | 3.1 |
| | 417677 | NM_016055 | Hs.82389 | CGI-118 protein | | 3.1 |
| | 443792 | AI763073 | Hs.204873 | ESTs | | 3.1 |
| 15 | 445861 | BE293423 | Hs.11809 | single Ig IL-1R-related molecule | TIR;TM; | 3.1 |
| | 407815 | AW373860 | Hs.183860 | hypothetical protein FLJ20277 | LRR,none | 3.1 |
| | 456689 | NM_002251 | Hs.117780 | potassium voltage-gated channel, de | ion_trans,K_tetra;TM;SS | 3.1 |
| | 446492 | AW205115 | Hs.161287 | ESTs | SPRY_zf-B_box,PAAD_D | 3.1 |
| | 427706 | AW971225 | Hs.293800 | ESTs, Weakly similar to ALU1_HUMAN | | 3.0 |
| 20 | 458008 | AA809314 | Hs.123295 | ESTs | SCAN_zf-C2H2,none | 3.0 |
| | 449708 | AI694598 | Hs.202126 | ESTs | | 3.0 |
| | 410132 | NM_003480 | Hs.300946 | Microfibril-associated glycoprotein | TM;SS | 3.0 |
| | 423778 | Y09267 | Hs.132821 | flavin containing monooxygenase 2 | FMO-like,pyr_redox;TM;S | 3.0 |
| | 425280 | U31519 | Hs.1872 | phosphoenolpyruvate carboxykinase 1 | PEPCK;TM; | 3.0 |
| 25 | 453177 | AW389509 | Hs.223747 | ESTs | zf-C2H2,none | 3.0 |
| | 416781 | AF072928 | Hs.79877 | myotubularin related protein 6 | | 3.0 |
| | 447582 | BE293520 | Hs.18910 | prostate cancer overexpressed gene | sugar_tr;TM;SS | 3.0 |
| | 417365 | D50683 | Hs.82028 | transforming growth factor, beta re | pkinase,WD40;TM; | 3.0 |
| | 452540 | AW161048 | Hs.150549 | ESTs, Weakly similar to T33997 hypo | | 2.9 |
| 30 | 430733 | AW367902 | Hs.236443 | Homo sapiens mRNA; cDNA DKFZp564N10 | PH,Ets,CH,spectrin,Ca_cha | 2.9 |
| | 418127 | BE243982 | Hs.83532 | membrane cofactor protein (CD46, tr | sushi;TM;SS | 2.9 |
| | 404445 | | | Target Exon | | 2.9 |
| | 423323 | AI951628 | Hs.127007 | potassium channel, subfamily K, mem | ion_trans;TM;SS | 2.9 |
| | 452093 | AA447453 | Hs.27860 | Homo sapiens mRNA; cDNA DKFZp586M07 | 7tm_1,none | 2.9 |
| 35 | 427981 | BE275986 | Hs.181311 | asparaginyl-tRNA synthetase | tRNA-synt_2,tRNA_anti,tRN | 2.9 |
| | 452242 | R50956 | Hs.159993 | glycosyltransferase | | 2.9 |
| | 440232 | AI766925 | Hs.112554 | ESTs | | 2.9 |
| | 444634 | AW611988 | Hs.197813 | ESTs | CKS | 2.9 |
| | 445889 | BE465186 | Hs.266958 | ESTs | TM; | 2.9 |
| 40 | 414483 | R25513 | Hs.10683 | ESTs | | 2.9 |
| | 453500 | AI478427 | Hs.43125 | esophageal cancer related gene 4 pr | TM;SS | 2.9 |
| | 419768 | T72104 | Hs.93194 | apolipoprotein A-I | Apolipoprotein;SS | 2.9 |
| | 427804 | AL049654 | Hs.180871 | protein kinase C, alpha binding pro | PDZ;SS | 2.9 |
| | 423753 | Y11312 | Hs.132463 | phosphoinositide-3-kinase, class 2, | C2,P13_P14_kinase,P13Ka,P | 2.9 |
| 45 | 430699 | AW969847 | Hs.292718 | ESTs, Weakly similar to RET2_HUMAN | lipocalin;SS | 2.9 |
| | 427842 | AW936961 | | gb:RC1-DT0029-160200-013-a12 DT0029 | efhand,mito_carr,none | 2.8 |
| | 432834 | F06459 | Hs.289113 | cytochrome b5 reductase 1 (BSR.1) | NAD_binding,FAD_binding_6 | 2.8 |
| | 421435 | AW972072 | Hs.372167 | ESTs | | 2.8 |
| | 402458 | | | C1002064:gij11993050jgb AAG42574.1 | TM;SS | 2.8 |
| 50 | 410036 | R57171 | Hs.57975 | calsequestrin 2 (cardiac muscle) | Calsequestrin;SS | 2.8 |
| | 412570 | AA033517 | Hs.74047 | electron-transfer-flavoprotein, bet | ETF_beta;SS | 2.8 |
| | 459439 | AW402931 | Hs.352411 | gb:U1-HF-BK0-abd-a-01-0-U1r1 NIH_M | | 2.8 |
| | 438622 | L03151 | | gb:Homo sapiens cell-type T-cell im | | 2.8 |
| | 417023 | AA192278 | Hs.301596 | ESTs, Moderately similar to S65657 | | 2.8 |
| 55 | 453281 | W46280 | Hs.55940 | ESTs, Weakly similar to A25704 syna | | 2.8 |
| | 403028 | | | Target Exon | trypsin,trefol | 2.8 |
| | 449029 | N28989 | Hs.22891 | solute carrier family 7 (cationic a | aa_permeases;TM;SS | 2.8 |
| | 425483 | AF231022 | Hs.158159 | FAT tumor suppressor (Drosophila) h | EGF,cadherin,laminin_G;TM | 2.8 |
| 60 | 406918 | M88357 | | gb:Homo sapiens DNA-binding protein | zf-C2H2,KRAB,zf-BED;TM; | 2.7 |
| | 435213 | AA092510 | Hs.5985 | non-kinase Cdc42 effector protein S | TM; | 2.7 |
| | 443990 | AW205085 | Hs.39557 | ESTs | | 2.7 |
| | 451698 | Y16187 | Hs.26880 | endothelin converting enzyme-like 1 | Peptidase_M13;TM; | 2.7 |
| | 431713 | AK000388 | Hs.267997 | EHM2 gene | Band_41;TM; | 2.7 |
| | 431469 | N49424 | Hs.124159 | ESTs | SH3 | 2.7 |
| 65 | 400386 | AF075290 | | gap junction protein, alpha 3, 46kD | connexin;TM;SS | 2.7 |
| | 406684 | X16354 | Hs.50964 | carcinoembryonic antigen-related ce | ig;TM;SS | 2.7 |
| | 449874 | AA135688 | Hs.10083 | Homo sapiens, clone IMAGE:4139786, | TM; | 2.7 |
| | 403213 | | | NM_019595:Homo sapiens intersecin | SH3,efhand,C2,PH,RhoGEF;T | 2.7 |
| | 459665 | BE159784 | Hs.47647 | gb:MRO-HT0408-220300-001-h06 HT0408 | | 2.7 |
| 70 | 421823 | N40850 | Hs.28625 | ESTs | | 2.7 |
| | 422693 | BE300073 | Hs.279860 | tumor protein, translationally-cont | TCTP,none | 2.7 |
| | 454906 | AI219323 | Hs.101077 | ESTs, Weakly similar to T22363 hypo | TM; | 2.7 |
| | 447075 | AV662037 | Hs.124740 | ESTs, Weakly similar to I38022 hypo | TM; | 2.7 |
| | 450273 | AW296454 | Hs.24743 | hypothetical protein FLJ20171 | tm,none | 2.7 |
| 75 | 434340 | AI193043 | Hs.128685 | ESTs, Weakly similar to T17226 hypo | | 2.7 |
| | 436972 | AA284679 | Hs.25640 | claudin 3 | PMP22_Claudin;TM;SS | 2.7 |
| | 441379 | AW175787 | Hs.334841 | selenium binding protein 1 | TM; | 2.7 |
| | 421143 | AB024536 | Hs.102171 | immunoglobulin superfamily containi | ig_LRR,LRNNT,LRRCCT;TM;S | 2.7 |
| | 422558 | NM_006420 | Hs.118249 | brefeldin A-inhibited guanine nucle | Sec7,none | 2.7 |
| 80 | 428900 | AA437189 | Hs.352324 | Human DNA sequence from clone RP1-6 | SS | 2.7 |
| | 421153 | AF009267 | Hs.102238 | Homo sapiens clone FBA1 Cri-du-chat | | 2.7 |
| | 427074 | AA527435 | Hs.178589 | hepatocellular carcinoma antigen ge | efhand;TM; | 2.6 |
| | 448133 | AA723157 | Hs.73769 | folate receptor 1 (adult) | Folate_rec,MIP;TM;SS | 2.6 |
| | 419158 | AF031475 | Hs.89648 | arginine vasopressin (neurophysin I | hormone5,hormone4;SS | 2.6 |

| | | | | | | |
|----|--------|-----------|-----------|-------------------------------------|---------------------------|-----|
| | 448406 | AW772298 | Hs.21103 | Homo sapiens mRNA; cDNA DKFZp564807 | | 2.6 |
| | 437176 | AW176909 | Hs.42346 | calcineurin-binding protein calsarc | Galactosyl_1;TM;SS | 2.6 |
| | 435075 | RS1094 | Hs.12400 | ESTs | | 2.6 |
| 5 | 403153 | | | Target Exon | | 2.6 |
| | 400387 | AF133131 | | double homeobox, 5 | | 2.6 |
| | 425940 | AB023184 | Hs.163990 | KIAA0967 protein | PDZ;SS | 2.6 |
| | 416157 | NM_003243 | Hs.342874 | transforming growth factor, beta re | zona_pellucida;TM;SS | 2.6 |
| | 452554 | AW452434 | Hs.58006 | ESTs, Weakly similar to ALUS_HUMAN | HLH,PAC,PAS,none | 2.6 |
| 10 | 453247 | T80198 | Hs.111806 | ESTs | wra,Cache,none | 2.6 |
| | 407744 | AB020629 | Hs.38095 | ATP-binding cassette, sub-family A | ABC_tran,PRK;TM;SS | 2.6 |
| | 432877 | AW974111 | Hs.292477 | ESTs | Est,SAM_PNT,none | 2.6 |
| | 450115 | AU591038 | Hs.38132 | ESTs | | 2.6 |
| | 406337 | | | C14000021:gi7242973[dbj]BAA92547.1 | Peptidase_M22 | 2.6 |
| 15 | 430877 | NM_005269 | Hs.2693 | glioma-associated oncogene homolog | zf-C2H2;SS | 2.6 |
| | 453874 | AW591783 | Hs.36131 | collagen, type XIV, alpha 1 (unduli | | 2.6 |
| | 450493 | M93718 | Hs.166373 | nitric oxide synthase 3 (endothelia | NAD_binding,flavodoxin,FA | 2.6 |
| | 427620 | NM_003705 | Hs.179866 | solute carrier family 25 (mitochond | ethand_mito_carr;TM;SS= | 2.6 |
| | 446585 | AV659397 | Hs.299668 | ESTs, Weakly similar to I38022 hypo | | 2.6 |
| 20 | 427223 | BE208189 | Hs.174031 | cytochrome c oxidase subunit Vlb | tubulin,FKBP,COX6B,7m_1, | 2.6 |
| | 428111 | S76617 | Hs.2243 | B lymphoid tyrosine kinase | SH2,SH3,kinase;SS | 2.6 |
| | 440133 | AI056255 | Hs.133349 | ESTs | | 2.6 |
| | 419693 | AA133749 | Hs.301350 | FXVD domain-containing ion transpor | ATP1G1_PLM_MAT8;TM;SS | 2.6 |
| | 417103 | Z33905 | Hs.81218 | hypothetical protein MGC3597 | TPR,zf-C3HC4,PHD;TM;SS= | 2.6 |
| 25 | 419100 | AA484362 | Hs.6748 | hypothetical protein PP1665 | squash,GOPD;TM; | 2.6 |
| | 449925 | AI342493 | Hs.24192 | Homo sapiens cDNA FLJ20767 fis, clo | | 2.6 |
| | 430937 | X53463 | Hs.2704 | glutathione peroxidase 2 (gastroint | GSHPx;SS | 2.6 |
| | 425640 | U34051 | Hs.158460 | cyclin-dependent kinase 5, regulato | CDK5_activator;TM; | 2.6 |
| | 409021 | AA156640 | Hs.49881 | fatty acid binding protein 3, muscl | Epocalin,none | 2.6 |
| 30 | 400538 | | | ENSP00000239776*.BA425A6.2 (similar | TM;SS | 2.6 |
| | 446947 | AF146747 | Hs.232165 | polycythemia rubra vera 1; cell sur | TM;SS | 2.6 |
| | 408310 | AW179023 | Hs.191705 | gb:PM3-ST0036-170899-001-e08 ST0036 | | 2.6 |
| | 433032 | AI084066 | Hs.20072 | myosin regulatory light chain inter | Band_41; | 2.6 |
| | 419389 | AI074951 | Hs.319095 | ESTs | DPPIV_N_term,none | 2.6 |
| 35 | 453145 | R63438 | Hs.183454 | Homo sapiens cDNA FLJ14883 fis, clo | STT3;TM;SS | 2.6 |
| | 443460 | AL050275 | Hs.9383 | DKFZP566D213 protein | EGF,laminin_EGF,EB;TM;S | 2.6 |
| | 421903 | AW079940 | Hs.15951 | ESTs, Weakly similar to S32436 coll | SS | 2.5 |
| | 421757 | Z20897 | Hs.296259 | paraoxonase 3 | Arylesterase;SS | 2.5 |
| | 428475 | AF172940 | Hs.184542 | CGI-127 protein | | 2.5 |
| 40 | 424657 | AA344719 | | gb:EST50901 Gall bladder II Homo sa | | 2.5 |
| | 432862 | AW004958 | Hs.236720 | amniotless protein | TM;SS | 2.5 |
| | 427195 | W27230 | Hs.173912 | eukaryotic translation initiation f | DEAD,helicase_C; | 2.5 |
| | 447770 | AB032417 | Hs.19545 | frizzled (Drosophila) homolog 4 | Fz,Frizzled,7m_2;TM;SS | 2.5 |
| | 456523 | AI083668 | Hs.50501 | hypothetical protein MGC10986 | kinase,none | 2.5 |
| 45 | 451846 | T65840 | Hs.11762 | ESTs | | 2.5 |
| | 432906 | BE265489 | Hs.3123 | lethal giant larvae (Drosophila) ho | WD40;TM; | 2.5 |
| | 453876 | AW021748 | Hs.110406 | ESTs, Weakly similar to I38022 hypo | | 2.5 |
| | 441488 | AW450935 | Hs.7862 | hypothetical protein FLJ20312 | TM; | 2.5 |
| | 444669 | F18939 | Hs.153827 | ESTs | | 2.5 |
| 50 | 452497 | AA732153 | Hs.27865 | Homo sapiens cDNA: FLJ21333 fis, cl | | 2.5 |

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|-------------|---------------------------------------|--|
| TABLE 31B: | | |
| Pkey: | Unique Eos probeset identifier number | |
| CAT number: | Gene cluster number | |
| Accession: | Genbank accession numbers | |

| Pkey | CAT Number | Accession |
|--------|------------|--|
| 439457 | 23338_1 | AF086274 W69434 W69517 |
| 413127 | 151610_1 | BG007296 BF330853 BF747375 BE066356 BE066292 BF330900 BF747142 BE066419 BF742510 BE066529 BE066298 BF742516 BF746603 |
| | | BE066274 BF334312 |
| 60 | 427842 | 1164138_1 |
| | 438622 | 46171_1 |
| | 424657 | 896375_1 |
| | | AW936960 AW936961 AA416706 R29415 |
| | | L03151 L03155 L03161 |
| | | AW963487 AA365077 AA344719 |

| | | |
|--------------|--|--|
| TABLE 31C: | | |
| Pkey: | Unique number corresponding to an Eos probeset | |
| Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. | |
| Strand: | Indicates DNA strand from which exons were predicted. | |
| NL_position: | Indicates nucleotide positions of predicted exons. | |

| Pkey | Ref | Strand | NL_position |
|--------|---------|--------|--|
| 401700 | 3176654 | Minus | 35416-35534 |
| 402449 | 9796674 | Plus | 59867-60039,62588-62828,63465-63623,6492 |
| 402632 | 9931268 | Plus | 101166-101419 |
| 404445 | 7596866 | Minus | 31112-31423 |
| 402458 | 9796782 | Plus | 170479-171134 |
| 403028 | 7670577 | Minus | 114150-114272 |
| 403213 | 7630897 | Minus | 162572-162739,164442-164540 |
| 403153 | 9799871 | Minus | 42232-43389 |
| 406337 | 9213455 | Plus | 90117-90337 |
| 400538 | 9797838 | Plus | 8752-9822 |

TABLE 32A: ABOUT 68 GENES UP-REGULATED IN GLIOMA COMPARED TO NORMAL ADULT TISSUES AND TO NON-MALIGNANT BRAIN TISSUES THAT ARE LIKELY TO ENCODE PROTEINS AMENABLE TO MODULATION BY SMALL MOLECULES, PEPTIDES, OR ANTIBODIES

Table 32A lists about 68 genes up-regulated in glioma compared to normal adult tissues and to non-malignant brain tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows: the ratio of "average" glioma to "average" normal adult tissues was greater than or equal to 2.5, the ratio of "average" glioma to "average" non-malignant brain tissues was greater than or equal to 2.0, the "average" glioma level was set to the 98th percentile value amongst various glioma specimens, the "average" normal adult tissue level was set to the 85th percentile value amongst various non-malignant tissues, the "average" non-malignant brain tissues level was set to the 90th percentile value amongst various non-malignant brain tissues, the "average" glioma value was greater than or equal to 50 units, and the predicted protein contained a structural domain that is indicative of having an oncogenic function or of transducing an intracellular signal, or of being modifiable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter). Predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 Protein Domains: Predicted Protein Domains
 R1: glioma vs. normal adult tissues and non-malignant brain tissues that are likely to encode proteins

| Pkey | ExAccn | UniGene ID | Unigene Title | Protein Domains | R1 |
|--------|-----------|------------|--|-----------------------------|-----|
| 424343 | AW956360 | Hs.4748 | adenylate cyclase activating polypeptide | 7tm_2,HRM | 8.8 |
| 418506 | AA084248 | Hs.85339 | Unknown protein for MGC:29643 (form | | 7.8 |
| 456723 | Z43902 | Hs.4748 | adenylate cyclase activating polypeptide | 7tm_2,HRM | 7.5 |
| 430228 | AW950939 | Hs.6382 | ESTs, Highly similar to T00391 hypo | | 7.1 |
| 436480 | AJ271643 | Hs.87469 | putative acid-sensing ion channel | ASC,TM; | 6.3 |
| 407603 | AW955705 | Hs.62604 | Homo sapiens, clone IMAGE:4299322, | TM; | 6.0 |
| 414825 | X06370 | Hs.77432 | epidermal growth factor receptor (a | Furin-like, pkinase, Recep_ | 6.0 |
| 423779 | AW071837 | Hs.57971 | ESTs | TNFR_c6 | 5.5 |
| 409638 | AW450420 | Hs.21335 | ESTs | 7tm_2,HRM | 5.3 |
| 442613 | A1004002 | Hs.130522 | Kv channel-interacting protein 1 | Neur_chan_LBD,Neur_c | 5.2 |
| 436456 | AW292677 | Hs.248122 | G protein-coupled receptor 24 | | 5.1 |
| 424340 | AA339036 | Hs.7033 | ESTs | lig_chan,ANF_receptor,non | 5.0 |
| 425115 | R44664 | Hs.123956 | ESTs | 7tm_1 | 4.7 |
| 446809 | AW590171 | Hs.101413 | ESTs | CaMBD,SK_channel,CaMBD,SK | 4.4 |
| 413278 | BE563085 | Hs.833 | interferon-stimulated protein, 15 k | ubiquitin;SS | 4.4 |
| 454360 | L78207 | Hs.54470 | ATP-binding cassette, sub-family C | ABC_tran,ABC_membrane,PRK | 4.2 |
| 414821 | M63835 | Hs.77424 | Fc fragment of IgG, high affinity I | ig;TM;SS | 4.2 |
| 428141 | D50402 | Hs.182611 | solute carrier family 11 (proton-co | Nramp;TM; | 4.1 |
| 435472 | AW977330 | Hs.283022 | triggering receptor expressed on my | ig;TM;SS | 4.1 |
| 435615 | Y15065 | Hs.4975 | potassium voltage-gated channel, KQ | ion_trans,KCNQ1_channel;T | 3.8 |
| 448204 | A1475124 | Hs.170561 | ESTs | lig_chan,SBP_bac_3 | 3.7 |
| 433290 | R20077 | Hs.302185 | Homo sapiens clone 23618 mRNA seque | lig_chan,SBP_bac_3,ANF_re | 3.6 |
| 408243 | Y00787 | Hs.624 | interleukin 8 | HLH,PAS,IL8;TM; | 3.6 |
| 415849 | R20529 | Hs.6806 | ESTs | 7tm_2,GPS,Gal_Lectin,HRM, | 3.5 |
| 451099 | R52795 | Hs.25954 | interleukin 13 receptor, alpha 2 | fn3;TM;SS | 3.4 |
| 445070 | NM_000677 | Hs.258 | adenosine A3 receptor | 7tm_1;TM;SS | 3.4 |
| 428037 | N47474 | Hs.89230 | potassium intermediate/small conduc | CaMBD,SK_channel | 3.2 |
| 444006 | BE395085 | Hs.10086 | type I transmembrane protein Fn14 | kd_recept_a,PKD,MHC_I;TM | 3.1 |
| 447143 | AW292408 | Hs.152290 | ESTs, Highly similar to JC2463 vaso | | 3.0 |
| 418054 | NM_002318 | Hs.83354 | lysyl oxidase-like 2 | SRCR,Lysyl_oxidase;TM;S | 3.0 |
| 424441 | X14850 | Hs.147097 | H2A histone family, member X | histone,CBFD_NFYB_HMF;TM= | 3.0 |
| 445057 | AJ420227 | Hs.366053 | Trp-p8 transient receptor potential | | 2.9 |
| 438204 | AJ589645 | Hs.128690 | ESTs | 7tm_1 | 2.9 |
| 431674 | AA098901 | Hs.301642 | G-protein coupled receptor | GCV_H | 2.9 |
| 424028 | AF055084 | Hs.153692 | Homo sapiens cDNA FLJ14354 fis, clo | | 2.9 |
| 415209 | F00183 | Hs.172004 | titin | | 2.8 |
| 438537 | AK000511 | Hs.6294 | hypothetical protein DKFZp434L1435 | IRNA-synt_1;TM; | 2.8 |
| 431053 | S40369 | Hs.249141 | Glutamate receptor subunit | lig_chan,ANF_receptor;TM= | 2.8 |
| 408482 | NM_000676 | Hs.45743 | adenosine A2b receptor | 7tm_1;TM;SS | 2.8 |
| 414774 | X02419 | Hs.77274 | plasminogen activator, urokinase | kringle,lysin,plant_thi | 2.8 |
| 426865 | D63476 | Hs.172813 | PAK-interacting exchange factor bet | SH3,PH,RhoGEF,Terpene_syn | 2.8 |
| 430897 | U71092 | Hs.248122 | G protein-coupled receptor 24 | 7tm_1;TM; | 2.7 |
| 438993 | AA828995 | | gb:od77b08.s1 NCI_CGAP_Ov2 Homo sap | EGF,metalthio,integrin_B, | 2.7 |
| 409552 | AL119675 | Hs.54929 | phosphorylase kinase, gamma 1 (musc | pkinase,Bac_DNA_binding;T | 2.7 |
| 412817 | AL037159 | Hs.74619 | proteasome (prosome, macropain) 26S | PC_rep;TM; | 2.7 |
| 419150 | AF120103 | Hs.197366 | smoothed (Drosophila) homolog | COX8,SHMT,MIF,GST_C,EF1G, | 2.7 |
| 419508 | AW997938 | Hs.90786 | ATP-binding cassette, sub-family C | ABC_tran,ABC_membrane;TM= | 2.7 |
| 417880 | BE241595 | Hs.82848 | selectin L (lymphocyte adhesion mol | EGF,lectin_c,sushi;TM;S | 2.7 |
| 432074 | AA525248 | Hs.149723 | ESTs | Y_phosphatase | 2.6 |
| 402154 | | | NM_031896:Homo sapiens calcium cha | PMP22_Claudin;TM;SS | 2.6 |
| 431222 | X56777 | Hs.273790 | zona pellucida glycoprotein 3A (spe | zona_pellucida;TM;SS | 2.6 |
| 419913 | AW270040 | Hs.34455 | ESTs | EPH_lbd,fn3,pkinase, | 2.6 |
| 412802 | U41518 | Hs.74602 | aquaporin 1 (channel-forming integr | MIP;TM;SS | 2.6 |
| 412070 | AW893260 | | gb:CM2-NN0010-100300-111-e09 NN0010 | 7tm_2,HRM | 2.6 |
| 422676 | D28481 | Hs.1570 | histamine receptor H1 | 7tm_1;TM;SS | 2.6 |
| 422311 | AF073515 | Hs.114948 | cytokine receptor-like factor 1 | fn3;TM; | 2.6 |
| 444381 | BE387335 | Hs.283713 | hypothetical protein BC014245 | Collagen;TM;SS | 2.6 |
| 419972 | AL041465 | Hs.182982 | golgin-67 | | 2.6 |
| 418526 | BE019020 | Hs.85838 | solute carrier family 16 (monocarbo | TM;SS | 2.6 |
| 421997 | R56740 | Hs.110613 | KIA0220 protein | aa_permeases,pyridoxal_de | 2.6 |
| 430181 | AF065314 | Hs.234785 | cyclic nucleotide gated channel alp | cNMP_binding,ion_trans;TM | 2.5 |
| 426318 | AA375125 | Hs.147112 | Homo sapiens cDNA: FLJ22322 fis, cl | EPH_lbd,pkinase,fn3,SAM,n | 2.5 |
| 434808 | AF155108 | Hs.256150 | NY-REN-41 antigen | TM; | 2.5 |
| 418843 | AJ251016 | Hs.89230 | potassium intermediate/small conduc | CaMBD,SK_channel;TM;SS= | 2.5 |
| 410290 | AA402307 | Hs.322844 | hypothetical protein DKFZp564A176 | Sema,PSI,TIG,integrin_B;T | 2.5 |

| | | | | | |
|--------|----------|-----------|-------------------------------------|--------------|-----|
| 424909 | S78187 | Hs.153752 | cell division cycle 25B | Rhodanese;SS | 2.5 |
| 408369 | R38438 | Hs.182575 | SLC15A2 Solute carrier family 15 (H | PTR2;TM; | 2.5 |
| 414561 | A1064813 | Hs.195155 | Homo sapiens amino acid transport s | Aa_trans;TM; | 2.5 |

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TABLE 32B:

| | |
|-------------|---------------------------------------|
| Pkey: | Unique Eos probeset identifier number |
| CAT number: | Gene cluster number |
| Accession: | Genbank accession numbers |

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| Pkey | CAT Number | Accession |
|--------|------------|---|
| 438993 | 2580163_1 | AJ926361 AA834879 AA828995 |
| 412070 | 287551_1 | BG820657 AW890808 BF904755 AW893260 BI034684 BF963423 BF961550 M85689 |

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TABLE 32C:

| | |
|--------------|---|
| Pkey: | Unique number corresponding to an Eos probeset |
| Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. |
| Strand: | Indicates DNA strand from which exons were predicted. |
| NT_position: | Indicates nucleotide positions of predicted exons. |

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| Pkey | Ref | Strand | NT_position |
|--------|---------|--------|---------------|
| 402154 | B516165 | Minus | 125299-125494 |

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TABLE 33A: ABOUT 798 GENES UP-REGULATED IN KIDNEY CANCER

Table 33A lists about 798 genes up-regulated in kidney cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" kidney cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" kidney cancer level was set to the 90th percentile amongst various kidney cancers. The "average" normal adult tissue level was set to the 90th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst the various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

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| | |
|----------------|---|
| Pkey: | Unique Eos probeset identifier number |
| ExAccn: | Exemplar Accession number, Genbank accession number |
| UnigeneID: | Unigene number |
| Unigene Title: | Unigene gene title |
| R1: | Ratio of tumor to normal tissue |

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| Pkey | ExAccn | UnigeneID | Unigene Title | R1 |
|--------|-----------|-----------|--|--------|
| 421471 | U90545 | Hs.104635 | solute carrier family 17 (sodium phospho | 1007.4 |
| 445178 | A1792241 | Hs.129614 | kidney-specific membrane protein | 438.0 |
| 452401 | NM_007115 | Hs.29352 | tumor necrosis factor, alpha-induced pro | 336.4 |
| 421727 | Y13153 | Hs.107318 | kynurenine 3-monooxygenase (kynurenine 3 | 323.6 |
| 440304 | BE159984 | Hs.125395 | ESTs | 295.0 |
| 436878 | BE465204 | Hs.47448 | ESTs | 258.8 |
| 452795 | AW392555 | Hs.18878 | hypothetical protein FLJ21620 | 258.6 |
| 421155 | H87879 | Hs.102267 | lysyl oxidase | 251.8 |
| 426471 | M22440 | Hs.170009 | transforming growth factor, alpha | 224.6 |
| 421478 | A1683243 | Hs.97258 | ESTs | 212.6 |
| 424086 | A1351010 | Hs.102267 | lysyl oxidase | 199.2 |
| 428296 | NM_003058 | Hs.183572 | solute carrier family 22 (organic cation | 186.4 |
| 426890 | AA393167 | Hs.41294 | ESTs | 183.4 |
| 441031 | A1110684 | Hs.7645 | fibrinogen, B beta polypeptide | 174.0 |
| 411642 | NM_014932 | Hs.71132 | neuroigin 1 | 172.4 |
| 452838 | U65011 | Hs.30743 | preferentially expressed antigen in mela | 161.4 |
| 425984 | AW836277 | Hs.165636 | hypothetical protein DKFZp761C07121 | 151.0 |
| 438966 | AW979074 | | gb:EST391184 MAGE resequences, MAGP Homo | 135.0 |
| 453165 | S74727 | Hs.32042 | aspartoacylase (aminoacylase 2, Canavan | 134.8 |
| 453160 | AJ263307 | Hs.146228 | ESTs | 132.6 |
| 452431 | U88879 | Hs.29499 | toll-like receptor 3 | 130.6 |
| 423508 | AW604297 | Hs.129711 | hepatitis A virus cellular receptor 1 | 120.4 |
| 420642 | AK001520 | Hs.99545 | Homo sapiens cDNA FLJ10658 fis, clone NT | 112.6 |
| 407975 | X89426 | Hs.41716 | endothelial cell-specific molecule 1 (NO | 111.8 |
| 431708 | A1698136 | Hs.108873 | ESTs | 109.8 |
| 446460 | AW013999 | Hs.150164 | ESTs | 103.6 |
| 443450 | N66045 | Hs.133529 | ESTs | 103.0 |
| 432865 | A1753709 | Hs.152484 | ESTs | 101.4 |
| 442438 | AA995998 | | gbros26b03.s1 NCI_CGAP_Kid5 Homo sapiens | 98.8 |
| 433447 | U29195 | Hs.3281 | neuronal pentraxin II | 98.5 |
| 440311 | A1733079 | Hs.125407 | ESTs, Moderately similar to ALUE_HUMAN ! | 98.2 |
| 415076 | NM_000857 | Hs.77890 | guanylate cyclase 1, soluble, beta 3 | 97.0 |
| 437157 | BE048860 | Hs.120655 | ESTs | 94.4 |
| 453319 | A1985369 | Hs.20117 | ESTs | 91.4 |
| 447046 | AA326187 | Hs.17170 | G protein-coupled receptor 4 | 90.2 |
| 439169 | A1912122 | Hs.41095 | ESTs | 86.6 |
| 431870 | AW449902 | Hs.105500 | ESTs | 84.4 |
| 438993 | AA828995 | | gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens | 83.8 |
| 445279 | R41900 | Hs.22245 | ESTs | 82.4 |
| 451592 | A1805416 | Hs.213897 | ESTs | 79.4 |
| 422966 | A1648419 | Hs.122613 | dimethylglycine dehydrogenase precursor | 78.8 |
| 423109 | M59305 | Hs.123655 | natriuretic peptide receptor C/guanylate | 78.0 |
| 415989 | A1267700 | Hs.111128 | ESTs | 77.0 |
| 422544 | AB018259 | Hs.118140 | KIAA0716 gene product | 74.8 |
| 425878 | AW964806 | Hs.38085 | ESTs, Weakly similar to putative glycine | 74.8 |
| 429352 | AK001512 | Hs.200097 | hypothetical protein FLJ10650 | 73.0 |

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|----|--------|-----------|-----------|---|------|
| | 453392 | U23752 | Hs.32964 | SRY (sex determining region Y)-box 11 | 72.2 |
| | 441665 | AI301355 | Hs.151285 | ESTs | 71.6 |
| | 435094 | AI560129 | Hs.277523 | EST | 71.2 |
| | 403345 | | | | 69.6 |
| 5 | 430440 | X52599 | Hs.2561 | nerve growth factor, beta polypeptide | 69.0 |
| | 440482 | AA886658 | Hs.50873 | ESTs | 67.6 |
| | 457100 | AA417878 | Hs.48401 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 67.0 |
| | 420637 | AW976153 | | gb:EST388262 MAGE resequences, MAGN Homo | 65.2 |
| 10 | 407905 | AW103655 | Hs.252905 | ESTs | 63.2 |
| | 422998 | AK000588 | Hs.122939 | hypothetical protein FLJ20581 | 61.8 |
| | 432267 | AK000872 | Hs.274227 | Homo sapiens cDNA FLJ10010 fis, clone HE | 61.2 |
| | 449448 | D60730 | Hs.57471 | ESTs | 60.6 |
| | 431941 | AK000106 | Hs.272227 | Homo sapiens cDNA FLJ20099 fis, clone CO | 59.8 |
| 15 | 419752 | AA249573 | Hs.152618 | ESTs | 58.4 |
| | 449579 | AW207260 | Hs.134014 | prostate cancer associated protein 6 | 58.2 |
| | 408609 | AA330431 | Hs.640 | calcitonin receptor | 57.4 |
| | 451009 | AA013140 | Hs.115707 | ESTs | 57.2 |
| | 435610 | AI852767 | Hs.114157 | ESTs, Weakly similar to putative p150 [H | 56.4 |
| 20 | 411893 | R82845 | Hs.273789 | ESTs | 56.2 |
| | 415227 | AW821113 | Hs.72402 | ESTs | 55.2 |
| | 433859 | AW896758 | Hs.163925 | ESTs | 55.0 |
| | 450459 | AI697193 | Hs.299254 | ESTs | 54.4 |
| | 400302 | N48056 | Hs.1915 | isolate hydrolase (prostate-specific memb | 53.4 |
| 25 | 421831 | AA298836 | Hs.22026 | ESTs | 52.8 |
| | 438817 | AI023799 | Hs.163242 | ESTs | 52.1 |
| | 449101 | AA205847 | Hs.23016 | G protein-coupled receptor | 52.0 |
| | 410025 | BE220489 | Hs.113592 | ESTs | 51.8 |
| | 423685 | BE350494 | Hs.49753 | Homo sapiens mRNA for KIAA1561 protein, | 48.0 |
| 30 | 436751 | AA732217 | Hs.294054 | ESTs | 46.6 |
| | 445424 | AB028945 | Hs.12696 | coractin SH3 domain-binding protein | 45.4 |
| | 444059 | R69743 | Hs.75442 | albumin | 44.8 |
| | 442671 | AI005668 | Hs.134779 | EST | 44.4 |
| | 445657 | AW612141 | Hs.279575 | ESTs | 44.3 |
| 35 | 452891 | N75582 | Hs.212875 | ESTs, Weakly similar to KIAA0357 [H.sapi | 44.0 |
| | 423735 | AA330259 | | gb:EST33963 Embryo, 12 week II Homo sapi | 43.8 |
| | 422553 | AI697720 | Hs.171455 | ESTs | 43.6 |
| | 452461 | N78223 | Hs.108106 | transcription factor | 42.8 |
| | 408430 | S79876 | Hs.44926 | dipeptidylpeptidase IV (CD26, adenosine | 42.6 |
| 40 | 452240 | AI591147 | Hs.61232 | ESTs | 41.7 |
| | 445186 | AW614544 | Hs.123641 | protein tyrosine phosphatase, receptor t | 41.4 |
| | 452788 | AW294571 | Hs.136040 | ESTs | 41.4 |
| | 419287 | X91906 | Hs.89872 | chloride channel 5 (nephrolithiasis 2, X | 40.6 |
| | 428822 | W28418 | Hs.301148 | potassium voltage-gated channel, Isk-rel | 40.2 |
| 45 | 412359 | AW837985 | | gb:QV3-LT0048-140200-083-e05 LT0048 Homo | 40.0 |
| | 434208 | T92641 | Hs.127648 | hypothetical protein PRO2176 | 39.2 |
| | 442168 | AI253165 | Hs.146022 | ESTs | 38.8 |
| | 400792 | AA635062 | Hs.50094 | Homo sapiens mRNA; cDNA DKFZp434O0515 (f | 38.6 |
| | 445900 | AF070526 | Hs.13429 | Homo sapiens clone 24787 mRNA sequence | 38.4 |
| | 444743 | AA045648 | Hs.11817 | nudix (nucleoside diphosphate linked moi | 38.4 |
| 50 | 428795 | R45503 | Hs.97469 | ESTs, Weakly similar to I49698 alpha-1,3 | 37.6 |
| | 406411 | | | | 37.6 |
| | 423657 | AL045128 | Hs.1691 | glucan (1,4-alpha-), branching enzyme 1 | 37.5 |
| | 417218 | AA005247 | Hs.285754 | met proto-oncogene (hepatocyte growth fa | 37.2 |
| 55 | 448788 | AI570286 | Hs.107070 | ESTs | 37.2 |
| | 441826 | AW503603 | Hs.129915 | phosphotriesterase related | 37.0 |
| | 409263 | AA069573 | Hs.50319 | ESTs | 36.8 |
| | 425577 | BE464496 | Hs.280977 | ESTs | 36.2 |
| | 452249 | BE394412 | Hs.61252 | ESTs | 34.8 |
| 60 | 435986 | AA703158 | Hs.187848 | ESTs | 34.4 |
| | 417236 | AI908497 | Hs.170737 | Homo sapiens cDNA: FLJ23251 fis, clone C | 33.8 |
| | 440234 | AW117264 | Hs.126252 | ESTs | 33.8 |
| | 435334 | R94223 | Hs.117747 | ESTs | 33.2 |
| | 410153 | BE311926 | Hs.15830 | Homo sapiens cDNA FLJ12691 fis, clone NT | 33.1 |
| 65 | 424871 | NM_004525 | Hs.153595 | low density lipoprotein-related protein | 32.8 |
| | 420908 | AL049974 | Hs.100261 | Homo sapiens mRNA; cDNA DKFZp564B222 (fr | 32.4 |
| | 423992 | AW898292 | Hs.137206 | Homo sapiens mRNA; cDNA DKFZp564H1663 (f | 32.4 |
| | 451050 | AW937420 | Hs.69662 | ESTs | 32.0 |
| | 449034 | AI624049 | | gb:ts41a09.x1 NCI_CGAP_U11 Homo sapiens | 31.6 |
| 70 | 434539 | AW748078 | Hs.214410 | ESTs | 31.0 |
| | 431595 | AA508196 | | gb:nh60f07.s1 NCI_CGAP_Pr8 Homo sapiens | 30.6 |
| | 449625 | NM_014253 | Hs.23796 | odx (odd Oz/ten-m, Drosophila) homolog 1 | 30.5 |
| | 448243 | AW369771 | Hs.77496 | small nuclear ribonucleoprotein polypept | 30.4 |
| | 413573 | AI733859 | Hs.149089 | ESTs | 30.2 |
| 75 | 421037 | AI684808 | Hs.197653 | ESTs | 30.2 |
| | 449353 | AA001220 | Hs.271369 | ESTs | 30.2 |
| | 416548 | H62953 | | gb:yr47f06.r1 Soares fetal liver spleen | 29.6 |
| | 423020 | AA383092 | Hs.1608 | replication protein A3 (14kD) | 29.6 |
| | 422420 | U03398 | Hs.1524 | tumor necrosis factor (ligand) superfam | 29.6 |
| 80 | 459508 | R83265 | Hs.205956 | ESTs | 29.2 |
| | 414245 | BE148072 | Hs.75850 | WAS protein family, member 1 | 28.8 |
| | 424565 | AW102723 | Hs.75295 | guanylate cyclase 1, soluble, alpha 3 | 28.6 |
| | 445925 | AI733820 | Hs.145664 | ESTs | 28.4 |
| | 412616 | AW970584 | Hs.291033 | ESTs | 28.0 |

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|----|--------|-----------|-----------|--|------|
| | 424638 | AJ472106 | Hs.49303 | Homo sapiens cDNA FLJ11663 fis, clone HE | 27.6 |
| | 445885 | AJ734009 | Hs.127699 | KIAA1603 protein | 27.6 |
| | 410247 | AF181721 | Hs.61345 | RU2S | 27.4 |
| 5 | 406414 | | | | 27.2 |
| | 435951 | AF269162 | Hs.41267 | c21orf7 form A-D | 27.2 |
| | 458680 | N73773 | Hs.282950 | ESTs | 27.0 |
| | 419948 | AB041035 | Hs.93847 | NADPH oxidase 4 | 26.4 |
| | 423276 | AC003034 | Hs.126261 | Homo sapiens Chromosome 16 BAC clone CIT | 26.3 |
| 10 | 427457 | AW779105 | Hs.164682 | ESTs, Weakly similar to ORF2 consensus s | 26.0 |
| | 446346 | AI290205 | | gb:q179g06.x1 Soares_NhHMPu_S1 Homo sapi | 26.0 |
| | 448595 | AB014544 | Hs.21572 | KIAA0644 gene product | 25.8 |
| | 419569 | AI971651 | Hs.91143 | jagged 1 (Alagille syndrome) | 25.6 |
| | 433242 | AB040938 | Hs.113940 | KIAA1505 protein | 25.6 |
| 15 | 453118 | AW195849 | Hs.252757 | ESTs | 25.6 |
| | 412209 | AW901456 | | gb:RC0-NN1012-270300-031-c07 NN1012 Homo | 25.2 |
| | 429710 | AI337113 | Hs.146025 | Homo sapiens cDNA: FLJ23594 fis, clone L | 25.2 |
| | 444783 | AK001468 | Hs.62180 | anillin (Drosophila Scraps homolog), act | 24.6 |
| | 436788 | AA766908 | Hs.259047 | ESTs | 24.4 |
| 20 | 427660 | AI741320 | Hs.114121 | Homo sapiens cDNA: FLJ23228 fis, clone C | 24.4 |
| | 419172 | AW338625 | Hs.22120 | ESTs | 24.3 |
| | 436061 | AI248584 | Hs.190745 | Homo sapiens cDNA: FLJ21326 fis, clone C | 24.2 |
| | 413623 | AA825721 | Hs.246973 | ESTs | 24.0 |
| | 407615 | AW753085 | | gb:PM1-CT0247-151299-005-a03 CT0247 Homo | 23.8 |
| 25 | 452466 | N84635 | Hs.29664 | Human DNA sequence from clone 682J15 on | 23.8 |
| | 432809 | AA565509 | Hs.131703 | ESTs | 23.7 |
| | 440102 | AI672443 | Hs.131190 | ESTs | 23.6 |
| | 451559 | AL119980 | Hs.128857 | ESTs | 23.2 |
| | 410811 | AW805687 | Hs.300648 | ESTs | 23.0 |
| 30 | 416778 | M16505 | Hs.79876 | steroid sulfatase (microsomal), arylsulf | 23.0 |
| | 453628 | AW243307 | Hs.170187 | ESTs | 22.8 |
| | 401352 | | | | 22.6 |
| | 451561 | N52812 | Hs.177403 | ESTs | 22.6 |
| | 401976 | | | | 22.4 |
| 35 | 410658 | AW105231 | Hs.192035 | ESTs | 22.4 |
| | 416220 | N49776 | Hs.121773 | ESTs | 22.2 |
| | 424073 | U03493 | Hs.138959 | gap junction protein, alpha 7, 45kD (con | 22.0 |
| | 444575 | AI264847 | Hs.22545 | Homo sapiens cDNA FLJ12935 fis, clone NT | 22.0 |
| | 444144 | BE159397 | Hs.7736 | hypothetical protein | 21.8 |
| 40 | 438504 | AW665281 | Hs.224625 | ESTs | 21.2 |
| | 439157 | AA912737 | Hs.20160 | ESTs | 20.8 |
| | 429006 | AA443143 | Hs.50929 | Homo sapiens cDNA FLJ13842 fis, clone TH | 20.5 |
| | 442006 | AW975183 | Hs.292663 | ESTs | 20.2 |
| | 409569 | AW573153 | Hs.256216 | ESTs | 19.8 |
| 45 | 421160 | AL080215 | Hs.102301 | Homo sapiens mRNA; cDNA DKFZp586J0323 (f | 19.8 |
| | 404200 | | | | 19.6 |
| | 446591 | H44186 | Hs.15456 | PDZ domain containing 1 | 19.2 |
| | 420218 | AW958037 | Hs.22437 | Homo sapiens cDNA: FLJ23366 fis, clone H | 18.9 |
| | 408390 | AA054222 | Hs.40400 | ESTs | 18.8 |
| 50 | 444038 | AW134509 | Hs.135077 | ESTs | 18.8 |
| | 446443 | AV659082 | Hs.134228 | ESTs | 18.8 |
| | 442204 | AI635450 | Hs.21914 | ESTs | 18.4 |
| | 451177 | AI969716 | Hs.13034 | ESTs | 18.2 |
| | 453931 | AL121278 | Hs.25144 | ESTs | 18.1 |
| 55 | 437212 | AI765021 | Hs.210775 | ESTs | 18.1 |
| | 431806 | AF186114 | Hs.270737 | tumor necrosis factor (ligand) superfamily | 18.0 |
| | 451659 | BE379761 | Hs.14248 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 17.8 |
| | 423909 | AJ223183 | Hs.135194 | immunoglobulin superfamily, member 6 | 17.6 |
| | 441082 | AW444804 | Hs.202655 | ESTs | 17.6 |
| 60 | 446259 | AA425204 | Hs.42278 | Homo sapiens cDNA FLJ13391 fis, clone PL | 17.6 |
| | 423609 | AA328348 | Hs.218289 | ESTs | 17.4 |
| | 428301 | AW628666 | Hs.98440 | ESTs | 17.4 |
| | 446364 | AB006624 | Hs.14912 | KIAA0286 protein | 17.4 |
| | 419983 | W55956 | Hs.94030 | Homo sapiens mRNA; cDNA DKFZp586E1624 (f | 17.0 |
| 65 | 424929 | AI640761 | Hs.224988 | ESTs | 17.0 |
| | 425695 | NM_005401 | Hs.159238 | protein tyrosine phosphatase, non-recept | 17.0 |
| | 449122 | AI631310 | Hs.196955 | ESTs | 17.0 |
| | 409519 | AA075368 | | gb:zm86h10.r1 Stratagene ovarian cancer | 16.8 |
| | 410947 | AK000305 | Hs.67055 | hypothetical protein FLJ20298 | 16.8 |
| 70 | 418053 | AA211493 | | gb:zn55d06.s1 Stratagene muscle 937209 H | 16.8 |
| | 433225 | AW816515 | Hs.173540 | ATPase, Class V, type 10D | 16.8 |
| | 443204 | AW205878 | Hs.29643 | Homo sapiens cDNA FLJ13103 fis, clone NT | 16.5 |
| | 421002 | AF116030 | Hs.100932 | transcription factor 17 | 16.5 |
| | 419296 | AA236115 | Hs.120785 | ESTs | 16.2 |
| 75 | 421659 | NM_014459 | Hs.106511 | protocadherin 17 | 16.0 |
| | 417589 | T82075 | Hs.13911 | ESTs | 16.0 |
| | 446057 | AI420227 | Hs.149358 | ESTs | 15.8 |
| | 434636 | AA083764 | Hs.241334 | ESTs | 15.6 |
| | 446797 | AI682536 | Hs.163495 | Homo sapiens cDNA FLJ13608 fis, clone PL | 15.6 |
| 80 | 443718 | AI083580 | Hs.221373 | ESTs | 15.4 |
| | 409748 | AI670776 | Hs.20961 | ESTs | 15.2 |
| | 443211 | AI128388 | Hs.143655 | ESTs | 15.0 |
| | 428911 | Z43846 | Hs.194478 | Homo sapiens mRNA; cDNA DKFZp434O1572 (f | 14.9 |
| | 444692 | AW779922 | Hs.145047 | ESTs | 14.8 |

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|----|--------|-----------|-----------|--|------|
| | 445436 | AI224105 | Hs.151408 | ESTs | 14.6 |
| | 408684 | R61377 | Hs.12727 | hypothetical protein FLJ21610 | 14.5 |
| | 405943 | | | | 14.4 |
| | 406291 | | | | 14.4 |
| 5 | 458679 | AW975460 | Hs.143563 | ESTs | 14.4 |
| | 450152 | AI138635 | Hs.22968 | ESTs | 14.4 |
| | 403899 | | | | 14.2 |
| | 454490 | AW797778 | | gb:CM2-UM0041-250200-104-d02 UM0041 Homo | 14.2 |
| | 451807 | W52854 | Hs.27099 | DKFZP564J0863 protein | 14.0 |
| 10 | 452453 | AI902519 | | gb:OV-BT009-101198-051 BT009 Homo sapien | 13.8 |
| | 447499 | AW262580 | Hs.147674 | KIAA1621 protein | 13.8 |
| | 406598 | | | | 13.6 |
| | 430939 | AI269471 | Hs.187018 | ESTs | 13.4 |
| | 443316 | AI478463 | Hs.18443 | ESTs | 13.4 |
| 15 | 408034 | N26639 | Hs.42192 | Human EST clone 251800 mariner transpos | 13.2 |
| | 428508 | BE252383 | Hs.184668 | SBB131 protein | 13.2 |
| | 447934 | AW631440 | Hs.165596 | ESTs | 13.2 |
| | 406671 | AA129547 | Hs.285754 | met proto-oncogene (hepatocyte growth fa | 13.1 |
| | 438199 | AW016531 | Hs.122147 | ESTs | 13.0 |
| 20 | 415511 | AI732617 | Hs.182362 | ESTs | 12.9 |
| | 426920 | AA393351 | Hs.132121 | ESTs | 12.8 |
| | 447311 | R37010 | Hs.33417 | Homo sapiens cDNA: FLJ22806 fis, clone K | 12.6 |
| | 423321 | AB013885 | Hs.126926 | beta-ureidopropionase | 12.5 |
| | 403622 | | | | 12.4 |
| 25 | 439759 | AL359055 | Hs.67709 | Homo sapiens mRNA full length insert cDN | 12.4 |
| | 422317 | NM_001147 | Hs.115181 | angiotensin 2 | 12.2 |
| | 428637 | AW979268 | | gb:EST391378 MAGE resequences, MAGP Homo | 12.2 |
| | 445717 | AW664658 | Hs.149332 | ESTs | 12.2 |
| | 418413 | R95735 | Hs.117753 | ESTs, Weakly similar to antigen of the m | 12.1 |
| 30 | 405336 | | | | 12.0 |
| | 437100 | AI761073 | Hs.14535 | Homo sapiens cDNA: FLJ22314 fis, clone H | 12.0 |
| | 428227 | AA321649 | Hs.2248 | small inducible cytokine subfamily B (Cy | 12.0 |
| | 414923 | AW445008 | Hs.77637 | homeo box A4 | 11.9 |
| | 432009 | AL137424 | | gb:Homo sapiens mRNA; cDNA DKFZp761G2123 | 11.8 |
| 35 | 433326 | AI379486 | Hs.159430 | ESTs | 11.8 |
| | 453955 | AW579207 | | gb:RC1-DT0029-120100-011-h01 DT0029 Homo | 11.8 |
| | 407510 | U96191 | | gb:Human trophoblast hypoxia-regulated f | 11.6 |
| | 433231 | AB040926 | Hs.143552 | KIAA1493 protein | 11.6 |
| | 451651 | AI097337 | Hs.88977 | hypothetical protein dJ511E16.2 | 11.6 |
| 40 | 443672 | AA323362 | Hs.9667 | butyrobetaine (gamma), 2-oxoglutarate di | 11.4 |
| | 405609 | | | | 11.4 |
| | 418912 | NM_000685 | Hs.89472 | angiotensin receptor 1 | 11.4 |
| | 421306 | AA806207 | Hs.125889 | ESTs | 11.4 |
| | 428721 | X02158 | Hs.2303 | erythropoietin | 11.4 |
| 45 | 419255 | AA235672 | Hs.87491 | ESTs | 11.4 |
| | 450006 | AI241555 | Hs.60171 | ESTs | 11.3 |
| | 435420 | AI928513 | Hs.59203 | ESTs | 11.2 |
| | 449802 | AW901804 | Hs.23984 | hypothetical protein FLJ20147 | 11.2 |
| | 424647 | W67751 | Hs.137308 | ESTs | 11.0 |
| 50 | 435758 | AI242163 | Hs.22670 | chromodomain helicase DNA binding protei | 11.0 |
| | 404347 | | | | 10.8 |
| | 438664 | AI911173 | Hs.213722 | ESTs | 10.8 |
| | 429125 | AA446854 | Hs.271004 | ESTs | 10.7 |
| | 416560 | R02818 | Hs.14102 | ESTs | 10.6 |
| 55 | 429945 | NM_006729 | Hs.226483 | diaphanous (Drosophila, homolog) 2 | 10.6 |
| | 435085 | AW130284 | Hs.192752 | ESTs, Moderately similar to NSD1 protein | 10.6 |
| | 442409 | BE208843 | Hs.129544 | ESTs, Weakly similar to ORF YLL027w [S.c | 10.6 |
| | 450644 | AW505496 | Hs.281215 | ESTs | 10.6 |
| | 448298 | AW137134 | Hs.187203 | ESTs | 10.4 |
| 60 | 404115 | | | | 10.2 |
| | 406242 | | | | 10.2 |
| | 420757 | X78592 | Hs.99915 | androgen receptor (dihydrotestosterone r | 10.2 |
| | 452588 | AA889120 | Hs.110637 | homeo box A10 | 10.2 |
| | 457233 | AI355009 | Hs.221698 | ESTs | 10.2 |
| 65 | 416185 | AW975861 | Hs.291995 | ESTs | 10.2 |
| | 446152 | AI292036 | Hs.150028 | ESTs | 10.1 |
| | 446298 | AF187813 | Hs.14637 | kidney- and liver-specific gene | 10.1 |
| | 423637 | AL137279 | Hs.130187 | Homo sapiens mRNA; cDNA DKFZp434O1214 (I | 10.0 |
| | 442405 | BE465247 | Hs.129530 | ESTs | 9.9 |
| 70 | 419213 | AW749146 | | gb:PM0-BT0340-170100-004-e03 BT0340 Homo | 9.8 |
| | 420840 | AI915836 | Hs.294008 | ESTs | 9.8 |
| | 423355 | AA324856 | Hs.257510 | ESTs | 9.8 |
| | 444929 | AI685841 | Hs.161354 | ESTs | 9.8 |
| | 423811 | AW299598 | Hs.50895 | homeo box C4 | 9.8 |
| 75 | 433527 | AW235613 | Hs.133020 | ESTs | 9.6 |
| | 429975 | AI167145 | Hs.165538 | ESTs | 9.6 |
| | 439979 | AW600291 | Hs.6823 | hypothetical protein FLJ10430 | 9.5 |
| | 433703 | AA210863 | Hs.3532 | nemo-like kinase | 9.2 |
| 80 | 417404 | NM_007350 | Hs.82101 | pleckstrin homology-like domain, family | 9.2 |
| | 451621 | AI879148 | Hs.26770 | fatty acid binding protein 7, brain | 9.2 |
| | 406992 | S82472 | | gb:beta-pol=DNA polymerase beta (exon a | 9.2 |
| | 419699 | AA248998 | Hs.31246 | ESTs | 9.2 |
| | 443740 | R56434 | Hs.21062 | ESTs | 9.2 |

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|----|--------|-----------|-----------|---|-----|
| | 422728 | AW937826 | Hs.103262 | ESTs | 9.2 |
| | 436961 | AW375974 | Hs.156704 | ESTs | 9.2 |
| | 431385 | BE178536 | Hs.11090 | high affinity immunoglobulin epsilon rec | 9.1 |
| | 411411 | AA345241 | Hs.55950 | ESTs, Weakly similar to KIAA1330 protein | 9.1 |
| 5 | 424115 | AA335497 | Hs.293965 | ESTs | 9.0 |
| | 402045 | | | | 9.0 |
| | 433426 | H69125 | Hs.133525 | ESTs | 9.0 |
| | 425493 | AW363582 | Hs.75323 | prohibiti | 9.0 |
| 10 | 447641 | BE619186 | | gb:601472933F1 NIH_MGC_68 Homo sapiens c | 9.0 |
| | 403095 | | | | 9.0 |
| | 407942 | AA378608 | Hs.5894 | hypothetical protein FLJ10305 | 8.8 |
| | 423126 | AA322245 | Hs.290155 | ESTs | 8.8 |
| | 408134 | AK000184 | Hs.42945 | acid sphingomyelinase-like phosphodiester | 8.8 |
| | 450375 | AA009647 | Hs.8850 | a disintegrin and metalloproteinase doma | 8.7 |
| 15 | 443647 | AV653846 | Hs.126261 | Homo sapiens Chromosome 16 BAC clone CIT | 8.6 |
| | 401439 | | | | 8.6 |
| | 449532 | W74653 | Hs.271593 | ESTs | 8.6 |
| | 453197 | AI916269 | Hs.109057 | ESTs, Weakly similar to ALU5_HUMAN ALU S | 8.6 |
| | 448450 | BE612490 | | gb:601451884F1 NIH_MGC_66 Homo sapiens c | 8.6 |
| 20 | 425176 | AW015644 | Hs.301430 | ESTs, Moderately similar to TEF1_HUMAN T | 8.5 |
| | 407721 | Y12735 | Hs.38018 | dual-specificity tyrosine-(Y)-phosphoryl | 8.4 |
| | 402921 | | | | 8.4 |
| | 428133 | AW167727 | Hs.11873 | ESTs | 8.4 |
| | 419503 | AA243642 | Hs.137422 | ESTs | 8.4 |
| 25 | 452644 | AW452616 | Hs.212481 | ESTs | 8.4 |
| | 452259 | AA317439 | Hs.28707 | signal sequence receptor, gamma (translo | 8.4 |
| | 409695 | AA296961 | | gb:EST112514 Adrenal gland tumor Homo sa | 8.3 |
| | 418076 | R61388 | Hs.6724 | ESTs | 8.3 |
| | 402696 | | | | 8.3 |
| 30 | 423099 | NM_002837 | Hs.123641 | protein tyrosine phosphatase, receptor 1 | 8.3 |
| | 413998 | AW103807 | Hs.243933 | ESTs | 8.3 |
| | 410008 | AA079552 | | gb:zm20h12.s1 Stratagene pancreas (93720 | 8.2 |
| | 416623 | N74925 | Hs.38761 | Homo sapiens cDNA: FLJ21564 fs, clone C | 8.2 |
| | 450001 | NM_001044 | Hs.406 | solute carrier family 6 (neurotransmitte | 8.2 |
| 35 | 435496 | AW840171 | Hs.265398 | ESTs, Weakly similar to transformation-r | 8.1 |
| | 413627 | BE182082 | Hs.246973 | ESTs | 8.0 |
| | 415713 | AW968573 | | gb:EST380649 MAGE resequences, MAGJ Homo | 8.0 |
| | 426695 | AW118191 | Hs.112729 | ESTs | 8.0 |
| | 452284 | AW451426 | Hs.252740 | ESTs | 8.0 |
| 40 | 454933 | BE141714 | | gb:QV0-HT0101-061099-032-c04 HT0101 Homo | 8.0 |
| | 426269 | H15302 | Hs.168950 | Homo sapiens mRNA; cDNA DKFZp566A1046 (f | 8.0 |
| | 418882 | NM_004996 | Hs.89433 | ATP-binding cassette, sub-family C (CFTR | 8.0 |
| | 444107 | T45839 | Hs.10319 | UDP glycosyltransferase 2 family, polype | 8.0 |
| | 445740 | T78281 | Hs.13226 | Homo sapiens clone 25181 mRNA sequence | 7.9 |
| 45 | 433190 | M26901 | Hs.3210 | renin | 7.9 |
| | 432777 | AA564991 | Hs.269477 | ESTs | 7.8 |
| | 449444 | AW818436 | Hs.23590 | solute carrier family 16 (monocarboxylic | 7.7 |
| | 444042 | NM_004915 | Hs.10237 | ATP-binding cassette, sub-family G (WHIT | 7.7 |
| 50 | 434032 | AW009951 | Hs.206892 | ESTs | 7.7 |
| | 419750 | AL079741 | Hs.183114 | Homo sapiens cDNA FLJ14236 fs, clone NT | 7.7 |
| | 439024 | R96696 | Hs.35598 | ESTs | 7.6 |
| | 437205 | AL110232 | | gb:Homo sapiens mRNA; cDNA DKFZp564D2071 | 7.6 |
| | 446030 | AF131805 | Hs.13544 | Homo sapiens clone 24850 mRNA sequence | 7.4 |
| 55 | 446311 | AW007294 | Hs.149795 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 7.4 |
| | 452883 | X80031 | Hs.150318 | ESTs | 7.4 |
| | 448253 | H25899 | Hs.201591 | ESTs | 7.4 |
| | 406030 | | | | 7.4 |
| | 437084 | AI911516 | Hs.127811 | ESTs | 7.4 |
| 60 | 435013 | H91923 | Hs.110024 | NADH:ubiquinone oxidoreductase MLRO subu | 7.3 |
| | 432143 | AL040183 | Hs.123484 | ESTs, Weakly similar to The KIAA0149 gen | 7.3 |
| | 409594 | AA076118 | | gb:zm18e06.s1 Stratagene pancreas (93720 | 7.3 |
| | 425151 | AA351814 | Hs.298678 | ESTs | 7.2 |
| | 448582 | AI538880 | Hs.94812 | ESTs | 7.2 |
| 65 | 455068 | AI807894 | Hs.27910 | centrosomal protein 2 | 7.2 |
| | 406504 | | | | 7.2 |
| | 428395 | AA427992 | Hs.104885 | ESTs, Weakly similar to zinc finger prot | 7.2 |
| | 421102 | AI470093 | Hs.89217 | ESTs | 7.2 |
| | 423161 | AL049227 | Hs.124776 | Homo sapiens mRNA; cDNA DKFZp564N1116 (f | 7.1 |
| 70 | 410534 | AW905138 | | gb:QV0-NN1071-280400-207-g07 NN1071 Homo | 7.1 |
| | 415084 | M19267 | Hs.77899 | tropomyosin 1 (alpha) | 7.0 |
| | 410274 | AA381807 | Hs.61762 | hypoxia-inducible protein 2 | 7.0 |
| | 439416 | W58294 | Hs.56254 | ESTs | 7.0 |
| | 420036 | R60336 | Hs.52792 | Homo sapiens mRNA; cDNA DKFZp586I1823 (f | 6.9 |
| 75 | 423349 | AF010258 | Hs.127428 | homeo box A9 | 6.8 |
| | 413070 | AA126776 | | gb:zm88c11.s1 Stratagene lung carcinoma | 6.8 |
| | 449361 | AW207890 | Hs.201918 | ESTs | 6.8 |
| | 459309 | AA040620 | Hs.109144 | ESTs | 6.8 |
| | 408771 | AW732573 | Hs.47584 | potassium voltage-gated channel, delayed | 6.8 |
| 80 | 416462 | W92845 | | gb:zh80f05.r1 Soares_fetal_liver_spleen_ | 6.8 |
| | 447835 | AW591623 | Hs.164129 | ESTs | 6.7 |
| | 403563 | | | | 6.7 |
| | 427897 | NM_017413 | Hs.181060 | apelin; peptide ligand for APJ receptor | 6.7 |
| | 422063 | BE156476 | | gb:QV0-HT0368-040100-082-c05 HT0368 Homo | 6.6 |

| | | | | | |
|----|--------|----------|-----------|--|-----|
| | 455275 | AW977806 | | gb:EST389810 MAGE resequences, MAGO Homo | 6.6 |
| | 441350 | AB020690 | Hs.7782 | paraneoplastic antigen MA2 | 6.6 |
| | 445575 | Z25368 | Hs.172004 | lin | 6.6 |
| | 446075 | AW451457 | Hs.279179 | ESTs | 6.6 |
| 5 | 405963 | | | | 6.6 |
| | 423049 | X59373 | Hs.188023 | ESTs | 6.6 |
| | 436456 | AW292677 | Hs.65909 | ESTs | 6.5 |
| | 420273 | AI652864 | Hs.197257 | ESTs | 6.5 |
| | 420831 | AA280824 | Hs.190035 | ESTs | 6.4 |
| 10 | 423739 | AA398155 | Hs.97600 | ESTs | 6.4 |
| | 441559 | AA338448 | Hs.259733 | ESTs | 6.4 |
| | 433999 | AA778212 | Hs.191869 | ESTs | 6.4 |
| | 439703 | AF086538 | Hs.196245 | ESTs | 6.4 |
| | 433757 | AI949974 | Hs.152670 | ESTs | 6.3 |
| 15 | 422095 | AI868872 | Hs.288966 | ceruloplasmin (ferroxidase) | 6.3 |
| | 415138 | C18356 | Hs.78045 | tissue factor pathway inhibitor 2 | 6.3 |
| | 448515 | H68441 | Hs.13528 | Homo sapiens cDNA FLJ14054 fs, clone HE | 6.3 |
| | 443595 | AF169312 | Hs.9613 | PPAR(gamma) angiopoietin related protein | 6.3 |
| | 429357 | AA779725 | Hs.164589 | ESTs | 6.3 |
| 20 | 404939 | | | | 6.3 |
| | 417071 | N58820 | Hs.275133 | ESTs | 6.2 |
| | 436209 | AW850417 | Hs.254020 | ESTs, Moderately similar to unnamed prot | 6.2 |
| | 403111 | | | | 6.2 |
| | 448796 | AA147829 | Hs.33193 | ESTs, Highly similar to AC007228 3 BC372 | 6.2 |
| 25 | 442353 | BE379594 | Hs.49136 | ESTs | 6.2 |
| | 451110 | AI955040 | Hs.301584 | ESTs | 6.1 |
| | 420092 | AA814043 | Hs.88045 | ESTs | 6.1 |
| | 441801 | AW242799 | Hs.211874 | ESTs | 6.0 |
| | 407500 | U43279 | | gb:Human nucleoporin nup 36 mRNA, comple | 6.0 |
| 30 | 450864 | R64139 | Hs.205225 | ESTs | 6.0 |
| | 455711 | BE069465 | | gb:RC2-BT0388-290100-012-a11 BT0388 Homo | 6.0 |
| | 405394 | | | | 6.0 |
| | 436476 | AA326108 | Hs.53631 | ESTs, Weakly similar to enhancer-of-spli | 6.0 |
| 35 | 454392 | BE260893 | | gb:601150677F1 NIH_MGC_19 Homo sapiens c | 6.0 |
| | 414575 | H11257 | Hs.295233 | ESTs | 5.9 |
| | 435767 | H73505 | Hs.117874 | ESTs | 5.9 |
| | 445495 | BE622641 | Hs.38489 | ESTs | 5.9 |
| | 428372 | AK000684 | Hs.183887 | hypothetical protein FLJ22104 | 5.9 |
| 40 | 436464 | AI016176 | Hs.269783 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 5.9 |
| | 415910 | U20350 | Hs.78913 | chemokine (C-X3-C) receptor 1 | 5.9 |
| | 402421 | | | | 5.8 |
| | 417038 | T85230 | | gb:yd33f02.r1 Soares fetal liver spleen | 5.8 |
| | 436461 | AW511956 | Hs.293261 | ESTs | 5.8 |
| 45 | 440870 | AI687284 | Hs.150539 | Homo sapiens cDNA FLJ13793 fs, clone TH | 5.8 |
| | 452281 | T93500 | Hs.28792 | Homo sapiens cDNA FLJ11041 fs, clone PL | 5.8 |
| | 417280 | AW173116 | Hs.262206 | ESTs | 5.7 |
| | 437259 | AI377755 | Hs.120695 | ESTs | 5.7 |
| | 425717 | X07282 | Hs.171495 | retinoic acid receptor, beta | 5.7 |
| 50 | 443614 | AV655386 | Hs.7645 | fibrinogen, B beta polypeptide | 5.7 |
| | 450625 | AW970107 | | gb:EST382188 MAGE resequences, MAGK Homo | 5.6 |
| | 425305 | AA363025 | Hs.155572 | Human clone 23801 mRNA sequence | 5.6 |
| | 430371 | D87466 | Hs.240112 | KIAA0276 protein | 5.6 |
| | 430499 | AW969408 | Hs.231991 | ESTs | 5.6 |
| 55 | 427920 | Z11502 | Hs.181107 | annexin A13 | 5.6 |
| | 449318 | AW236021 | Hs.108788 | ESTs, Weakly similar to zeste [D.melanog | 5.6 |
| | 407864 | AF069291 | Hs.40539 | chromosome 8 open reading frame 1 | 5.5 |
| | 410754 | T63840 | | gb:yc16b10.s1 Stratagene lung (937210) H | 5.5 |
| | 415286 | AW249540 | Hs.72548 | ESTs | 5.5 |
| 60 | 443297 | AI049864 | Hs.133029 | ESTs | 5.5 |
| | 440138 | AB033023 | Hs.6982 | hypothetical protein FLJ10201 | 5.5 |
| | 441006 | AW605267 | Hs.7627 | CGI-60 protein | 5.4 |
| | 409348 | AI401535 | Hs.146090 | ESTs | 5.4 |
| | 449679 | AI823951 | Hs.295668 | Homo sapiens cDNA FLJ11846 fs, clone HE | 5.4 |
| 65 | 408938 | AA059013 | Hs.22607 | ESTs | 5.4 |
| | 456411 | AA603305 | | gb:np12d11.s1 NCI_CGAP_Pr3 Homo sapiens | 5.4 |
| | 443756 | AW089799 | Hs.153665 | ESTs | 5.4 |
| | 422232 | D43945 | Hs.113274 | transcription factor EC | 5.4 |
| | 424574 | BE408618 | Hs.150748 | malonyl-CoA decarboxylase | 5.3 |
| 70 | 424834 | AK001432 | Hs.153408 | Homo sapiens cDNA FLJ10570 fs, clone NT | 5.3 |
| | 440589 | BE397763 | Hs.194478 | Homo sapiens mRNA; cDNA DKFZp434O1572 (f | 5.3 |
| | 425782 | U66468 | Hs.159525 | cell growth regulatory with EF-hand doma | 5.3 |
| | 450236 | AW162998 | Hs.24684 | KIAA1376 protein | 5.3 |
| | 418110 | R43523 | Hs.217754 | Homo sapiens cDNA: FLJ22202 fs, clone H | 5.3 |
| 75 | 427061 | AB032971 | Hs.173392 | KIAA1145 protein | 5.3 |
| | 413841 | M34276 | Hs.75576 | plasminogen | 5.3 |
| | 432358 | AI093491 | Hs.72830 | ESTs | 5.2 |
| | 416805 | F13271 | Hs.79981 | Human clone 23560 mRNA sequence | 5.2 |
| | 438475 | W03856 | Hs.13188 | ESTs, Highly similar to Gene product wit | 5.2 |
| 80 | 443305 | AI050693 | Hs.133318 | ESTs | 5.2 |
| | 413930 | M86153 | Hs.75618 | RAB11A, member RAS oncogene family | 5.1 |
| | 451859 | H44491 | Hs.252938 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 5.1 |
| | 429826 | N93266 | Hs.40747 | ESTs | 5.1 |
| | 436032 | AA150797 | Hs.109276 | latexin protein | 5.1 |

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|----|--------|-----------|-----------|---|-----|
| | 447081 | Y13896 | Hs.17287 | potassium inwardly-rectifying channel, s | 5.1 |
| | 438297 | AW515196 | Hs.258238 | ESTs, Moderately similar to ALU1_HUMAN A | 5.1 |
| | 421126 | M74587 | Hs.102122 | insulin-like growth factor binding prote | 5.1 |
| 5 | 440238 | AW451970 | Hs.155644 | paired box gene 2 | 5.1 |
| | 426651 | AU076646 | Hs.171683 | nuclear receptor subfamily 1, group H, m | 5.0 |
| | 425813 | AA364136 | Hs.210553 | ESTs, Weakly similar to hypothetical pro | 5.0 |
| | 432328 | AI572739 | Hs.195471 | 6-phosphofructo-2-kinase/fructose-2,6-bi | 5.0 |
| | 430682 | AW971949 | Hs.291252 | ESTs | 5.0 |
| 10 | 410049 | AW579475 | | gb:RC0-DT0076-110100-031-d10 DT0076 Homo | 5.0 |
| | 429222 | AI457692 | Hs.99164 | ESTs | 5.0 |
| | 446317 | AI287367 | Hs.150906 | ESTs | 5.0 |
| | 409506 | NM_006153 | Hs.54589 | NCK adaptor protein 1 | 5.0 |
| | 407768 | AW002841 | Hs.29475 | ESTs | 5.0 |
| 15 | 437938 | AI950087 | | gb:wc05c02.x1 NCI_CGAP_Kid12 Homo sapien | 5.0 |
| | 430403 | AF039390 | Hs.241382 | tumor necrosis factor (ligand) superfam | 4.9 |
| | 426215 | AW963419 | Hs.155223 | stanniocalcin 2 | 4.9 |
| | 448570 | AI923944 | Hs.30913 | ESTs | 4.9 |
| | 445034 | AW293376 | Hs.160323 | ESTs | 4.9 |
| 20 | 410361 | BE391804 | Hs.62661 | guanylate binding protein 1, interferon- | 4.8 |
| | 453891 | AB037751 | Hs.36353 | Homo sapiens mRNA full length insert cDN | 4.8 |
| | 438492 | AW340048 | Hs.293188 | ESTs | 4.8 |
| | 446417 | AI299050 | | gb:qn14d12.x1 NCI_CGAP_Lu5 Homo sapien | 4.8 |
| | 409578 | BE041386 | | gb:hk88c02.x1 NCI_CGAP_Lu21 Homo sapien | 4.8 |
| 25 | 447269 | NM_004861 | Hs.17958 | cerebroside (3'-phosphoadenylylsulfate:g | 4.8 |
| | 413795 | AL040178 | Hs.142003 | ESTs | 4.8 |
| | 422357 | AF016272 | Hs.115418 | cadherin 16, KSP-cadherin | 4.8 |
| | 452208 | AA024792 | Hs.31895 | ESTs, Weakly similar to B9 [H.sapien] | 4.7 |
| | 422711 | D60641 | Hs.21739 | Homo sapiens mRNA; cDNA DKFZp586i1518 (f | 4.7 |
| 30 | 441392 | AW451831 | Hs.222119 | ESTs, Weakly similar to K1CQ_HUMAN KERAT | 4.7 |
| | 439221 | AA737106 | Hs.32250 | ESTs | 4.7 |
| | 431956 | AK002032 | Hs.272245 | Homo sapiens cDNA FLJ11170 fis, clone PL | 4.7 |
| | 417355 | D13168 | Hs.82002 | endothelin receptor type B | 4.7 |
| | 414700 | H63202 | Hs.38163 | ESTs | 4.7 |
| 35 | 402739 | | | | 4.6 |
| | 403170 | | | | 4.6 |
| | 443486 | NM_003428 | Hs.9450 | zinc finger protein 84 (HPF2) | 4.6 |
| | 408380 | AF123050 | Hs.44532 | diubiquitin | 4.6 |
| | 427899 | AA829286 | Hs.181062 | serum amyloid A1 | 4.6 |
| 40 | 446302 | AI285848 | Hs.149757 | ESTs | 4.5 |
| | 414812 | X72755 | Hs.77367 | monokine induced by gamma interferon | 4.5 |
| | 424063 | NM_002019 | Hs.138671 | fms-related tyrosine kinase 1 (vascular | 4.4 |
| | 413384 | NM_000401 | Hs.75334 | exostoses (multiple) 2 | 4.4 |
| | 421298 | AW172431 | Hs.13012 | ESTs | 4.4 |
| 45 | 420789 | AI670057 | Hs.199882 | ESTs | 4.4 |
| | 453558 | AI417023 | Hs.40478 | ESTs | 4.4 |
| | 453745 | AA952989 | Hs.63908 | Homo sapiens HSPC316 mRNA, partial cds | 4.4 |
| | 451762 | AF222980 | Hs.26985 | disrupted in schizophrenia 1 | 4.4 |
| | 410334 | AW979261 | Hs.291993 | ESTs | 4.4 |
| 50 | 457030 | AI301740 | Hs.173381 | dihydropyrimidinase-like 2 | 4.4 |
| | 452194 | AI694413 | Hs.298262 | ESTs, Weakly similar to dJ88J8.1 [H.sapi | 4.4 |
| | 410407 | X66839 | Hs.63287 | carbonic anhydrase IX | 4.3 |
| | 401157 | | | | 4.3 |
| | 432004 | BE018302 | Hs.2894 | placental growth factor, vascular endothe | 4.3 |
| 55 | 426866 | U02330 | Hs.172816 | neuregulin 1 | 4.3 |
| | 446115 | AI733075 | Hs.292682 | ESTs, Weakly similar to S69913 hypertens | 4.3 |
| | 424704 | AI263293 | Hs.152096 | cytochrome P450, subfamily IIJ (arachido | 4.2 |
| | 446619 | AU076643 | Hs.313 | secreted phosphoprotein 1 (osteopontin, | 4.2 |
| | 433578 | BE336886 | Hs.3416 | adipose differentiation-related protein | 4.2 |
| 60 | 407065 | Y10141 | | gb:H.sapien DAT1 gene, partial, VNTR. | 4.2 |
| | 407182 | AA312551 | Hs.230157 | ESTs | 4.2 |
| | 416565 | AW000960 | Hs.44970 | ESTs | 4.2 |
| | 442230 | BE219088 | Hs.279547 | ESTs | 4.2 |
| | 440680 | AA903098 | | gb:ok46f08.s1 NCI_CGAP_Lu2 Homo sapien | 4.2 |
| 65 | 413802 | AW964490 | Hs.32241 | ESTs | 4.2 |
| | 438370 | AA843242 | Hs.48523 | ESTs | 4.2 |
| | 432731 | R31178 | Hs.287820 | fibronectin 1 | 4.2 |
| | 409745 | AA077391 | | gb:7B14E12 Chromosome 7 Fetal Brain cDNA | 4.2 |
| | 441484 | AA935481 | Hs.58972 | ESTs | 4.2 |
| 70 | 411213 | AA676939 | Hs.69285 | neuropilin 1 | 4.2 |
| | 453045 | AW418979 | Hs.224502 | ESTs | 4.2 |
| | 407999 | AI126271 | Hs.49433 | ESTs, Weakly similar to HYPOTHETICAL PRO | 4.2 |
| | 409770 | AW499536 | | gb:U1-HF-BR0p-aj-c-12-0-U1.r1 NIH_MGC_5 | 4.1 |
| | 449856 | AA203155 | Hs.18200 | ESTs | 4.1 |
| 75 | 430806 | S69377 | Hs.247978 | T-cell acute lymphocytic leukemia 2 | 4.1 |
| | 412672 | BE006341 | | gb:RC2-BN0127-240300-011-b05 BN0127 Homo | 4.1 |
| | 430719 | AA488988 | Hs.293796 | ESTs | 4.1 |
| | 409637 | AA323948 | Hs.55407 | Homo sapiens mRNA; cDNA DKFZp434K0621 (f | 4.1 |
| | 414696 | AF002020 | Hs.76918 | Niemann-Pick disease, type C1 | 4.1 |
| 80 | 444670 | H58373 | Hs.37494 | ESTs | 4.1 |
| | 448090 | AI608821 | Hs.270289 | ESTs | 4.1 |
| | 408830 | AK001709 | Hs.48403 | hypothetical protein FLJ10847 | 4.1 |
| | 419088 | AI538323 | Hs.77496 | small nuclear ribonucleoprotein polypept | 4.1 |
| | 416655 | AW968613 | Hs.79428 | BCL2/adenovirus E1B 19kD-interacting pro | 4.1 |

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|----|--------|----------|-----------|---|-----|
| | 435772 | AW975688 | Hs.250867 | zona peflucida glycoprotein 3A (sperm re | 4.1 |
| | 442556 | AL137761 | Hs.8379 | Homo sapiens mRNA; cDNA DKFZp586L2424 (f | 4.1 |
| | 459595 | AL040421 | | gb:DKFZp434B0714_r1 434 (synonym: htes3) | 4.1 |
| 5 | 438859 | AI559626 | Hs.164973 | ESTs, Weakly similar to AF231024 1 proto | 4.0 |
| | 423279 | AW959861 | Hs.290943 | ESTs | 4.0 |
| | 441592 | AW137071 | Hs.127211 | ESTs | 4.0 |
| | 411836 | AW901879 | | gb:QV0-NN1021-280400-212-110 NN1021 Homo | 4.0 |
| | 426384 | AI472078 | | gb:ij85h03.x1 Soares_NSF_F8_9W_OT_PA_P_S | 4.0 |
| 10 | 412494 | AL133900 | Hs.792 | ADP-ribosylation factor domain protein 1 | 4.0 |
| | 413583 | AL120806 | Hs.5888 | ESTs | 4.0 |
| | 415610 | L44319 | | gb:HUMEST1D10 Human thymus NSTH II Homo | 4.0 |
| | 430009 | AA894564 | Hs.22242 | ESTs | 4.0 |
| | 449539 | W80363 | Hs.58446 | ESTs | 4.0 |
| 15 | 438929 | AW195515 | Hs.253177 | ESTs | 4.0 |
| | 416000 | R82342 | Hs.79856 | ESTs | 4.0 |
| | 429616 | AI982722 | Hs.120845 | ESTs | 4.0 |
| | 458471 | AV648609 | Hs.194240 | ESTs | 4.0 |
| | 453195 | BE241876 | Hs.32352 | hypothetical protein DKFZp434K1210 | 4.0 |
| 20 | 459046 | AA910339 | Hs.26216 | Homo sapiens cDNA: FLJ22811 fis, clone K | 3.9 |
| | 438177 | BE327015 | Hs.281391 | ESTs | 3.9 |
| | 422438 | AA445925 | Hs.270896 | ESTs | 3.9 |
| | 450382 | AA397658 | Hs.60257 | Homo sapiens cDNA FLJ135598 fis, clone PL | 3.9 |
| | 449611 | AI970394 | Hs.197075 | ESTs | 3.9 |
| 25 | 452030 | AL137578 | Hs.27607 | Homo sapiens mRNA; cDNA DKFZp564N2464 (f | 3.9 |
| | 452881 | AW135220 | Hs.241921 | ESTs | 3.9 |
| | 414729 | BE466928 | Hs.281901 | ESTs | 3.9 |
| | 428816 | AA004986 | Hs.193852 | ATP-binding cassette, sub-family C (CFTR | 3.9 |
| | 405908 | | | | 3.8 |
| 30 | 445452 | H92975 | Hs.246046 | ESTs, Weakly similar to RET1_HUMAN RETIN | 3.8 |
| | 447961 | W32791 | Hs.170405 | ESTs | 3.8 |
| | 446639 | AI016826 | Hs.132501 | ESTs | 3.8 |
| | 401189 | | | | 3.8 |
| | 429548 | AW138872 | Hs.135288 | ESTs | 3.8 |
| 35 | 431523 | N55759 | Hs.163674 | ESTs | 3.8 |
| | 430014 | H59354 | Hs.182485 | actinin, alpha 4 | 3.8 |
| | 429250 | H56585 | Hs.198308 | tryptophan rich basic protein | 3.8 |
| | 451988 | AF263928 | Hs.27410 | papillomavirus regulatory factor PRF-1 | 3.8 |
| | 437939 | AW298600 | Hs.141840 | ESTs, Weakly similar to S59501 interlero | 3.8 |
| 40 | 427510 | Z47542 | Hs.179312 | small nuclear RNA activating complex, po | 3.8 |
| | 433522 | AI821730 | Hs.116524 | ESTs | 3.8 |
| | 443843 | AW878864 | Hs.13528 | Homo sapiens cDNA FLJ14054 fis, clone HE | 3.7 |
| | 407305 | AA715284 | | gb:nv35f03.r1 NCI_CGAP_Br5 Homo sapiens | 3.7 |
| | 434613 | AI821826 | Hs.187786 | ESTs, Moderately similar to ALUB_HUMAN ! | 3.7 |
| 45 | 410276 | AI554545 | Hs.68301 | ESTs | 3.7 |
| | 422504 | AA311407 | | gb:EST182167 Jurkat T-cells V Homo sapie | 3.7 |
| | 421013 | M62397 | Hs.1345 | mutated in colorectal cancers | 3.7 |
| | 437949 | U78519 | Hs.41654 | ESTs | 3.7 |
| | 431840 | AA534908 | Hs.2860 | POU domain, class 5, transcription facto | 3.7 |
| 50 | 409446 | AI561173 | Hs.67688 | ESTs | 3.7 |
| | 415263 | AA948033 | Hs.130853 | ESTs | 3.7 |
| | 450206 | AI796450 | Hs.201600 | ESTs | 3.7 |
| | 439444 | AI277652 | Hs.54578 | ESTs | 3.7 |
| | 437828 | AW976806 | Hs.291805 | ESTs | 3.7 |
| 55 | 453238 | AA033991 | Hs.269234 | ESTs | 3.7 |
| | 420041 | AB005142 | Hs.94592 | Idolho | 3.7 |
| | 448458 | AW614367 | Hs.171054 | ESTs | 3.7 |
| | 435080 | AI831760 | Hs.155111 | ESTs | 3.7 |
| | 444249 | T87398 | Hs.205816 | ESTs | 3.7 |
| 60 | 426595 | AW971980 | Hs.62402 | p21/Cdc42/Rac1-activated kinase 1 (yeast | 3.7 |
| | 417715 | AW969587 | Hs.86366 | ESTs | 3.7 |
| | 432579 | AF043244 | Hs.278439 | nucleolar protein 3 (apoptosis repressor | 3.6 |
| | 440048 | AA897461 | Hs.158469 | ESTs, Weakly similar to envelope protein | 3.6 |
| | 430091 | AB032958 | Hs.233023 | KIAA1132 protein | 3.6 |
| 65 | 438030 | X98427 | Hs.122634 | ESTs | 3.6 |
| | 453496 | AA442103 | Hs.33084 | solute carrier family 2 (facilitated glu | 3.6 |
| | 446636 | AC002563 | Hs.15767 | citron (rho-interacting, serine/threonin | 3.6 |
| | 417860 | AW408557 | Hs.235498 | Homo sapiens cDNA FLJ14075 fis, clone HE | 3.6 |
| | 435794 | H72108 | Hs.13704 | ESTs | 3.6 |
| 70 | 449695 | AA164569 | Hs.34550 | ESTs | 3.6 |
| | 411485 | AW848125 | | gb:IL3-CT0214-301299-048-G04 CT0214 Homo | 3.6 |
| | 426274 | D38122 | Hs.2007 | tumor necrosis factor (ligand) superfam | 3.6 |
| | 458201 | AI989961 | Hs.233477 | ESTs, Moderately similar to A Chain A, S | 3.6 |
| | 440987 | AA911705 | Hs.130229 | ESTs | 3.6 |
| 75 | 425178 | H16097 | Hs.161027 | ESTs | 3.6 |
| | 419080 | AW150835 | Hs.18878 | hypothetical protein FLJ21620 | 3.6 |
| | 436091 | AA704705 | Hs.181044 | ESTs, Weakly similar to A Chain A, Human | 3.6 |
| | 452671 | AW861074 | Hs.225833 | ESTs | 3.6 |
| | 437222 | AL117588 | Hs.299963 | ESTs | 3.6 |
| 80 | 437809 | AL137723 | Hs.5855 | Homo sapiens mRNA; cDNA DKFZp434D0818 (f | 3.5 |
| | 411545 | AW850818 | | gb:IL3-CT0220-091199-026-A03 CT0220 Homo | 3.5 |
| | 414799 | AI752416 | Hs.77326 | insulin-like growth factor binding prote | 3.5 |
| | 439882 | AA847856 | Hs.124565 | ESTs | 3.5 |
| | 419229 | AI827237 | Hs.282884 | ESTs | 3.5 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 431889 | AA521277 | Hs.124946 | ESTs | |
| | 422660 | AW297582 | Hs.237062 | ESTs | 3.5 |
| | 415122 | D60708 | Hs.22245 | ESTs | 3.5 |
| | 444127 | N63620 | Hs.13281 | ESTs | 3.5 |
| 5 | 416913 | AW934714 | | gb:RC1-DT0001-031299-011-a11 DT0001 Homo | 3.5 |
| | 409044 | AI129586 | Hs.33033 | ESTs | 3.5 |
| | 453365 | AA035211 | Hs.17404 | ESTs | 3.5 |
| | 452355 | N54926 | Hs.29202 | G protein-coupled receptor 34 | 3.5 |
| 10 | 423246 | AL119114 | Hs.23107 | ESTs | 3.5 |
| | 434131 | AI858275 | Hs.143659 | ESTs | 3.5 |
| | 425304 | AA463844 | Hs.31339 | fibroblast growth factor 11 | 3.5 |
| | 453775 | NM_002916 | Hs.35120 | replication factor C (activator 1) 4 (37 | 3.5 |
| | 426559 | AB001914 | Hs.170414 | paired basic amino acid cleaving system | 3.4 |
| 15 | 456311 | AA225632 | Hs.190016 | ESTs | 3.4 |
| | 420737 | L08096 | Hs.99899 | tumor necrosis factor (ligand) superfamily | 3.4 |
| | 448733 | NM_005629 | Hs.187958 | solute carrier family 6 (neurotransmitter) | 3.4 |
| | 401811 | | | | 3.4 |
| | 404021 | | | | 3.4 |
| 20 | 447175 | AI365208 | Hs.293606 | ESTs | 3.4 |
| | 453743 | AL120480 | | gb:DKFZp761K098_r1 761 (synonym: hamy2) | 3.4 |
| | 455070 | AW854675 | | gb:MR1-CT0258-290300-206-a01 CT0258 Homo | 3.4 |
| | 419546 | AA244199 | | gb:nc06c05.s1 NCI_CGAP_Pr1 Homo sapiens | 3.4 |
| | 449441 | AI656040 | Hs.196532 | ESTs | 3.4 |
| 25 | 441606 | R37263 | Hs.21065 | ESTs | 3.4 |
| | 446594 | AI311917 | Hs.16292 | ESTs | 3.4 |
| | 424684 | AI432572 | Hs.164221 | ESTs | 3.4 |
| | 413719 | BE439580 | Hs.75498 | small inducible cytokine subfamily A (Cy | 3.4 |
| | 427914 | AA417350 | Hs.20575 | ESTs | 3.4 |
| 30 | 438257 | AW474419 | Hs.224794 | ESTs | 3.4 |
| | 412642 | BE244598 | Hs.809 | hepatocyte growth factor (hepatopoietin A; | 3.4 |
| | 454690 | AW854639 | | gb:MR1-CT0258-140100-203-d10 CT0258 Homo | 3.3 |
| | 428046 | AW812795 | Hs.155381 | ESTs, Moderately similar to 138022 hypot | 3.3 |
| | 407331 | AI570416 | Hs.99910 | phosphofructokinase, platelet | 3.3 |
| 35 | 440472 | AA866169 | Hs.169071 | ESTs | 3.3 |
| | 421893 | NM_001078 | Hs.109225 | vascular cell adhesion molecule 1 | 3.3 |
| | 403797 | | | | 3.3 |
| | 417924 | AU077231 | Hs.82932 | cyclin D1 (PRAD1; parathyroid adenomas | 3.3 |
| | 410623 | AW958932 | Hs.293833 | ESTs | 3.3 |
| 40 | 449338 | H73444 | Hs.394 | adrenomedullin | 3.3 |
| | 441024 | AW081530 | Hs.137088 | ESTs | 3.3 |
| | 405257 | | | | 3.3 |
| | 450396 | AU077002 | Hs.24950 | regulator of G-protein signalling 5 | 3.3 |
| | 416892 | L24498 | Hs.80409 | growth arrest and DNA-damage-inducible, | 3.3 |
| 45 | 444471 | AB020684 | Hs.11217 | KIAA0877 protein | 3.3 |
| | 431689 | AA305688 | Hs.267695 | UDP-Gal:betaGlcNAc beta 1,3-galactosyltr | 3.3 |
| | 452093 | AA447453 | Hs.27860 | Homo sapiens mRNA; cDNA DKFZp586M0723 (f | 3.3 |
| | 425236 | AW067800 | Hs.155223 | stanniocalcin 2 | 3.3 |
| | 428824 | W23624 | Hs.173059 | ESTs | 3.2 |
| 50 | 450101 | AV649989 | Hs.24385 | Human hbc647 mRNA sequence | 3.2 |
| | 425260 | L47726 | Hs.1870 | phenylalanine hydroxylase | 3.2 |
| | 443830 | AI142095 | Hs.143273 | ESTs | 3.2 |
| | 415245 | N59650 | Hs.27252 | ESTs | 3.2 |
| | 405953 | | | | 3.2 |
| 55 | 430812 | L10405 | Hs.247992 | DNA binding protein for surfactant prote | 3.2 |
| | 418946 | AI798841 | Hs.132103 | ESTs | 3.2 |
| | 424750 | D29956 | Hs.152818 | ubiquitin specific protease 8 | 3.2 |
| | 435342 | AW979168 | Hs.163270 | ESTs | 3.2 |
| | 458860 | AW873557 | Hs.212739 | ESTs | 3.2 |
| 60 | 430172 | AA468591 | Hs.161889 | ESTs | 3.2 |
| | 431842 | NM_005764 | Hs.271473 | epithelial protein up-regulated in carci | 3.2 |
| | 451221 | AI949701 | Hs.210589 | ESTs | 3.2 |
| | 436211 | AK001581 | Hs.80961 | polymerase (DNA directed), gamma | 3.2 |
| | 433727 | C16221 | Hs.112608 | ESTs | 3.2 |
| 65 | 424897 | D63216 | Hs.153684 | frizzled-related protein | 3.2 |
| | 414821 | M63835 | Hs.77424 | Fc fragment of IgG, high affinity Ia, re | 3.1 |
| | 418030 | BE207573 | Hs.83321 | neuromedin B | 3.1 |
| | 417919 | AI928203 | Hs.86379 | ESTs | 3.1 |
| | 430437 | AI768801 | Hs.169943 | Homo sapiens cDNA FLJ13569 fis, clone PL | 3.1 |
| 70 | 409663 | AI743750 | Hs.65862 | ESTs | 3.1 |
| | 454024 | AA993527 | Hs.16281 | hypothetical protein FLJ23403 | 3.1 |
| | 424980 | L42172 | Hs.154078 | lipopolysaccharide-binding protein | 3.1 |
| | 421633 | AF121860 | Hs.106260 | sorting nexin 10 | 3.1 |
| | 436002 | R68529 | Hs.120967 | ESTs | 3.1 |
| 75 | 437682 | AA476652 | Hs.94952 | Homo sapiens cDNA: FLJ23371 fis, clone H | 3.1 |
| | 439451 | AF086270 | Hs.278554 | heterochromatin-like protein 1 | 3.1 |
| | 430183 | BE010038 | | gb:PM3-BN0176-100400-001-g04 BN0176 Homo | 3.1 |
| | 428479 | Y00272 | Hs.184572 | cell division cycle 2, G1 to S and G2 to | 3.1 |
| | 441285 | NM_002374 | Hs.167 | microtubule-associated protein 2 | 3.1 |
| 80 | 456386 | W28481 | | gb:47e1 Human retina cDNA randomly prime | 3.1 |
| | 451130 | AI762250 | Hs.211347 | ESTs | 3.1 |
| | 439702 | AW085525 | Hs.134182 | ESTs | 3.1 |
| | 453331 | AI240665 | Hs.8895 | ESTs | 3.1 |
| | 428841 | AI418430 | Hs.104935 | ESTs | 3.1 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 449899 | AI610700 | Hs.103280 | ESTs | 3.1 |
| | 436009 | H57130 | Hs.120925 | ESTs | 3.1 |
| | 448966 | AW372914 | Hs.287462 | Homo sapiens cDNA FLJ11875 fis, clone HE | 3.1 |
| | 408239 | AA053401 | Hs.271827 | ESTs, Moderately similar to ALU7_HUMAN A | 3.1 |
| 5 | 418526 | BE019020 | Hs.85838 | solute carrier family 16 (monocarboxylic | 3.1 |
| | 401260 | | | | 3.1 |
| | 450705 | U90304 | Hs.25351 | iroquois-class homeodomain protein | 3.1 |
| | 447233 | AW246333 | Hs.17901 | Homo sapiens cDNA: FLJ21974 fis, clone H | 3.1 |
| 10 | 424415 | NM_001975 | Hs.146580 | enolase 2, (gamma, neuronal) | 3.0 |
| | 403346 | | | | 3.0 |
| | 446319 | AW207590 | Hs.160711 | ESTs | 3.0 |
| | 432757 | AF113013 | Hs.278919 | PRO0806 protein | 3.0 |
| | 407921 | AI378617 | Hs.23100 | Homo sapiens cDNA FLJ12592 fis, clone NT | 3.0 |
| 15 | 414618 | AI204600 | Hs.96978 | ESTs | 3.0 |
| | 434398 | AA121098 | Hs.3838 | serum-inducible kinase | 3.0 |
| | 440113 | AI916532 | Hs.188272 | ESTs | 3.0 |
| | 424539 | L02911 | Hs.150402 | activin A receptor, type I | 3.0 |
| | 428945 | AW192803 | Hs.98974 | ESTs | 3.0 |
| 20 | 458297 | R54033 | Hs.21245 | ESTs | 3.0 |
| | 424405 | AI076838 | Hs.12967 | ESTs | 3.0 |
| | 411290 | AW835544 | | gb:QV4-LT0016-271299-068-f03 LT0016 Homo | 3.0 |
| | 459068 | BE464396 | Hs.118468 | ESTs | 3.0 |
| | 459065 | AI373532 | Hs.157910 | ESTs | 3.0 |
| 25 | 437693 | AI754443 | Hs.185951 | ESTs | 3.0 |
| | 429418 | AI381028 | Hs.99283 | ESTs | 3.0 |
| | 406117 | | | | 3.0 |
| | 415492 | R41674 | Hs.16491 | ESTs | 3.0 |
| | 419854 | AW664873 | Hs.87836 | Homo sapiens PAC clone RPS-1087M19 from | 3.0 |
| 30 | 453688 | AW381270 | Hs.194110 | Homo sapiens mRNA; cDNA DKFZp434C0814 (f | 3.0 |
| | 408119 | W26213 | | gb:22d10 Human retina cDNA randomly prim | 3.0 |
| | 438358 | AL035992 | Hs.210278 | ESTs | 3.0 |
| | 412372 | R65998 | Hs.118615 | ESTs | 3.0 |
| | 431984 | AL080239 | Hs.272284 | Human DNA sequence from clone GS1-256022 | 3.0 |
| 35 | 403782 | | | | 3.0 |
| | 443183 | R16258 | Hs.6217 | Homo sapiens cDNA FLJ12521 fis, clone NT | 3.0 |
| | 456388 | W28557 | | gb:48d8 Human retina cDNA randomly prime | 3.0 |
| | 447922 | Z92910 | Hs.20019 | hemochromatosis | 3.0 |
| | 428857 | AF008192 | Hs.194283 | putative GR6 protein | 3.0 |
| 40 | 406991 | S82185 | | (NONE) | 3.0 |
| | 432596 | AJ224741 | Hs.278461 | matrilin 3 | 3.0 |
| | 453202 | AW085781 | Hs.26270 | Homo sapiens cDNA FLJ11588 fis, clone HE | 3.0 |
| | 414132 | AI801235 | Hs.48480 | ESTs | 3.0 |
| | 409122 | W07089 | Hs.297873 | ESTs | 3.0 |
| 45 | 405547 | | | | 3.0 |
| | 422219 | AW978073 | | gb:EST390182 MAGE resequences, MAGO Homo | 3.0 |
| | 417227 | T57776 | Hs.191094 | ESTs | 3.0 |
| | 448592 | N69546 | Hs.141706 | ESTs | 3.0 |
| | 421477 | AI904743 | Hs.104650 | hypothetical protein FLJ10292 | 3.0 |
| 50 | 400368 | BE779978 | Hs.69149 | proline-serine-threonine phosphatase int | 3.0 |
| | 455362 | AW902635 | | gb:QV3-NN1024-100500-181-b02 NN1024 Homo | 3.0 |
| | 443578 | R97191 | Hs.134106 | ESTs | 3.0 |
| | 419348 | AA236645 | Hs.98274 | ESTs | 3.0 |
| | 439138 | AI742605 | Hs.193696 | ESTs | 3.0 |
| 55 | 449547 | H93543 | Hs.117963 | ESTs | 3.0 |
| | 455180 | AW863503 | | gb:MR3-SN0009-180400-110-c12 SN0009 Homo | 3.0 |
| | 444228 | AV648612 | Hs.282396 | ESTs | 3.0 |
| | 423496 | U91963 | Hs.129700 | toll-like 1 | 3.0 |
| | 401707 | | | | 3.0 |
| 60 | 419276 | BE165909 | Hs.134682 | Homo sapiens cDNA: FLJ23161 fis, clone L | 3.0 |
| | 441677 | AW271702 | Hs.93739 | ESTs | 3.0 |
| | 459587 | AA031956 | | gb:zk15e04.s1 Soares_pregnant_uterus_NbH | 3.0 |
| | 431311 | AA502552 | Hs.188980 | ESTs | 3.0 |
| | 426326 | BE165753 | Hs.250528 | ESTs, Weakly similar to unnamed protein | 3.0 |
| 65 | 412685 | BE092186 | | gb:IL2-BT0734-200400-075-H05 BT0734 Homo | 3.0 |
| | 414752 | BE503505 | Hs.248689 | ESTs | 3.0 |
| | 403144 | | | | 3.0 |
| | 407539 | X91103 | | gb:H.sapiens mRNA for Hr44 protein. | 3.0 |
| | 412379 | AW947581 | | gb:RC0-MT0004-140300-031-d08 MT0004 Homo | 3.0 |
| 70 | 407937 | AW297944 | Hs.242811 | ESTs | 3.0 |
| | 456976 | AI681882 | Hs.270428 | ESTs | 3.0 |
| | 417066 | AA329572 | Hs.172004 | titin | 3.0 |
| | 406007 | | | | 3.0 |
| | 416940 | N75620 | Hs.43157 | ESTs | 3.0 |
| 75 | 433322 | H50621 | Hs.134156 | ESTs | 3.0 |
| | 406088 | | | | 3.0 |
| | 416573 | R10356 | Hs.18865 | ESTs, Weakly similar to AC007228 2 BC372 | 3.0 |
| | 423130 | AW897586 | Hs.21213 | ESTs | 3.0 |
| | 412721 | AW183165 | Hs.95600 | ESTs | 3.0 |
| 80 | 418375 | NM_003081 | Hs.84389 | synaptosomal-associated protein, 25kD | 3.0 |
| | 422992 | AF016833 | Hs.122785 | maltase-glucoamylase (alpha-glucosidase) | 3.0 |
| | 406506 | | | | 3.0 |
| | 413472 | BE242870 | Hs.75379 | solute carrier family 1 (glial high affi | 3.0 |
| | 422650 | D42055 | Hs.1556 | neural precursor cell expressed, develop | 3.0 |

| | | | | | |
|------------|-------------|------------------------------------|--|--|-----|
| 5 | 400325 | M85292 | Hs.247924 | Homo sapiens endogenous HIV-1 related se | 3.0 |
| | 401078 | | | | 3.0 |
| | 446645 | AI336596 | Hs.156294 | ESTs | 3.0 |
| | 446704 | AI337228 | Hs.197083 | ESTs | 3.0 |
| | 427072 | H38046 | | gb:yp58c10.r1 Soares fetal liver spleen | 3.0 |
| TABLE 338: | | | | | |
| 10 | Pkey: | Unique Eos probe/identifier number | | | |
| | CAT number: | Gene cluster number | | | |
| | Accession: | Genbank accession numbers | | | |
| 15 | Pkey | CAT number | Accession | | |
| | 407615 | 1005404_1 | AW753085 AW753082 AW054744 AW753107 AW753087 | | |
| | 408119 | 1040172_1 | W26213 H08055 Z44031 AW954559 R17434 | | |
| | 409519 | 113722_1 | AA075368 AA075369 | | |
| | 409578 | 1140976_1 | BE041386 AW419449 AW663595 | | |
| 20 | 409594 | 114249_1 | AA076118 AA975618 AA076220 | | |
| | 409695 | 114876_1 | AA296961 AA296889 AA076945 AA077528 AA077497 | | |
| | 409745 | 115237_1 | AA077391 AJ347618 AJ361453 AJ088754 AW207491 AW960912 AA921874 AA286833 AA150722 BE152353 AW188822 BE152450 | | |
| | 409770 | 1154048_1 | AW499536 AW499553 AW502138 AW499537 AW502136 AW501743 | | |
| | 410008 | 116812_1 | AA079552 BE142525 BE142527 | | |
| 25 | 410049 | 1172307_1 | AW579475 AW939654 AW939655 | | |
| | 410534 | 1207247_1 | AW905138 AW753008 R13818 Z43519 | | |
| | 410754 | 1219733_1 | T63840 AW801569 AW801568 | | |
| | 411290 | 1237738_1 | AW835544 AW835613 AW835711 AW835697 AW835703 BE092535 BE092199 411485 1247181_1 AW848125 AW848124 AW848203 AW846695 | | |
| | | | AW848633 AW848693 BE350771 | | |
| 30 | 411545 | 1249138_1 | AW850818 AW850833 AW851100 | | |
| | 411836 | 1260619_1 | AW901879 AW901875 AW866247 BE011294 BE504813 | | |
| | 412209 | 1283610_1 | AW901456 AW901450 AW901441 | | |
| | 412359 | 129085_1 | AW837985 AW837938 AA101955 AW837913 AW837935 | | |
| | 412379 | 1292479_1 | AW947581 AW947546 AW947545 AW947544 | | |
| 35 | 412685 | 1321663_1 | BE092186 BE092157 AW983859 | | |
| | 412872 | 1333898_1 | BE006341 BE006307 BE006311 | | |
| | 413070 | 134815_1 | AA126776 AA133984 BE148613 BE063475 AA358219 | | |
| | 415610 | 1540554_1 | L44319 F12851 T75057 | | |
| | 415713 | 154859_1 | AW968573 AA167225 AA491129 | | |
| 40 | 416462 | 1595954_1 | W92845 H57479 | | |
| | 416548 | 1600181_1 | H52953 N76608 N72413 | | |
| | 416913 | 163001_1 | AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499 | | |
| | 417038 | 164390_1 | T85230 AA192508 T89190 | | |
| | 418053 | 171810_1 | AA211493 AW817839 AW817836 | | |
| 45 | 419213 | 182860_1 | AW749146 AW749138 AW749123 AW749130 AA235142 | | |
| | 419546 | 185766_1 | AA244199 AA244272 H57440 | | |
| | 420637 | 195241_1 | AW976153 AA278945 AA747691 | | |
| | 422063 | 210852_1 | BE156476 BE156473 BE156474 BE156475 AA302839 | | |
| | 422219 | 213547_1 | AW978073 AW978072 AA807550 AA306567 | | |
| 50 | 422504 | 217160_1 | AA311407 AW958321 N23583 R70050 | | |
| | 423735 | 231498_1 | AA330259 AA661806 AA502431 AW974633 AA649496 | | |
| | 426384 | 266211_1 | AI472078 AA377209 AA865807 | | |
| | 427072 | 274884_1 | H38046 W69645 AA397968 H38047 | | |
| | 428637 | 293660_1 | AW979268 AA878419 AA431342 AA431628 | | |
| 55 | 430183 | 31412_2 | BE010038 AA676833 AJ311783 T86895 W68032 BE064393 BE064394 BE157228 BE183282 AI936370 AA552514 T67280 AA039909 | | |
| | 431595 | 335512_1 | AA508196 BE142920 AI280311 AI205616 D61709 | | |
| | 432009 | 34025_1 | AL137424 BE007148 T52277 | | |
| | 432705 | 43463_1 | AL110232 N94765 | | |
| | 437938 | 44573_2 | AI950087 N70208 R97040 N36809 AJ308119 AW967677 N35320 AI251473 H59397 AW971573 R97278 W01059 AW967671 AA908598 AA251875 | | |
| 60 | | | AI820501 AI820532 W87891 T85904 U71456 T82391 BE328571 T75102 R34725 AA884922 BE328517 AI219788 AA84444 N92578 F13493 AA927794 | | |
| | | | AI560251 AW874068 AL134043 AW235363 AA663345 AW008282 AA488964 AA283144 AI890387 AI950344 AI714346 AI689062 AA282915 AW102898 | | |
| | | | AI872193 AJ763273 AW173586 AW150329 AJ653832 AI762668 AA988777 AA488892 AI356394 AW103813 AI539642 AA642789 AA856975 AW505512 | | |
| | | | AI961530 AW629970 BE612881 AW276997 AW513601 AW512843 AA044209 AW856538 AA180009 AA337499 AW961101 AA251669 AA251874 | | |
| | | | AI819225 AW205862 AI683338 AI858509 AW276905 AI633006 AA972584 AA908741 AW072629 AW513996 AA293273 AA969759 N75628 N23388 | | |
| 65 | | | H84729 H60052 T92487 AI022058 AA780419 AA551005 W80701 AW613456 AJ373032 AI564269 F00531 H83488 W37181 W78802 R66056 AI002839 | | |
| | | | R67840 AA300207 AW959581 T63226 F04005 | | |
| | 438966 | 467436_1 | AW979074 AA834841 AA828650 | | |
| | 438993 | 467651_1 | AA828995 AA834879 AI926361 | | |
| | 440680 | 500121_1 | AA903098 AW836693 BE160824 AW606818 AW582699 AW836766 | | |
| 70 | 442438 | 542469_1 | AA995998 AI916584 R61781 T77332 F07756 F08149 F07647 | | |
| | 446346 | 673545_1 | AI290205 AW235762 AI651268 | | |
| | 446417 | 676384_1 | AI299050 BE256910 | | |
| | 447641 | 73043_1 | BE619186 BE264952 R26042 | | |
| | 448450 | 76399_1 | BE612490 T05205 AA481187 | | |
| 75 | 449034 | 794817_1 | AI624049 AW117770 AI858360 | | |
| | 450625 | 84032_1 | AW970107 AA513951 AA010406 | | |
| | 452453 | 918300_1 | AI902519 AI902518 AI902516 | | |
| | 453743 | 979813_1 | AL120480 AW836448 AW176802 | | |
| | 453955 | 989877_1 | AW579207 AW936883 AW008026 N88905 | | |
| 80 | 454392 | 115882_1 | BE260893 AA078319 R85057 AW803024 H85811 AA078293 | | |
| | 454490 | 1217172_1 | AW797778 AW797781 AW797780 | | |
| | 454690 | 1229106_1 | AW854639 AW854719 AW854718 BE145880 AW854692 BE145866 AW816154 AW854698 AW854654 AW813335 AW854699 | | |
| | 454933 | 1245515_1 | BE141714 AW845993 AW845989 | | |
| | 455070 | 1252209_1 | AW854675 AW854685 AW854716 AW854690 AW854615 AW854624 AW854623 AW854641 AW854632 AW854695 AW854661 | | |
| | 455180 | 1258658_1 | AW863503 AW863362 | | |
| | 455275 | 1272255_1 | AW977806 AW887923 AW886321 | | |

455362 1284507_1 AW902635 AW902574 BE011167 BE011329 AW902808 AW902651
 455711 1352369_1 BE069465 BE069505
 456386 1842693_-1 W28481
 456388 1842839_-1 W28557
 456411 185688_1 AA603305 AA244095 AA244183
 459587 94893_1 AA031956
 459595 969956_1 AL040421

TABLE 33C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

| Pkey | Ref | Strand | NL_position |
|--------|---------|--------|---|
| 401078 | 3687273 | Plus | 105052-105171 |
| 401157 | 9438289 | Minus | 114133-114247,114567-114645 |
| 401189 | 9690246 | Minus | 90815-90929 |
| 401260 | 8076883 | Minus | 86008-86355 |
| 401352 | 9931258 | Minus | 26064-26208 |
| 401439 | 8246737 | Plus | 92993-94026 |
| 401707 | 2951946 | Plus | 21972-22104 |
| 401811 | 6730720 | Plus | 107002-107209 |
| 401976 | 3095020 | Minus | 17594-17709,21068-21175 |
| 402045 | 7923943 | Plus | 5964-6128 |
| 402421 | 9796341 | Minus | 46609-46662,46758-46811,86293-86346,89776-89829,90048-90101,102817-102924 |
| 402696 | 7328818 | Minus | 23600-23731 |
| 402739 | 9212192 | Plus | 60456-61019 |
| 402921 | 7981303 | Minus | 52242-52384,55599-55858,57124-57309,59633-59761,59957-60123 |
| 403095 | 8954339 | Plus | 150025-150240,151564-151690 |
| 403111 | 8980970 | Plus | 175012-175159 |
| 403144 | 9454649 | Minus | 166200-166628 |
| 403170 | 9838134 | Plus | 40955-41356 |
| 403345 | 8569726 | Plus | 77890-78069 |
| 403346 | 8569726 | Plus | 92752-93015 |
| 403563 | 8101139 | Plus | 2800-3501 |
| 403622 | 8569879 | Plus | 1941-2388,2580-2761 |
| 403782 | 8078608 | Plus | 41326-41633 |
| 403797 | 8099896 | Minus | 123065-125008 |
| 403899 | 7381715 | Minus | 9144-9350 |
| 404021 | 8655966 | Plus | 192534-193489 |
| 404115 | 9621489 | Plus | 232707-232982 |
| 404200 | 6010176 | Minus | 7066-7210 |
| 404347 | 9838195 | Plus | 74493-74829 |
| 404939 | 6862697 | Plus | 175318-175476 |
| 405257 | 7329310 | Plus | 73121-73273 |
| 405336 | 6094635 | Plus | 33267-33563 |
| 405394 | 6624123 | Minus | 31900-32373 |
| 405547 | 1054740 | Plus | 124361-124520,124914-125050 |
| 405609 | 5757553 | Minus | 42814-43010,43583-43783,44863-45033,46429-46554,47815-48018,49961-50153,51624-51727,51823-51959,52702-52918,55469-55601,57111-57307,58169-58296,60215-60332,61482-61727 |
| 405908 | 6758795 | Plus | 97969-98715 |
| 405943 | 6758796 | Plus | 20605-20812 |
| 405953 | 7960374 | Minus | 65101-65574 |
| 405963 | 8247786 | Plus | 4056-4699 |
| 406007 | 8247802 | Minus | 13484-13829 |
| 406030 | 8312328 | Minus | 96123-96547 |
| 406088 | 9123919 | Minus | 65772-66270 |
| 406117 | 9142932 | Plus | 54304-54584 |
| 406242 | 7417725 | Minus | 36736-36951 |
| 406291 | 5686274 | Plus | 9562-9867 |
| 406411 | 9256407 | Plus | 7400-7527 |
| 406414 | 9256407 | Plus | 49593-49850 |
| 406504 | 7711360 | Minus | 107068-107277 |
| 406506 | 7711374 | Minus | 6843-8077 |
| 406598 | 8248614 | Plus | 56373-56849 |

TABLE 34A: ABOUT 197 GENES UP-REGULATED IN KIDNEY CANCER

Table 34A lists about 197 genes up-regulated in kidney cancer compared to normal adult tissues that are likely to be extracellular or cell-surface proteins. These were selected as for Table 33A and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig, fn3, egf, 7tm domains). Predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 PSDomain: Protein Structural Domain
 R1: Ratio of tumor to normal tissue

| Pkey | ExAccn | UnigenelD | UnigeneTitle | PSDomain | R1 |
|--------|-----------|-----------|-----------------|---------------------|--------|
| 421471 | U90545 | Hs.104635 | solute carrier | TM,SS | 1007.4 |
| 452401 | NM_007115 | Hs.29352 | tumor necrosis | TM,SS,Xlink,CUB | 336.4 |
| 421727 | Y13153 | Hs.107318 | kynurenine 3-mo | TM,SS,Monooxygenase | 323.6 |

| | | | | | | |
|----|--------|-----------|-----------|------------------|---------------------------------------|-------|
| 5 | 426471 | M22440 | Hs.170009 | transforming gr | TM,SS,EGF | 224.6 |
| | 441031 | AI110684 | Hs.7645 | fibrinogen, B b | fibrinogen_C | 174.0 |
| | 411642 | NM_014932 | Hs.71132 | neurologin 1 | TM,SS,COesterase | 172.4 |
| | 452838 | U65011 | Hs.30743 | preferentially | TM | 161.4 |
| | 425984 | AW836277 | Hs.165636 | hypothetical pr | TM | 151.0 |
| | 453165 | S74727 | Hs.32042 | aspartoacylase | TM | 134.8 |
| | 452431 | U88879 | Hs.29499 | tol-like recep | TM,SS,TIR,LRRCT | 130.6 |
| 10 | 423508 | AW604297 | Hs.129711 | hepatitis A vir | TM,SS,ig | 120.4 |
| | 407975 | X89426 | Hs.41716 | endothelial cel | SS,IGFBP | 111.8 |
| | 415076 | NM_000857 | Hs.77890 | guanylate cycl | TM,guanylate_cyc | 97.0 |
| | 447046 | AA326187 | Hs.17170 | G protein-coupl | TM,7tm_1 | 90.2 |
| | 423109 | M59305 | Hs.123655 | natriuretic pep | TM,SS,ANF_receptor | 78.0 |
| | 422544 | AB018259 | Hs.118140 | KIAA0716 gene p | TM | 74.8 |
| 15 | 429352 | AK001512 | Hs.200097 | hypothetical pr | TM | 73.0 |
| | 453392 | U23752 | Hs.32964 | SRY (sex determ | TM,HMG_box | 72.2 |
| | 403345 | | | | TM,alpha-amylase | 69.6 |
| | 430440 | X52599 | Hs.2561 | nerve growth fa | TM,SS,NGF | 69.0 |
| | 408609 | AA330431 | Hs.640 | calcitonin rece | TM,SS,7tm_2 | 57.4 |
| 20 | 449101 | AA205847 | Hs.23016 | G protein-coupl | TM,7tm_1 | 52.0 |
| | 423685 | BE350494 | Hs.49753 | Homo sapiens mR | TM,Myosin_tail | 48.0 |
| | 452891 | N75582 | Hs.212875 | ESTs, Weakly si | SS | 44.0 |
| | 408430 | S79876 | Hs.44926 | dipeptidylpepti | TM,SS,DPPIV_N_term,Peptidase_S9 | 42.6 |
| | 412887 | X91906 | Hs.89872 | chloride channe | TM,CBS,voltage_CLC | 40.6 |
| 25 | 428822 | W28418 | Hs.301148 | potassium volta | TM | 40.2 |
| | 434208 | T92641 | Hs.127648 | hypothetical pr | TM,SS | 39.2 |
| | 400792 | AA635062 | Hs.50094 | Homo sapiens mR | TM,BIR,CARD,zf-C3HC4 | 38.6 |
| | 444743 | AA045648 | Hs.11817 | nudix (nucleosi | TM,muIT | 38.4 |
| | 406411 | | | | TM,vwa,FG-GAP | 37.6 |
| 30 | 423657 | AL045128 | Hs.1691 | glucan (1,4-alp | TM,alpha-amylase | 37.5 |
| | 424871 | NM_004525 | Hs.153595 | low density lip | TM,SS,EGF,kid_receptL_a,kid_receptL_b | 32.8 |
| | 449625 | NM_014253 | Hs.23796 | odz (odd Oz/ten | SH2,EGF | 30.5 |
| | 423020 | AA383092 | Hs.1608 | replication pro | TM | 29.6 |
| | 422420 | U03398 | Hs.1524 | tumor necrosis | TM,TNF | 29.6 |
| 35 | 414245 | BE148072 | Hs.75850 | WAS protein fam | TM,WH2 | 28.8 |
| | 410247 | AF181721 | Hs.61345 | RU2S | TM | 27.4 |
| | 406414 | | | | TM,vwa,FG-GAP | 27.2 |
| | 435951 | AF269162 | Hs.41267 | c21orf7 form A - | TM | 27.2 |
| | 419948 | AB041035 | Hs.93847 | NADPH oxidase 4 | TM,SS,Ferri_reduct | 26.4 |
| 40 | 448595 | AB014544 | Hs.21572 | KIAA0644 gene p | TM,SS,LRRCT,LRR | 25.8 |
| | 419569 | AI971651 | Hs.91143 | jagged 1 (Alagi | TM,SS,DSL,EGF | 25.6 |
| | 43242 | AB040938 | Hs.113940 | KIAA1505 protei | SS | 25.6 |
| | 416778 | M16505 | Hs.79876 | steroid sulfata | TM,Sulfatase | 23.0 |
| | 401352 | | | | TM | 22.6 |
| 45 | 404200 | | | | SS | 19.6 |
| | 446591 | H44186 | Hs.15456 | PDZ domain cont | TM,PDZ | 19.2 |
| | 431806 | AF186114 | Hs.270737 | tumor necrosis | TM,SS | 18.0 |
| | 423909 | AJ223183 | Hs.135194 | immunoglobulin | TM,SS,ig | 17.6 |
| 50 | 446364 | AB006624 | Hs.14912 | KIAA0286 protei | TM | 17.4 |
| | 425695 | NM_005401 | Hs.159238 | protein tyrosin | TM,Band_41,Y_phosphatase | 17.0 |
| | 410947 | AK000305 | Hs.67055 | hypothetical pr | TM | 16.8 |
| | 421002 | AF116030 | Hs.100932 | transcription f | TM,KRAB,zf-C2H2 | 16.5 |
| | 421659 | NM_014459 | Hs.106511 | protocadherin 1 | TM,SS,cadherin | 16.0 |
| 55 | 458679 | AW975460 | Hs.143563 | ESTs | SS | 14.4 |
| | 406598 | | | | SS | 13.6 |
| | 428508 | BE252383 | Hs.184668 | SBB131 protein | TM,PX | 13.2 |
| | 423321 | AB013885 | Hs.126926 | beta-ureidoprop | TM,SS,CN_hydrolase | 12.5 |
| | 422317 | NM_001147 | Hs.115181 | angiopoietin 2 | fibrinogen_C | 12.2 |
| 60 | 428227 | AA321649 | Hs.2248 | small inducible | IL8 | 12.0 |
| | 414923 | AW445008 | Hs.77637 | homeo box A4 | TM,homeobox | 11.9 |
| | 433231 | AB040926 | Hs.143552 | KIAA1493 protei | SS | 11.6 |
| | 443672 | AA323362 | Hs.9667 | butyrobetaine (| TM | 11.4 |
| | 405609 | | | | TM,Myosin_tail,myosin_head | 11.4 |
| | 418912 | NM_000685 | Hs.89472 | angiotensin rec | TM,7tm_1 | 11.4 |
| 65 | 449802 | AW901804 | Hs.23984 | hypothetical pr | TM | 11.2 |
| | 404347 | | | | SS | 10.8 |
| | 429945 | NM_006729 | Hs.226483 | diaphanous (Dro | TM,FH2 | 10.6 |
| | 435085 | AW130284 | Hs.192752 | ESTs, Moderate | TM | 10.6 |
| | 404115 | | | | SS | 10.2 |
| 70 | 420757 | X78592 | Hs.99915 | androgen recept | TM,Androgen_recep,hormone_rec,zf-C4 | 10.2 |
| | 446298 | AF187813 | Hs.14637 | kidney- and liv | TM,Acetyltransf | 10.1 |
| | 433703 | AA210863 | Hs.3532 | nemo-like kinas | TM,ptkinase | 9.2 |
| | 417404 | NM_007350 | Hs.82101 | pleckstrin homo | TM | 9.2 |
| | 451621 | AJ879148 | Hs.26770 | fatty acid bind | TM,SS,lipocalin | 9.2 |
| 75 | 402045 | | | | TM,SS | 9.0 |
| | 403095 | | | | SS,PAX,homeobox | 8.8 |
| | 401439 | | | | TM | 8.6 |
| | 407721 | Y12735 | Hs.38018 | dual-specificit | TM,ptkinase | 8.4 |
| 80 | 402921 | | | | TM | 8.4 |
| | 419503 | AA243642 | Hs.137422 | ESTs | TM | 8.4 |
| | 452259 | AA317439 | Hs.28707 | signal sequence | TM | 8.4 |
| | 402696 | | | | TM | 8.3 |
| | 450001 | NM_001044 | Hs.406 | solute carrier | TM,SS,SNF | 8.1 |
| | 433190 | M26901 | Hs.3210 | renin | SS,asp | 7.8 |

| | | | | | | |
|----|--------|-----------|-----------|-----------------|--|-----|
| | 449444 | AW818436 | Hs.23590 | solute carrier | TM,MCT | 7.7 |
| | 444042 | NM_004915 | Hs.10237 | ATP-binding cas | TM,ABC_tran | 7.7 |
| | 452883 | X80031 | Hs.150318 | ESTs | TM,C4.Collagen | 7.4 |
| | 425151 | AA351814 | Hs.298678 | ESTs | TM | 7.2 |
| 5 | 455068 | AI807894 | Hs.27910 | centrosomal pro | TM,SS | 7.2 |
| | 406504 | | | | TM | 7.2 |
| | 410274 | AA381807 | Hs.61762 | hypoxia-inducib | SS | 7.0 |
| | 423349 | AF010258 | Hs.127428 | homeo box A9 | TM,homeobox | 6.8 |
| | 408771 | AW732573 | Hs.47584 | potassium volta | TM,K_tetra,ion_trans | 6.8 |
| 10 | 445575 | Z25368 | Hs.172004 | titin | TM | 6.6 |
| | 415138 | C18356 | Hs.78045 | tissue factor p | Kunitz_BPTI,G-gamma | 6.3 |
| | 443595 | AF169312 | Hs.9613 | PPAR(gamma) ang | TM,SS,fibrinogen_C | 6.3 |
| | 404939 | | | | TM | 6.3 |
| | 436209 | AW850417 | Hs.254020 | ESTs, Moderatel | TM,SS | 6.2 |
| 15 | 403111 | | | | TM | 6.2 |
| | 405394 | | | | TM | 6.0 |
| | 454392 | BE260893 | | gb:601150677F1 | TM,SS | 6.0 |
| | 415910 | U20350 | Hs.78913 | chemokine (C-X3 | TM,7tm_1 | 5.9 |
| | 402421 | | | | TM | 5.8 |
| 20 | 425717 | X07282 | Hs.171495 | retinoic acid r | TM,hormone_rec,zf-C4 | 5.7 |
| | 427920 | Z11502 | Hs.181107 | annexin A13 | TM,annexin | 5.6 |
| | 407864 | AF069291 | Hs.40539 | chromosome 8 op | TM,FHA,BRCT | 5.5 |
| | 441006 | AW605267 | Hs.7627 | CGI-60 protein | TM | 5.4 |
| | 422232 | D43945 | Hs.113274 | transcription f | TM,HLH | 5.4 |
| 25 | 425782 | U66468 | Hs.159525 | cell growth reg | SS | 5.3 |
| | 450236 | AW162998 | Hs.24684 | KIAA1376 protei | TM,SS | 5.3 |
| | 413841 | M34276 | Hs.75576 | plasminogen | SS,trypsin,kringle,PAN | 5.3 |
| | 436032 | AA150797 | Hs.109276 | latexin protein | TM | 5.1 |
| | 447081 | Y13896 | Hs.17287 | potassium inwar | TM,IRK | 5.1 |
| 30 | 421126 | M74585 | Hs.102122 | insulin-like gr | SS,thyroglobulin_1,IgFBP | 5.1 |
| | 426651 | AU076646 | Hs.171683 | nuclear recepto | TM,zf-C4,hormone_rec | 5.0 |
| | 432328 | AI572739 | Hs.195471 | 6-phosphofructo | TM,6PF2K,PGAM | 5.0 |
| | 409506 | NM_006153 | Hs.54589 | NCK adaptor pro | TM,SH2,SH3 | 5.0 |
| | 410361 | BE391804 | Hs.62661 | guanylate bindi | TM,SS,GBP | 4.8 |
| 35 | 453891 | AB037751 | Hs.36353 | Homo sapiens mR | TM | 4.8 |
| | 447269 | NM_004861 | Hs.17958 | cerebroside (3 | TM,SS | 4.8 |
| | 422357 | AF016272 | Hs.115418 | cadherin 16, KS | TM,cadherin | 4.8 |
| | 417355 | D13168 | Hs.82002 | endothelin rece | TM,SS,7tm_1,zf-C3HC4 | 4.7 |
| | 402739 | | | | SS | 4.6 |
| 40 | 443486 | NM_003428 | Hs.9450 | zinc finger pro | TM,KRAB,zf-C2H2 | 4.6 |
| | 408380 | AF123050 | Hs.44532 | diubiquitin | TM,ubiquitin,7tm_3,ANF_receptor,sushi,7tm_1 | 4.6 |
| | 414812 | X72755 | Hs.77367 | monokine induce | SS,IL8 | 4.4 |
| | 424063 | NM_002019 | Hs.138671 | tns-related tyr | TM,SS,kinase,ig | 4.4 |
| | 413384 | NM_000401 | Hs.75334 | exostoses (mult | TM | 4.4 |
| 45 | 457030 | AJ301740 | Hs.173381 | dihydropyrimidi | TM,SS,Dihydroorotase | 4.4 |
| | 410407 | X66839 | Hs.63287 | carbonic anhydr | TM,SS,carb_anhydrase | 4.3 |
| | 401157 | | | | TM,citrate_synt | 4.3 |
| | 432004 | BE018302 | Hs.2894 | placental growt | SS,PDGF | 4.3 |
| 50 | 424704 | AI263293 | Hs.152096 | cytochrome P450 | SS,p450 | 4.2 |
| | 407065 | Y10141 | | gb:H.sapiens DA | TM,SS,SNF | 4.2 |
| | 411213 | AA676939 | Hs.69285 | neurotrophin 1 | TM,CUB,F5_F8_type_C,MAM | 4.2 |
| | 430806 | S69377 | Hs.247978 | T-cell acute ly | TM,HLH | 4.1 |
| | 414696 | AF002020 | Hs.76918 | Niemann-Pick di | TM,SS,Patched | 4.1 |
| 55 | 408830 | AK001709 | Hs.48403 | hypothetical pr | TM,UPF0013 | 4.1 |
| | 416655 | AW968613 | Hs.79428 | BCL2/adenovirus | TM | 4.1 |
| | 412494 | AL133900 | Hs.792 | ADP-ribosylatio | TM,arf,zf-B_box,zf-C3HC4 | 4.0 |
| | 453195 | BE241876 | Hs.32352 | hypothetical pr | TM | 4.0 |
| | 428816 | AA004986 | Hs.193852 | ATP-binding cas | TM,ABC_membrane,ABC_tran,COX15-CtaA | 3.9 |
| 60 | 401189 | | | | TM,SET,PHD,HMG_box | 3.8 |
| | 451988 | AF263928 | Hs.27410 | papillomavirus | TM | 3.8 |
| | 421013 | M62397 | Hs.1345 | mutated in colo | TM | 3.7 |
| | 420041 | AB005142 | Hs.94592 | klortho | TM,SS,Glyco_hydro_1 | 3.7 |
| | 432579 | AF043244 | Hs.278439 | nucleolar prote | TM | 3.6 |
| 65 | 453496 | AA442103 | Hs.33084 | solute carrier | TM,SS,sugar_tr | 3.6 |
| | 446636 | AC002563 | Hs.15767 | citron (rho-int | TM,CNH,DAG_PE-bind,PH,kinase,kinase_C | 3.6 |
| | 426274 | D38122 | Hs.2007 | tumor necrosis | TM,TNF | 3.6 |
| | 452355 | N54926 | Hs.29202 | G protein-coupl | TM,7tm_1 | 3.5 |
| | 453775 | NM_002916 | Hs.35120 | replication fac | TM,SS,AAA | 3.4 |
| 70 | 426559 | AB001914 | Hs.170414 | paired basic am | TM,Peptidase_S8,P | 3.4 |
| | 420737 | L08096 | Hs.98899 | tumor necrosis | TM,TNF | 3.4 |
| | 448733 | NM_005629 | Hs.187958 | solute carrier | TM,SNF,ABC_tran,isodh,kinase,Ribosomal_L18ae | 3.4 |
| | 413719 | BE439580 | Hs.75498 | small inducible | SS,IL8 | 3.4 |
| | 427914 | AA417350 | Hs.20575 | ESTs | TM,GAS2 | 3.4 |
| | 412642 | BE244598 | Hs.809 | hepatocyte grow | kringle,PAN,trypsin | 3.4 |
| 75 | 421893 | NM_001078 | Hs.109225 | vascular cell a | TM,SS,ig | 3.3 |
| | 417924 | AU077231 | Hs.82932 | cyclin D1 (PRAD | TM,cyclin | 3.3 |
| | 405257 | | | | TM | 3.3 |
| | 450396 | AU077002 | Hs.24950 | regulator of G- | TM,RGS | 3.3 |
| 80 | 416892 | L24498 | Hs.80409 | growth arrest a | TM,Ribosomal_L7Ae | 3.3 |
| | 425236 | AW067800 | Hs.155223 | stanniocalcin 2 | SS | 3.3 |
| | 430812 | L10405 | Hs.247992 | DNA binding pro | TM,SS | 3.2 |
| | 431842 | NM_005764 | Hs.271473 | epithelial prot | TM,SS | 3.2 |
| | 424897 | D63216 | Hs.153684 | fizzled-relate | TM,Fz,NTR | 3.2 |

| | | | | | | |
|--------|--------------|---|---|---|---|-----|
| 5 | 414821 | M63835 | Hs.77424 | Fc fragment of | TM,SS,ig | 3.1 |
| | 418030 | BE207573 | Hs.83321 | neuromedin B | SS | 3.1 |
| | 421633 | AF121860 | Hs.106260 | sorting nexin 1 | TM,PX | 3.1 |
| | 441285 | NM_002374 | Hs.167 | microtubule-ass | SS,tubulin-binding | 3.1 |
| | 418526 | BE019020 | Hs.85838 | solute carrier | TM,MCT | 3.1 |
| | 401260 | | | | TM,SS | 3.1 |
| | 450705 | U90304 | Hs.25351 | iroquois-class | TM,homeobox | 3.1 |
| | 424415 | NM_001975 | Hs.146580 | enolase 2, (gam | TM,SS,enolase | 3.1 |
| | 403346 | | | | TM,alpha-amylase | 3.0 |
| | 10 | 432757 | AF113013 | Hs.278919 | PRO0806 protein | TM |
| 434398 | | AA121098 | Hs.3838 | serum-inducible | TM,pkinase,POLO_box | 3.0 |
| 424539 | | L02911 | Hs.150402 | activin A recep | TM,Activin_rec,pkinase | 3.0 |
| 406117 | | | | | SS | 3.0 |
| 408119 | | W26213 | | gb:22d10 Human | TM,SS | 3.0 |
| 15 | 431984 | AL080239 | Hs.272284 | Human DNA seque | TM | 3.0 |
| | 403782 | | | | TM | 3.0 |
| | 447822 | Z92910 | Hs.20019 | hemochromatosis | TM,SS,ig,MHC_I,histone,SPRY,zf-B_box,zf-C3HC4 | 3.0 |
| | 428857 | AF008192 | Hs.194283 | putative GR6 pr | SS | 3.0 |
| | 432596 | AJ224741 | Hs.278461 | matrilin 3 | SS | 3.0 |
| 20 | 453202 | AW085781 | Hs.26270 | Homo sapiens cD | TM | 3.0 |
| | 405547 | | | | TM,SS,ABC_membrane,ABC_tran | 3.0 |
| | 423496 | U91963 | Hs.129700 | tblold-like 1 | TM,SS,EGF,CUB,Astacin | 3.0 |
| | 401707 | | | | SS | 3.0 |
| | 403144 | | | | TM,ion_trans,K_tetra | 3.0 |
| 25 | 418375 | NM_003081 | Hs.84389 | synaptosomal-as | TM,NA | 3.0 |
| | 422992 | AF016833 | Hs.122785 | maltese-glucoam | TM,Glyco_hydro_31,trefol | 3.0 |
| | 406506 | | | | TM | 3.0 |
| | 413472 | BE242870 | Hs.75379 | solute carrier | TM,SDF | 3.0 |
| | | | | | | 3.0 |
| 30 | TABLE 34B: | | | | | |
| | Pkey: | Unique Eos probeset identifier number | | | | |
| | CAT number: | Gene cluster number | | | | |
| | Accession: | Genbank accession numbers | | | | |
| 35 | Pkey | CAT number | Accession | | | |
| | 408119 | 1040172_1 | W26213 H08055 Z44031 AW954559 R17434 | | | |
| | 454392 | 115882_1 | BE260893 AA078319 R85057 AW803024 H85811 AA078293 | | | |
| 40 | TABLE 34C: | | | | | |
| | Pkey: | Unique number corresponding to an Eos probeset | | | | |
| | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA | | | | |
| | Strand: | sequence of human chromosome 22" Dunham, et al. (1999) <u>Nature</u> 402:489-495. | | | | |
| | Nt_position: | Indicates DNA strand from which exons were predicted. | | | | |
| 45 | | Indicates nucleotide positions of predicted exons. | | | | |
| | Pkey | Ref | Strand | Nt_position | | |
| | 401157 | 9438289 | Minus | 114133-114247,114567-114645 | | |
| | 401189 | 9690246 | Minus | 90815-90929 | | |
| 50 | 401260 | 8076883 | Minus | 86008-86355 | | |
| | 401352 | 9931258 | Minus | 26064-26208 | | |
| | 401439 | 8246737 | Plus | 92993-94026 | | |
| | 401707 | 2951946 | Plus | 21972-22104 | | |
| | 402045 | 7923943 | Plus | 5964-6128 | | |
| 55 | 402421 | 9796341 | Minus | 46609-46662,46758-46811,86293-86346,89776-89829,90048-90101,102817-102924 | | |
| | 402696 | 7328818 | Minus | 23600-23731 | | |
| | 402739 | 9212192 | Plus | 60456-61019 | | |
| | 402921 | 7981303 | Minus | 52242-52384,55599-55858,57124-57309,59633-59761,59957-60123 | | |
| | 403095 | 8954339 | Plus | 150025-150240,151564-151690 | | |
| 60 | 403111 | 8980970 | Plus | 175012-175159 | | |
| | 403144 | 9454649 | Minus | 166200-166628 | | |
| | 403345 | 8569726 | Plus | 77890-78069 | | |
| | 403346 | 8569726 | Plus | 92752-93015 | | |
| | 403782 | 8078608 | Plus | 41326-41633 | | |
| 65 | 404115 | 9621489 | Plus | 232707-232982 | | |
| | 404200 | 6010176 | Minus | 7066-7210 | | |
| | 404347 | 9838195 | Plus | 74493-74829 | | |
| | 404939 | 6862697 | Plus | 175318-175476 | | |
| | 405257 | 7329310 | Plus | 73121-73273 | | |
| 70 | 405394 | 6624123 | Minus | 31900-32373 | | |
| | 405547 | 1054740 | Plus | 124361-124520,124914-125050 | | |
| | 405609 | 5757553 | Minus | 42814-43010,43583-43783,44863-45033,46429-46554,47815-48018,49961-50153,51624-51727,51823-51959,52702-52918,55469-55601,57111-57307,58169-58296,60215-60332,61482-61727 | | |
| | 406117 | 9142932 | Plus | 54304-54584 | | |
| 75 | 406411 | 9256407 | Plus | 7400-7527 | | |
| | 406414 | 9256407 | Plus | 49593-49850 | | |
| | 406504 | 7711360 | Minus | 107068-107277 | | |
| | 406506 | 7711374 | Minus | 6843-8077 | | |
| | 406598 | 8248614 | Plus | 56373-56849 | | |

TABLE 35A: ABOUT 532 GENES UP-REGULATED IN KIDNEY CANCER

Table 35A lists about 532 genes up-regulated in kidney cancer compared to normal kidney. These were selected as for Table 33A except using an "average" of the 70th percentile for both the numerator and the denominator and using non-malignant kidney specimens in determining the denominator value.

| | | | | |
|----------------|--------|---|-----------|--|
| Pkey: | | Unique Eos probeset identifier number | | |
| ExAccn: | | Exemplar Accession number, Genbank accession number | | |
| UnigeneID: | | Unigene number | | |
| Unigene Title: | | Unigene gene title | | |
| R1: | | Ratio of tumor to normal tissue | | |
| 5 | | | | |
| | Pkey | ExAccn | UnigeneID | UnigeneTitle |
| | 424704 | AI263293 | Hs.152096 | cytochrome P450, subfamily IIJ (arachido |
| | 426559 | AB001914 | Hs.170414 | paired basic amino acid cleaving system |
| 10 | 458079 | AI796870 | Hs.54277 | ESTs |
| | 433447 | U29195 | Hs.3281 | neuronal pentraxin II |
| | 439979 | AW600291 | Hs.6823 | hypothetical protein FLJ10430 |
| | 446921 | AB012113 | Hs.16530 | small inducible cytokine subfamily A (Cy |
| 15 | 435359 | T60843 | Hs.189679 | ESTs |
| | 450152 | AI138635 | Hs.22968 | ESTs |
| | 452401 | NM_007115 | Hs.29352 | tumor necrosis factor, alpha-induced pro |
| | 440304 | BE159984 | Hs.125395 | ESTs |
| | 414821 | M63835 | Hs.77424 | Fc fragment of IgG, high affinity Ia, re |
| 20 | 421155 | H87879 | Hs.102267 | lysyl oxidase |
| | 452795 | AW392555 | Hs.18878 | hypothetical protein FLJ21620 |
| | 414812 | X72755 | Hs.77367 | monokine induced by gamma interferon |
| | 426471 | M22440 | Hs.170009 | transforming growth factor, alpha |
| | 427897 | NM_017413 | Hs.181060 | apelin; peptide ligand for APJ receptor |
| 25 | 449523 | NM_000579 | Hs.54443 | chemokine (C-C motif) receptor 5 |
| | 436961 | AW375974 | Hs.156704 | ESTs |
| | 447499 | AW262580 | Hs.147674 | KIAA1621 protein |
| | 438817 | AI023799 | Hs.163242 | ESTs |
| | 430630 | AW269920 | Hs.2621 | cystatin A (stefin A) |
| 30 | 428227 | AA321649 | Hs.2248 | small inducible cytokine subfamily B (Cy |
| | 424086 | AI351010 | Hs.102267 | lysyl oxidase |
| | 425289 | AW139342 | Hs.155530 | interferon, gamma-inducible protein 16 |
| | 436476 | AA326108 | Hs.53631 | ESTs, Weakly similar to enhancer-of-spli |
| | 415286 | AW249540 | Hs.72548 | ESTs |
| | 428157 | AI738719 | Hs.298668 | ESTs |
| 35 | 456804 | AI421645 | Hs.139851 | caveolin 2 |
| | 429490 | AI971131 | Hs.293684 | ESTs, Weakly similar to alternatively sp |
| | 429732 | U20158 | Hs.2488 | lymphocyte cytosolic protein 2 (SH2 doma |
| | 433757 | AI949974 | Hs.152670 | ESTs |
| 40 | 400419 | AF084545 | Hs.81800 | chondroitin sulfate proteoglycan 2 (vers |
| | 428046 | AW812795 | Hs.155381 | ESTs, Moderately similar to I38022 hypot |
| | 411642 | NM_014932 | Hs.71132 | neurotigin 1 |
| | 444381 | BE387335 | Hs.283713 | ESTs, Weakly similar to CA54_HUMAN COLLA |
| | 435767 | H73505 | Hs.117874 | ESTs |
| 45 | 427581 | NM_014788 | Hs.179703 | KIAA0129 gene product |
| | 448019 | AW947164 | Hs.195641 | ESTs |
| | 406671 | AA129547 | Hs.285754 | met proto-oncogene (hepatocyte growth fa |
| | 447835 | AW591623 | Hs.164129 | ESTs |
| | 448520 | AB002367 | Hs.21355 | doublecortin and CaM kinase-like 1 |
| 50 | 417308 | H60720 | Hs.81892 | KIAA0101 gene product |
| | 432731 | R31178 | Hs.287820 | fibronectin 1 |
| | 421566 | NM_000399 | Hs.1395 | early growth response 2 (Krox-20 (Drosop |
| | 419235 | AW470411 | Hs.288433 | neurotrophin |
| | 426490 | NM_001621 | Hs.170087 | aryl hydrocarbon receptor |
| 55 | 421485 | AA243499 | Hs.104800 | hypothetical protein FLJ10134 |
| | 422603 | BE242587 | Hs.118651 | hematopoietically expressed homeobox |
| | 418110 | R43523 | Hs.217754 | Homo sapiens cDNA: FLJ22202 fis, clone H |
| | 425984 | AW836277 | Hs.165636 | hypothetical protein DKFZp761C07121 |
| | 432606 | NM_002104 | Hs.3066 | granzyme K (serine protease, granzyme 3; |
| 60 | 436772 | AW975688 | Hs.250867 | zona pellucida glycoprotein 3A (sperm re |
| | 444969 | AI203334 | Hs.160628 | ESTs |
| | 426890 | AA393167 | Hs.41294 | ESTs |
| | 437330 | AL353944 | Hs.50115 | Homo sapiens mRNA: cDNA DKFZp761J1112 (f |
| | 458809 | AW972512 | Hs.20985 | sin3-associated polypeptide, 30kD |
| 65 | 446627 | AI973016 | Hs.15725 | hypothetical protein SBB148 |
| | 452960 | AK001335 | Hs.31137 | Homo sapiens cDNA: FLJ22681 fis, clone H |
| | 417280 | AW173116 | Hs.262206 | ESTs |
| | 422173 | BE385828 | Hs.250619 | phorbol-like protein MDS019 |
| | 420552 | AK000492 | Hs.98806 | hypothetical protein |
| 70 | 425188 | AK002052 | Hs.155071 | hypothetical protein FLJ11190 |
| | 427871 | AW992405 | Hs.59622 | ESTs, Weakly similar to unknown [H.sapie |
| | 446152 | AI292036 | Hs.150028 | ESTs |
| | 426560 | AA381661 | Hs.119878 | ESTs |
| | 419034 | NM_002110 | Hs.89555 | hemopoietic cell kinase |
| 75 | 456508 | AA502764 | Hs.123469 | ESTs, Weakly similar to AF208855 1 BM-01 |
| | 452281 | T93500 | Hs.28792 | Homo sapiens cDNA FLJ11041 fis, clone PL |
| | 442932 | AA457211 | Hs.8858 | bromodomain adjacent to zinc finger doma |
| | 426075 | AW513691 | Hs.270149 | ESTs |
| | 434398 | AA121098 | Hs.3838 | serum-inducible kinase |
| 80 | 450506 | NM_004460 | Hs.418 | fibroblast activation protein, alpha |
| | 425782 | U66468 | Hs.159525 | cell growth regulatory with EF-hand doma |
| | 426108 | AA622037 | Hs.166468 | programmed cell death 5 |
| | 416000 | R82342 | Hs.79856 | ESTs |
| | 450236 | AW162998 | Hs.24684 | KIAA1376 protein |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 449679 | AJ823951 | Hs.296668 | Homo sapiens cDNA FLJ11846 fis. clone HE | 11.6 |
| | 441350 | AB020690 | Hs.7782 | paraneoplastic antigen MA2 | 11.4 |
| | 442227 | AW771958 | Hs.175437 | ESTs | 11.4 |
| 5 | 414004 | AA737033 | Hs.7155 | ESTs, Weakly similar to 2115357A TYG pr | 11.4 |
| | 447056 | N67879 | Hs.157695 | ESTs | 11.4 |
| | 444863 | AW384082 | Hs.301323 | ESTs | 11.3 |
| | 452838 | U65011 | Hs.30743 | preferentially expressed antigen in mela | 11.3 |
| | 426780 | BE242284 | Hs.172199 | adenylate cyclase 7 | 11.2 |
| 10 | 453160 | AI263307 | Hs.146228 | ESTs | 11.1 |
| | 449539 | W80363 | Hs.58446 | ESTs | 11.1 |
| | 415323 | BE269352 | Hs.949 | neutrophil cytosolic factor 2 (65kD, chr | 11.1 |
| | 423508 | AW604297 | Hs.129711 | hepatitis A virus cellular receptor 1 | 11.0 |
| | 408380 | AF123050 | Hs.44532 | diubiquitin | 11.0 |
| 15 | 448410 | AK000227 | Hs.21126 | hypothetical protein FLJ20220 | 11.0 |
| | 451277 | AK001123 | Hs.26176 | hypothetical protein FLJ10261 | 11.0 |
| | 453165 | S74727 | Hs.32042 | aspartoacylase (aminoacylase 2, Canavan | 10.8 |
| | 435380 | AA679001 | Hs.192221 | ESTs | 10.8 |
| | 447183 | AI554733 | Hs.173182 | ESTs | 10.7 |
| 20 | 438330 | AW450572 | Hs.257316 | ESTs | 10.7 |
| | 441392 | AW451831 | Hs.222119 | ESTs, Weakly similar to K1CQ_HUMAN KERAT | 10.6 |
| | 418036 | Z37976 | Hs.83337 | latent transforming growth factor beta b | 10.5 |
| | 452862 | AW378065 | Hs.8587 | ESTs | 10.5 |
| | 431512 | BE270734 | Hs.2795 | lactate dehydrogenase A | 10.4 |
| 25 | 421478 | AI683243 | Hs.97258 | ESTs | 10.3 |
| | 413879 | AA132961 | Hs.212533 | Homo sapiens cDNA: FLJ22572 fis. clone H | 10.3 |
| | 411800 | N39342 | Hs.5184 | TH1 drosophila homolog | 10.3 |
| | 433862 | D85960 | Hs.3610 | KIAA0205 gene product | 10.3 |
| | 440594 | AW445167 | Hs.126036 | ESTs | 10.3 |
| 30 | 414504 | AW069181 | Hs.293523 | ESTs, Weakly similar to transformation-r | 10.2 |
| | 431211 | M86849 | Hs.5566 | gap junction protein, beta 2, 25kD (conn | 10.2 |
| | 437682 | AA476652 | Hs.94952 | Homo sapiens cDNA: FLJ23371 fis. clone H | 10.2 |
| | 430097 | AI523245 | Hs.127638 | ESTs | 10.1 |
| | 432579 | AF043244 | Hs.278439 | nucleolar protein 3 (apoptosis repressor | 10.1 |
| 35 | 434927 | H46612 | Hs.293815 | Homo sapiens HSPC285 mRNA, partial cds | 10.0 |
| | 424113 | AI743880 | Hs.12876 | ESTs | 9.9 |
| | 439981 | AI348408 | Hs.124675 | ESTs, Weakly similar to unnamed protein | 9.9 |
| | 411937 | AW876626 | | gb:RC3-PT0028-120200-013-d08 PT0028 Homo | 9.9 |
| | 439653 | AW021103 | Hs.6631 | hypothetical protein FLJ20373 | 9.9 |
| 40 | 428862 | NM_000346 | Hs.2316 | SRY (sex-determining region Y)-box 9 (ca | 9.9 |
| | 424623 | AW963062 | Hs.165809 | ESTs | 9.8 |
| | 410762 | AF226053 | Hs.66170 | HSKM-B protein | 9.8 |
| | 433285 | AW975944 | Hs.237396 | ESTs | 9.8 |
| | 413795 | AL040178 | Hs.142003 | ESTs | 9.7 |
| 45 | 434392 | AW983709 | Hs.268051 | ESTs | 9.6 |
| | 435542 | AA687376 | Hs.269533 | ESTs | 9.6 |
| | 430887 | N66801 | Hs.260287 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 9.6 |
| | 410339 | AI916499 | Hs.298258 | ESTs | 9.5 |
| | 452431 | U88879 | Hs.29499 | loll-like receptor 3 | 9.5 |
| 50 | 405121 | AB028989 | Hs.88500 | mitogen-activated protein kinase 8 inter | 9.5 |
| | 408134 | AK000184 | Hs.42945 | acid sphingomyelinase-like phosphodiester | 9.4 |
| | 438966 | AW979074 | | gb:EST391184 MAGE resequences, MAGP Homo | 9.4 |
| | 449625 | NM_014253 | Hs.23796 | odt (odd Ozten-m, Drosophila) homolog 1 | 9.4 |
| | 441024 | AW081530 | Hs.137088 | ESTs | 9.4 |
| 55 | 445900 | AF070526 | Hs.13429 | Homo sapiens clone 24787 mRNA sequence | 9.3 |
| | 433001 | AF217513 | Hs.279905 | clone HQ0310 PRO0310p1 | 9.2 |
| | 440074 | AA863045 | Hs.199057 | ESTs, Weakly similar to T00050 hypothesi | 9.2 |
| | 421659 | NM_014459 | Hs.106511 | protocadherin 17 | 9.2 |
| | 434542 | AA769310 | Hs.61260 | hypothetical protein FLJ13164 | 9.2 |
| 60 | 427283 | AL119796 | Hs.174185 | ectonucleotide pyrophosphatase/phosphodi | 9.1 |
| | 428820 | AA436187 | Hs.172631 | integrin, alpha M (complement component | 9.1 |
| | 419441 | AW023731 | Hs.274368 | Homo sapiens mRNA: cDNA DKFZp586i1524 (f | 9.1 |
| | 407856 | AA045281 | Hs.266175 | phosphoprotein associated with GEMs | 9.0 |
| | 431941 | AK000106 | Hs.272227 | Homo sapiens cDNA FLJ20099 fis. clone CO | 9.0 |
| 65 | 446460 | AW013999 | Hs.150164 | ESTs | 9.0 |
| | 452598 | AI831594 | Hs.68647 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 8.9 |
| | 407975 | X89426 | Hs.41716 | endothelial cell-specific molecule 1 (NO | 8.9 |
| | 437259 | AI377755 | Hs.120695 | ESTs | 8.9 |
| | 420235 | AA256756 | Hs.31178 | ESTs | 8.7 |
| 70 | 436959 | AL133076 | Hs.5354 | hypothetical protein FLJ12716 | 8.7 |
| | 413554 | AA319146 | Hs.75426 | secretogranin II (chromogranin C) | 8.7 |
| | 435894 | AI076667 | Hs.188011 | ESTs | 8.6 |
| | 418693 | AI750878 | Hs.87409 | thrombospondin 1 | 8.6 |
| | 425770 | NM_014363 | Hs.159492 | spastic ataxia of Charlevoix-Saguenay (s | 8.6 |
| 75 | 456249 | AI206144 | Hs.82508 | HRI/HFB2206 protein | 8.6 |
| | 437672 | AW748265 | Hs.5741 | flavohemoprotein b5-b5R | 8.6 |
| | 430268 | AK000737 | Hs.237480 | hypothetical protein FLJ20730 | 8.6 |
| | 417225 | AA815048 | Hs.24078 | Homo sapiens cDNA FLJ12649 fis. clone NT | 8.5 |
| | 435266 | AK001942 | Hs.4863 | Homo sapiens cDNA FLJ11080 fis. clone PL | 8.5 |
| 80 | 447974 | R76886 | | gb:y64b03.s1 Soares placenta Nb2HP Homo | 8.4 |
| | 447850 | AB018298 | Hs.19822 | SEC24 (S. cerevisiae) related gene famil | 8.4 |
| | 429525 | N92540 | Hs.205353 | ectonucleoside triphosphate diphosphohyd | 8.4 |
| | 435717 | AF227905 | Hs.105794 | UDP-glucose:glycoprotein glucosyltransfe | 8.3 |
| | 445784 | AI253155 | Hs.146065 | ESTs | 8.3 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 454024 | AA933527 | Hs.16281 | hypothetical protein FLJ23403 | 8.3 |
| | 443885 | H91806 | Hs.15284 | ESTs | 8.3 |
| | 403713 | | | | 8.3 |
| 5 | 433376 | AJ249361 | Hs.74122 | caspase 4, apoptosis-related cysteine pr | 8.2 |
| | 419490 | NM_006144 | Hs.90708 | granzyme A (granzyme 1, cytotoxic T-lymp | 8.2 |
| | 444670 | H58373 | Hs.37494 | ESTs | 8.2 |
| | 408761 | AA057264 | Hs.238936 | ESTs | 8.2 |
| | 453033 | AA325869 | Hs.31463 | KIAA0281 gene product | 8.2 |
| 10 | 441224 | AU076964 | Hs.7753 | calumenin | 8.1 |
| | 441689 | AI123705 | Hs.106932 | ESTs | 8.1 |
| | 440283 | AI732892 | Hs.190489 | ESTs | 8.1 |
| | 429598 | AA811257 | Hs.269710 | ESTs | 8.1 |
| | 424775 | AB014540 | Hs.153026 | SWAP-70 protein | 8.1 |
| 15 | 451292 | AB037716 | Hs.26204 | KIAA1295 protein | 8.0 |
| | 453951 | AI676235 | Hs.24789 | ESTs | 8.0 |
| | 416200 | AI188972 | Hs.44257 | Homo sapiens mRNA; cDNA DKFZp762O2215 (f | 8.0 |
| | 431087 | H12723 | Hs.290791 | ESTs | 8.0 |
| | 432328 | AI572739 | Hs.195471 | 6-phosphofructo-2-kinase/fructose-2,6-bi | 7.9 |
| 20 | 419474 | AW968619 | Hs.155849 | ESTs | 7.9 |
| | 418342 | BE002723 | Hs.293504 | ESTs, Moderately similar to ALU1_HUMAN A | 7.9 |
| | 408088 | AW157022 | Hs.4947 | Homo sapiens cDNA: FLJ22584 fis, clone H | 7.9 |
| | 413719 | BE439580 | Hs.75498 | small inducible cytokine subfamily A (Cy | 7.9 |
| | 440987 | AA911705 | Hs.130229 | ESTs | 7.9 |
| 25 | 412448 | L12864 | Hs.73895 | tumor necrosis factor receptor superfam | 7.9 |
| | 415737 | AA167626 | Hs.118743 | ESTs | 7.9 |
| | 412959 | D87458 | Hs.75090 | KIAA0282 protein | 7.8 |
| | 424247 | X14008 | Hs.234734 | lysosome (renal amyloidosis) | 7.8 |
| | 453331 | AI240665 | Hs.8895 | ESTs | 7.8 |
| 30 | 421991 | NM_014918 | Hs.110488 | KIAA0990 protein | 7.8 |
| | 443450 | N66045 | Hs.133529 | ESTs | 7.8 |
| | 431876 | AA521183 | Hs.269678 | ESTs | 7.8 |
| | 432582 | AI623817 | Hs.168457 | ESTs | 7.7 |
| | 445800 | AA126419 | Hs.301632 | ESTs | 7.7 |
| 35 | 424636 | AA453734 | Hs.10198 | ESTs | 7.7 |
| | 432134 | AI816782 | Hs.122583 | Homo sapiens cDNA: FLJ21934 fis, clone H | 7.7 |
| | 446873 | AI554439 | Hs.30724 | ESTs | 7.7 |
| | 400793 | AA635062 | Hs.50094 | Homo sapiens mRNA; cDNA DKFZp434O0515 (f | 7.7 |
| | 436061 | AI248584 | Hs.190745 | Homo sapiens cDNA: FLJ21326 fis, clone C | 7.7 |
| 40 | 442028 | AI239437 | Hs.48945 | ESTs | 7.7 |
| | 442760 | BE075297 | Hs.10067 | ESTs, Weakly similar to KIAA1205 protein | 7.7 |
| | 442152 | R39246 | Hs.239666 | Homo sapiens cDNA FLJ13495 fis, clone PL | 7.7 |
| | 427944 | AA417878 | Hs.48401 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 7.6 |
| | 414646 | AA353776 | Hs.901 | CD48 antigen (B-cell membrane protein) | 7.6 |
| 45 | 407634 | AW016569 | Hs.301280 | ESTs, Highly similar to AF241831 1 intra | 7.6 |
| | 418372 | AA311833 | Hs.84318 | replication protein A1 (70kD) | 7.6 |
| | 434666 | AF151103 | Hs.112259 | T cell receptor gamma locus | 7.6 |
| | 442432 | BE093589 | Hs.38178 | Homo sapiens cDNA: FLJ23468 fis, clone H | 7.6 |
| | 408418 | AW963897 | Hs.44743 | KIAA1435 protein | 7.6 |
| 50 | 418805 | AI829520 | Hs.227513 | ESTs | 7.5 |
| | 425354 | U62027 | Hs.155935 | complement component 3a receptor 1 | 7.5 |
| | 408743 | AL110246 | Hs.47367 | hypothetical protein from EUROIMAGE 7836 | 7.5 |
| | 444836 | AI589825 | Hs.173504 | ESTs, Weakly similar to JCS238 galactosy | 7.5 |
| | 421810 | AK001718 | Hs.108530 | hypothetical protein FLJ10856 | 7.4 |
| 55 | 432753 | NM_014075 | Hs.278915 | PRO0593 protein | 7.4 |
| | 420061 | AW024937 | Hs.29410 | ESTs | 7.4 |
| | 432865 | AI753709 | Hs.152484 | ESTs | 7.4 |
| | 419070 | AW979068 | Hs.182503 | ESTs | 7.4 |
| | 430172 | AA468591 | Hs.161889 | ESTs | 7.4 |
| 60 | 446343 | AW771414 | Hs.8314 | ESTs | 7.4 |
| | 424125 | M31669 | Hs.1735 | inhibin, beta B (activin AB beta polypep | 7.4 |
| | 453818 | BE256832 | Hs.10711 | Homo sapiens cDNA FLJ13449 fis, clone PL | 7.4 |
| | 447046 | AA326187 | Hs.17170 | G protein-coupled receptor 4 | 7.4 |
| | 410577 | X91911 | Hs.64639 | glioma pathogenesis-related protein | 7.4 |
| 65 | 452240 | AI591147 | Hs.61232 | ESTs | 7.3 |
| | 450375 | AA009647 | Hs.8850 | a disintegrin and metalloproteinase doma | 7.3 |
| | 422631 | BE218919 | Hs.118793 | hypothetical protein FLJ10688 | 7.3 |
| | 450205 | AI219748 | Hs.11356 | ESTs | 7.3 |
| | 437212 | AI765021 | Hs.210775 | ESTs | 7.3 |
| 70 | 440193 | AW902312 | Hs.7037 | pallid (mouse) homolog, pallidin | 7.2 |
| | 417022 | NM_014737 | Hs.80905 | Ras association (RalGDS/AF-6) domain fam | 7.2 |
| | 451818 | AI819018 | | gb:ts54f01.x1 NCI_CGAP_Kd8 Homo sapiens | 7.2 |
| | 453013 | AA031407 | | gb:zk15g12.r1 Soares_pregnanL uterus_NbH | 7.2 |
| | 430105 | X70297 | Hs.2540 | cholinergic receptor, nicotinic, alpha p | 7.2 |
| 75 | 451621 | AI879148 | Hs.26770 | fatty acid binding protein 7, brain | 7.2 |
| | 442438 | AA995998 | | gb:os26b03.s1 NCI_CGAP_Kd5 Homo sapiens | 7.2 |
| | 415138 | C18356 | Hs.78045 | tissue factor pathway inhibitor 2 | 7.2 |
| | 407305 | AA715284 | | gb:nv35f03.r1 NCI_CGAP_Br5 Homo sapiens | 7.2 |
| | 452814 | AI092790 | Hs.55016 | hypothetical protein FLJ21935 | 7.2 |
| 80 | 425028 | NM_001110 | Hs.172028 | a disintegrin and metalloproteinase doma | 7.2 |
| | 443462 | AI064690 | Hs.171176 | ESTs | 7.2 |
| | 422060 | R20893 | Hs.75613 | CD36 antigen (collagen type I receptor, | 7.2 |
| | 434096 | AW662958 | Hs.75825 | pleiomorphic adenoma gene-like 1 | 7.1 |
| | 443161 | AI038316 | | gb:ox48c08.x1 Soares_total_fetus_Nb2HF8_ | 7.1 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| 5 | 458725 | AW970192 | Hs.171942 | ras responsive element binding protein 1 | 7.1 |
| | 426423 | NM_012446 | Hs.169833 | single-stranded-DNA-binding protein | 7.1 |
| | 412783 | BE276738 | Hs.74578 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypep | 7.1 |
| | 435664 | AI032087 | Hs.269819 | ESTs | 7.0 |
| | 431708 | AI698136 | Hs.108873 | ESTs | 7.0 |
| | 426501 | AW043782 | Hs.293616 | ESTs | 7.0 |
| | 453548 | AL079983 | Hs.75442 | albumin | 7.0 |
| | 426595 | AW971980 | Hs.62402 | p21/Cdc42/Rac1-activated kinase 1 (yeast | 7.0 |
| 10 | 412490 | AW803564 | Hs.268850 | Homo sapiens cDNA: FLJ22528 fis, clone H | 7.0 |
| | 431556 | AF016028 | Hs.260039 | sarcospan (Kras oncogene-associated gene | 7.0 |
| | 420018 | U56387 | Hs.94376 | proprotein convertase subtilisin/kexin 1 | 6.9 |
| | 418986 | AI123555 | Hs.81796 | ESTs | 6.9 |
| | 430290 | AI734110 | Hs.136355 | ESTs | 6.9 |
| 15 | 427472 | AA522539 | Hs.131250 | transposon-derived Buster3 transposase-I | 6.9 |
| | 444042 | NM_004915 | Hs.10237 | ATP-binding cassette, sub-family G (WHIT | 6.9 |
| | 414737 | AI160386 | Hs.125087 | ESTs | 6.9 |
| | 420479 | AW183695 | Hs.186572 | ESTs | 6.9 |
| | 432656 | NM_000246 | Hs.3076 | MHC class II transactivator | 6.9 |
| 20 | 414217 | AI309298 | Hs.279898 | Homo sapiens cDNA: FLJ23165 fis, clone L | 6.9 |
| | 431870 | AW449902 | Hs.105500 | ESTs | 6.9 |
| | 415788 | AW628686 | Hs.78851 | KIAA0217 protein | 6.9 |
| | 430066 | AI929659 | Hs.237825 | signal recognition particle 72kD | 6.9 |
| | 437156 | AI916600 | Hs.121194 | Homo sapiens cDNA: FLJ21569 fis, clone C | 6.9 |
| 25 | 401539 | | | | 6.8 |
| | 412782 | AI189211 | Hs.173044 | ESTs | 6.8 |
| | 416058 | L08895 | Hs.78995 | MADS box transcription enhancer factor 2 | 6.8 |
| | 437205 | AL110232 | | gb:Homo sapiens mRNA; cDNA DKFZp564D2071 | 6.8 |
| 30 | 458814 | AI498957 | Hs.170861 | ESTs | 6.7 |
| | 452106 | AI141031 | Hs.21342 | ESTs | 6.7 |
| | 413249 | AF167160 | Hs.75251 | DEAD/H (Asp-Glu-Ala-Asp/His) box binding | 6.7 |
| | 420910 | AL049437 | Hs.100292 | Homo sapiens mRNA; cDNA DKFZp586E1120 (f | 6.7 |
| | 445527 | W39694 | Hs.83286 | ESTs | 6.7 |
| | 424063 | NM_002019 | Hs.138671 | fms-related tyrosine kinase 1 (vascular | 6.7 |
| 35 | 421977 | W94197 | Hs.110165 | ribosomal protein L26 homolog | 6.7 |
| | 430280 | AA361258 | Hs.237868 | interleukin 7 receptor | 6.7 |
| | 415989 | AI267700 | Hs.111128 | ESTs | 6.7 |
| | 418026 | BE379727 | Hs.83213 | fatty acid binding protein 4, adipocyte | 6.6 |
| | 425295 | AA431366 | Hs.37251 | ESTs | 6.6 |
| 40 | 438619 | AB032773 | Hs.6341 | TUJ2B1-TY protein | 6.6 |
| | 424916 | AW867440 | Hs.23096 | ESTs | 6.6 |
| | 429697 | AW296451 | Hs.24605 | ESTs | 6.6 |
| | 408741 | M73720 | Hs.646 | carboxypeptidase A3 (mast cell) | 6.6 |
| | 403549 | | | | 6.6 |
| 45 | 449008 | AW578003 | Hs.22826 | tropomodulin 3 (ubiquitous) | 6.6 |
| | 435798 | BE395289 | Hs.12720 | elF4E-transporter | 6.6 |
| | 447217 | BE465754 | Hs.17778 | neuropilin 2 | 6.6 |
| | 453070 | AK001465 | Hs.31575 | SEC63, endoplasmic reticulum translocon | 6.6 |
| | 410276 | AI554545 | Hs.68301 | ESTs | 6.6 |
| 50 | 435391 | AA704588 | Hs.58934 | ESTs | 6.6 |
| | 421878 | AA299652 | Hs.111496 | Homo sapiens cDNA FLJ11643 fis, clone HE | 6.6 |
| | 452092 | BE245374 | Hs.27842 | hypothetical protein FLJ11210 | 6.6 |
| | 448789 | BE539108 | Hs.22051 | Homo sapiens mRNA; cDNA DKFZp4340119 (f | 6.5 |
| | 425331 | AW962128 | | gb:EST374201 MAGE resequences, MAGG Homo | 6.5 |
| 55 | 431956 | AK002032 | Hs.272245 | Homo sapiens cDNA FLJ11170 fis, clone PL | 6.5 |
| | 444880 | AW118683 | Hs.154150 | ESTs | 6.5 |
| | 434131 | AI858275 | Hs.143659 | ESTs | 6.5 |
| | 446658 | AI440137 | Hs.164989 | ESTs | 6.5 |
| | 408150 | BE620274 | Hs.43112 | Homo sapiens mRNA; cDNA DKFZp434B1620 (f | 6.5 |
| | 403790 | | | | 6.5 |
| 60 | 417129 | AI381800 | Hs.143275 | Homo sapiens cDNA FLJ13233 fis, clone OV | 6.5 |
| | 452119 | AI656378 | Hs.33461 | ESTs | 6.5 |
| | 437396 | BE140396 | Hs.21621 | hypothetical protein DKFZp7620076 | 6.4 |
| | 458946 | AA009716 | Hs.42311 | ESTs | 6.4 |
| 65 | 452110 | T47667 | Hs.28005 | Homo sapiens mRNA; cDNA DKFZp564G2463 (f | 6.4 |
| | 449318 | AW236021 | Hs.108788 | ESTs. Weakly similar to zeste [D.melanog | 6.4 |
| | 408308 | AL033377 | Hs.44197 | hypothetical protein DKFZp564D0462 | 6.4 |
| | 402474 | | | | 6.4 |
| | 430712 | AW044647 | Hs.196284 | ESTs | 6.4 |
| 70 | 418299 | AA279530 | Hs.83968 | integrin, beta 2 (antigen CD18 (p95), ty | 6.4 |
| | 432683 | AW995441 | Hs.10475 | ESTs | 6.4 |
| | 423764 | AF054589 | Hs.132739 | ESTs | 6.4 |
| | 409571 | AA504249 | Hs.187585 | ESTs | 6.4 |
| 75 | 401600 | BE247275 | Hs.151787 | U5 snRNP-specific protein, 116 kD | 6.4 |
| | 415076 | NM_000857 | Hs.77890 | guanylate cyclase 1, soluble, beta 3 | 6.4 |
| | 432925 | AA878324 | Hs.192734 | ESTs | 6.4 |
| | 427528 | AL0077143 | Hs.179565 | minichromosome maintenance deficient [S. | 6.4 |
| | 453894 | AW937825 | Hs.56847 | Homo sapiens cDNA FLJ12874 fis, clone NT | 6.4 |
| | 430335 | D80007 | Hs.239499 | KIAA0185 protein | 6.4 |
| 80 | 453370 | AI470523 | Hs.182356 | ESTs. Moderately similar to translation | 6.3 |
| | 421327 | AA837295 | Hs.188802 | ESTs | 6.3 |
| | 450654 | AI245587 | Hs.25275 | Kruppel-type zinc finger protein | 6.3 |
| | 413497 | BE177661 | | gb:RC1-HT0598-020300-011-h02 HT0598 Homo | 6.3 |
| | 445279 | R41900 | Hs.22245 | ESTs | 6.3 |

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|----|--------|-----------|-----------|--|-----|
| | 429747 | M87507 | Hs.2490 | caspase 1, apoptosis-related cysteine pr | 6.3 |
| | 421252 | AA765930 | Hs.130878 | ESTs | 6.3 |
| | 432140 | AK000404 | Hs.272688 | hypothetical protein FLJ20397 | 6.3 |
| | 434203 | BE262677 | Hs.283558 | hypothetical protein PRO1855 | 6.2 |
| 5 | 419436 | AA991639 | Hs.15036 | ESTs, Highly similar to AF161358 1 HSPC0 | 6.2 |
| | 430287 | AW182459 | Hs.125759 | ESTs, Weakly similar to tumor suppressor | 6.2 |
| | 409690 | W45393 | Hs.94642 | ESTs, Highly similar to ATFa [H.sapiens] | 6.2 |
| | 420101 | AW500529 | Hs.95180 | Homo sapiens mRNA; cDNA DKFZp434A205 (tr | 6.1 |
| | 435889 | AJ249107 | Hs.269901 | ESTs | 6.1 |
| 10 | 417259 | AW903838 | Hs.81800 | chondroitin sulfate proteoglycan 2 (vers | 6.1 |
| | 448030 | N30714 | Hs.20161 | HDCME31P protein | 6.1 |
| | 442571 | C06338 | Hs.165464 | ESTs | 6.1 |
| | 421202 | AF193339 | Hs.102506 | eukaryotic translation initiation factor | 6.1 |
| | 415558 | AA885143 | Hs.125719 | ESTs | 6.1 |
| 15 | 408042 | AL049233 | Hs.42244 | Homo sapiens mRNA; cDNA DKFZp564A023 (tr | 6.1 |
| | 438086 | AA336519 | Hs.301167 | Homo sapiens cDNA: FLJ21545 fis, clone C | 6.1 |
| | 427390 | AJ432163 | Hs.268231 | Homo sapiens cDNA: FLJ23111 fis, clone L | 6.0 |
| | 440749 | W22335 | Hs.7392 | Homo sapiens mRNA; cDNA DKFZp761E0323 (f | 6.0 |
| | 448822 | BE149845 | Hs.289038 | Homo sapiens cDNA: FLJ20994 fis, clone C | 6.0 |
| 20 | 424806 | AA382523 | Hs.105689 | ESTs | 6.0 |
| | 435185 | AA669490 | Hs.289109 | dimethylarginine dimethylaminohydrolase | 6.0 |
| | 452235 | AL039743 | Hs.28514 | Homo sapiens mRNA; cDNA DKFZp434H092 (tr | 6.0 |
| | 432415 | T16971 | Hs.289014 | ESTs | 6.0 |
| | 436345 | AA873008 | Hs.121572 | ESTs | 6.0 |
| 25 | 439451 | AF086270 | Hs.278554 | heterochromatin-like protein 1 | 6.0 |
| | 434674 | AA831879 | Hs.136985 | ESTs | 6.0 |
| | 429653 | NM_005955 | Hs.211581 | metal-regulatory transcription factor 1 | 6.0 |
| | 446822 | AB037794 | Hs.16229 | KIAA1373 protein | 6.0 |
| | 423590 | AW952412 | Hs.65874 | ESTs | 6.0 |
| 30 | 424026 | AI798295 | Hs.123218 | ESTs | 5.9 |
| | 423246 | AL119114 | Hs.23107 | ESTs | 5.9 |
| | 420982 | AW576160 | Hs.100729 | KIAA0692 protein | 5.9 |
| | 435008 | AF150262 | Hs.162898 | ESTs | 5.9 |
| | 420092 | AA814043 | Hs.88045 | ESTs | 5.9 |
| 35 | 444484 | AK002126 | Hs.11260 | hypothetical protein FLJ11264 | 5.9 |
| | 410193 | AJ132592 | Hs.59757 | zinc finger protein 281 | 5.9 |
| | 450534 | AI570189 | Hs.25132 | KIAA0470 gene product | 5.9 |
| | 440146 | AW014231 | Hs.90790 | Homo sapiens cDNA: FLJ22930 fis, clone K | 5.9 |
| | 425361 | AA355933 | Hs.132221 | Homo sapiens cDNA FLJ12401 fis, clone MA | 5.9 |
| 40 | 425174 | D87450 | Hs.154978 | KIAA0261 protein | 5.9 |
| | 458287 | AA987556 | Hs.12867 | ESTs | 5.9 |
| | 433793 | AW975959 | Hs.107513 | ESTs, Moderately similar to KIAA1058 pro | 5.8 |
| | 443228 | W24781 | Hs.293798 | ESTs | 5.8 |
| | 419983 | W55956 | Hs.94030 | Homo sapiens mRNA; cDNA DKFZp586E1624 (f | 5.8 |
| 45 | 410361 | BE391804 | Hs.62661 | guanylate binding protein 1, interferon- | 5.8 |
| | 415714 | NM_002290 | Hs.78672 | laminin, alpha 4 | 5.8 |
| | 421689 | N87820 | Hs.106826 | hypothetical protein | 5.8 |
| | 431176 | AI026984 | Hs.293662 | ESTs | 5.8 |
| | 443837 | AI984625 | Hs.9884 | spindle pole body protein | 5.8 |
| 50 | 410623 | AW958932 | Hs.293833 | ESTs | 5.8 |
| | 421298 | AW172431 | Hs.13012 | ESTs | 5.8 |
| | 449052 | AW029507 | Hs.161102 | ESTs | 5.8 |
| | 433043 | W57554 | Hs.125019 | ESTs, Highly similar to KIAA0886 protein | 5.8 |
| | 439444 | AI277652 | Hs.54578 | ESTs | 5.7 |
| 55 | 428698 | AA852773 | Hs.297939 | ESTs, Weakly similar to T17344 hypotheti | 5.7 |
| | 411928 | AA888624 | Hs.19121 | adaptor-related protein complex 2, alpha | 5.7 |
| | 442242 | AV647908 | Hs.90424 | Homo sapiens cDNA: FLJ23285 fis, clone H | 5.7 |
| | 417315 | AI080042 | Hs.180450 | ribosomal protein S24 | 5.7 |
| | 422544 | AB018259 | Hs.118140 | KIAA0716 gene product | 5.7 |
| 60 | 412584 | X54870 | Hs.74085 | DNA segment on chromosome 12 (unique) 24 | 5.7 |
| | 433505 | AW504027 | Hs.15301 | Homo sapiens NY-REN-25 antigen mRNA, par | 5.7 |
| | 410425 | BE278367 | Hs.63510 | KIAA0141 gene product | 5.7 |
| | 457292 | AI921270 | Hs.214178 | Homo sapiens cDNA FLJ14251 fis, clone OV | 5.7 |
| | 457100 | AA417878 | Hs.48401 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 5.7 |
| 65 | 436995 | AI160015 | Hs.118112 | ESTs | 5.7 |
| | 426283 | NM_003937 | Hs.169139 | kynureninase (L-kynurenine hydrolase) | 5.7 |
| | 441518 | AW161697 | Hs.294150 | ESTs | 5.7 |
| | 448807 | AI571940 | Hs.7549 | ESTs | 5.7 |
| | 449556 | AA002008 | Hs.188633 | ESTs | 5.7 |
| 70 | 439211 | AI890347 | Hs.271923 | Homo sapiens cDNA: FLJ22785 fis, clone K | 5.7 |
| | 430440 | X52599 | Hs.2561 | nerve growth factor, beta polypeptide | 5.7 |
| | 413551 | BE242639 | Hs.75425 | ubiquitin associated protein | 5.7 |
| | 441633 | AW958544 | Hs.112242 | ESTs | 5.7 |
| | 427093 | AA398118 | Hs.97579 | ESTs | 5.6 |
| 75 | 418250 | U29926 | Hs.83918 | adenosine monophosphate deaminase (isof | 5.6 |
| | 432267 | AK000872 | Hs.274227 | Homo sapiens cDNA FLJ10010 fis, clone HE | 5.6 |
| | 419839 | U24577 | Hs.93304 | phospholipase A2, group VII (platelet-ac | 5.6 |
| | 430253 | AK001514 | Hs.236844 | hypothetical protein FLJ10652 | 5.6 |
| | 450447 | AF212223 | Hs.25010 | hypothetical protein P15-2 | 5.6 |
| 80 | 434623 | AB023163 | Hs.4014 | KIAA0946 protein; Huntingtin interacting | 5.6 |
| | 420642 | AK001520 | Hs.99545 | Homo sapiens cDNA FLJ10658 fis, clone NT | 5.6 |
| | 414020 | NM_002984 | Hs.75703 | small inducible cytokine A4 (homologous | 5.6 |
| | 420825 | AI656727 | | gbt153f12.x1 NCI_CGAP_GC6 Homo sapiens | 5.6 |

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|----|--------|-----------|-----------|---|-----|
| | 422363 | T55979 | Hs.115474 | replication factor C (activator 1) 3 (38 | 5.6 |
| | 452046 | AB018345 | Hs.27657 | KIAA0802 protein | 5.6 |
| | 408911 | AW294772 | Hs.98321 | Homo sapiens cDNA FLJ14103 fis, clone MA | 5.6 |
| 5 | 414844 | AA296874 | Hs.77494 | deoxyguanosine kinase | 5.6 |
| | 416498 | U33632 | Hs.79351 | potassium channel, subfamily K, member 1 | 5.6 |
| | 430512 | AF182294 | Hs.241578 | U6 snRNA-associated Sm-like protein LSml8 | 5.6 |
| | 430339 | W28608 | Hs.239625 | integral membrane protein 28 | 5.6 |
| | 420153 | N22120 | Hs.75277 | hypothetical protein FLJ13910 | 5.6 |
| 10 | 420892 | AW975076 | Hs.172589 | nuclear phosphoprotein similar to S. cer | 5.6 |
| | 441568 | AI733322 | Hs.127176 | ESTs | 5.6 |
| | 414575 | H11257 | Hs.295233 | ESTs | 5.5 |
| | 419929 | U90268 | Hs.93810 | cerebral cavernous malformations 1 | 5.5 |
| | 438613 | C05569 | Hs.243122 | hypothetical protein FLJ13057 similar to | 5.5 |
| 15 | 453064 | R40334 | Hs.301395 | Homo sapiens cDNA: FLJ21204 fis, clone C | 5.5 |
| | 433409 | AI278802 | Hs.25661 | ESTs | 5.5 |
| | 407094 | AF000574 | Hs.22405 | leukocyte immunoglobulin-like receptor, | 5.5 |
| | 425234 | AW152225 | Hs.165909 | ESTs | 5.5 |
| | 447644 | AW881622 | Hs.108846 | Homo sapiens cDNA FLJ12534 fis, clone NT | 5.5 |
| 20 | 411653 | AF070578 | Hs.71168 | Homo sapiens clone 24674 mRNA sequence | 5.5 |
| | 446534 | AI307356 | Hs.175225 | ESTs | 5.5 |
| | 452355 | N54926 | Hs.29202 | G protein-coupled receptor 34 | 5.5 |
| | 434715 | BE005346 | Hs.116410 | ESTs | 5.5 |
| | 440486 | BE243513 | Hs.7212 | hypothetical protein PP1044 | 5.5 |
| 25 | 444825 | AW167613 | Hs.248 | mitogen-activated protein kinase kinase | 5.5 |
| | 419172 | AW338625 | Hs.22120 | ESTs | 5.5 |
| | 444931 | AV652066 | Hs.75113 | general transcription factor IIA | 5.4 |
| | 413940 | AI633205 | Hs.159914 | ESTs | 5.4 |
| | 410480 | R97457 | Hs.63984 | cadherin 13, H-cadherin (heart) | 5.4 |
| 30 | 447072 | D61594 | Hs.17279 | tyrosylprotein sulfotransferase 1 | 5.4 |
| | 434361 | AF129755 | Hs.117772 | ESTs | 5.4 |
| | 453392 | U23752 | Hs.32964 | SRY (sex determining region Y)-box 11 | 5.4 |
| | 445175 | AV652851 | Hs.300846 | ESTs | 5.4 |
| | 411213 | AA676839 | Hs.69285 | neuropilin 1 | 5.4 |
| 35 | 412530 | AA766268 | Hs.266273 | Homo sapiens cDNA FLJ13346 fis, clone OV | 5.4 |
| | 422667 | H25642 | Hs.133471 | ESTs | 5.4 |
| | 434064 | AL049045 | Hs.180758 | hypothetical protein PRO0082 | 5.4 |
| | 429688 | BE245169 | Hs.211610 | CUG triplet repeat, RNA-binding protein | 5.4 |
| | 452060 | W26980 | Hs.153612 | ATP-binding cassette, sub-family F (GCN2 | 5.4 |
| 40 | 419093 | AI804054 | Hs.112885 | ESTs | 5.4 |
| | 436267 | AW450938 | Hs.180115 | ESTs | 5.4 |
| | 405257 | | | | 5.4 |
| | 431154 | AW971228 | Hs.290259 | ESTs | 5.4 |
| | 415511 | AI732617 | Hs.182362 | ESTs | 5.4 |
| 45 | 419175 | AW270037 | Hs.179507 | KIAA0779 protein | 5.4 |
| | 454117 | BE410100 | Hs.40368 | adaptor-related protein complex 1, sigma | 5.3 |
| | 423720 | AL044191 | Hs.23388 | Homo sapiens cDNA: FLJ21310 fis, clone C | 5.3 |
| | 409995 | AW960597 | Hs.30164 | ESTs | 5.3 |
| | 414911 | NM_000107 | Hs.77602 | damage-specific DNA binding protein 2 (4 | 5.3 |
| 50 | 455716 | BE070263 | | gb:QV4-BT0407-280100-090-e07 BT0407 Homo | 5.3 |
| | 430598 | AK001764 | Hs.247112 | hypothetical protein FLJ10902 | 5.3 |
| | 419985 | H66373 | Hs.15973 | ESTs, Highly similar to bA393U16.3 [Hsa | 5.3 |
| | 428753 | AW939252 | Hs.192927 | hypothetical protein FLJ20251 | 5.3 |
| | 423099 | NM_002837 | Hs.123641 | protein tyrosine phosphatase, receptor t | 5.3 |
| | 404176 | | | | 5.3 |
| 55 | 431475 | AI567669 | Hs.287316 | ESTs | 5.3 |
| | 406625 | Y13647 | Hs.119597 | stearoyl-CoA desaturase (delta-9-desatur | 5.3 |
| | 405475 | | | | 5.3 |
| | 430180 | AA331406 | Hs.75456 | A kinase (PRKA) anchor protein 10 | 5.3 |
| 60 | 446183 | AA354991 | Hs.14222 | Homo sapiens mRNA; cDNA DKFZp761P019 (fr | 5.3 |
| | 417381 | AF164142 | Hs.82042 | solute carrier family 23 (nucleobase tra | 5.3 |
| | 433029 | NM_014322 | Hs.279926 | opsin 3 (encephalopsin) | 5.3 |
| | 442837 | AI022082 | Hs.50492 | ESTs | 5.3 |
| | 437140 | AA312799 | Hs.283689 | activator of CREM in testis | 5.3 |
| 65 | 408989 | AW361666 | Hs.49500 | KIAA0746 protein | 5.3 |
| | 417355 | D13168 | Hs.82002 | endothelin receptor type B | 5.3 |
| | 407361 | AA744622 | Hs.292645 | ESTs, Weakly similar to ALU5_HUMAN ALU S | 5.3 |
| | 437734 | AA693951 | Hs.180284 | ESTs | 5.3 |
| | 452234 | AW084176 | Hs.223296 | ESTs | 5.3 |
| 70 | 423057 | AW961597 | Hs.130816 | ESTs | 5.3 |
| | 439593 | BE073597 | Hs.124863 | ESTs | 5.3 |
| | 446501 | AI302616 | Hs.150819 | ESTs | 5.3 |
| | 416406 | D86961 | Hs.79299 | lipoma HMGIC fusion partner-like 2 | 5.3 |
| | 427164 | AB037721 | Hs.173871 | KIAA1300 protein | 5.2 |
| 75 | 416815 | U41514 | Hs.80120 | UDP-N-acetyl-alpha-D-galactosamine:polyp | 5.2 |
| | 448212 | AI475858 | | gb:tc87d07.x1 NCI_CGAP_CLL1 Homo sapiens | 5.2 |
| | 412420 | AL035668 | Hs.73853 | bone morphogenetic protein 2 | 5.2 |
| | 416975 | NM_004131 | Hs.1051 | granzyme B (granzyme 2, cytotoxic T-lymp | 5.2 |
| | 406815 | AA833930 | Hs.288036 | tRNA isopentenylpyrophosphate transferas | 5.2 |
| 80 | 451418 | BE387790 | Hs.26369 | hypothetical protein FLJ20287 | 5.2 |
| | 425322 | U63630 | Hs.155637 | protein kinase, DNA-activated, catalytic | 5.2 |
| | 451156 | AI983569 | Hs.232042 | ESTs | 5.2 |
| | 415910 | U20350 | Hs.78913 | chemokine (C-X3-C) receptor 1 | 5.2 |
| | 423024 | AA593731 | Hs.75613 | CD36 antigen (collagen type I receptor, | 5.2 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| 5 | 428593 | AW207440 | Hs.185973 | degenerative spermatocyte (homolog Dros | 5.2 |
| | 451149 | AL047586 | Hs.10283 | ESTs | 5.2 |
| | 429458 | BE161832 | Hs.292689 | ESTs | 5.2 |
| | 422241 | Y00062 | Hs.170121 | protein tyrosine phosphatase, receptor I | 5.2 |
| | 432383 | AK000144 | Hs.274449 | Homo sapiens cDNA FLJ20137 fis, clone CO | 5.2 |
| | 417696 | BE241624 | Hs.82401 | CD69 antigen (p60, early T-cell activati | 5.2 |
| | 442991 | BE281238 | Hs.8886 | hypothetical protein FLJ20424 | 5.2 |
| | 426711 | AA383471 | Hs.180669 | conserved gene amplified in osteosarcoma | 5.2 |
| 10 | 438995 | AI277986 | Hs.164875 | ESTs | 5.1 |
| | 438582 | AI521310 | Hs.283365 | ESTs, Weakly similar to ALU5_HUMAN ALU S | 5.1 |
| | 424859 | U92014 | Hs.153527 | Homo sapiens pTM5 mariner-like transpos | 5.1 |
| | 445563 | AW873606 | Hs.149006 | ESTs | 5.1 |
| | 416852 | AF283776 | Hs.80285 | Homo sapiens mRNA; cDNA DKFZp586C1723 (f | 5.1 |
| 15 | 420567 | AK000812 | Hs.98874 | similar to protein-rich protein 48 | 5.1 |
| | 420530 | AL133101 | Hs.99508 | Homo sapiens mRNA; cDNA DKFZp434O0921 (f | 5.1 |
| | 455510 | AA422029 | Hs.143540 | ESTs, Weakly similar to hyperpolarizatio | 5.1 |
| | 412676 | NM_000165 | Hs.74471 | gap junction protein, alpha 1, 43kD (con | 5.1 |
| | 438146 | Z36842 | Hs.57548 | ESTs | 5.1 |
| 20 | 423430 | AF112481 | Hs.128501 | RAD54, S. cerevisiae, homolog of, B | 5.1 |
| | 421633 | AF121860 | Hs.106260 | sorting nexin 10 | 5.1 |
| | 447197 | R36075 | | gb:yh88b01.s1 Soares placenta Nb2HP Homo | 5.1 |
| | 436943 | AA773838 | Hs.5353 | caspase 10, apoptosis-related cysteine p | 5.1 |
| | 456210 | N49729 | Hs.156875 | ESTs | 5.1 |
| 25 | 411893 | R82845 | Hs.273789 | ESTs | 5.1 |
| | 432331 | W37862 | Hs.274368 | Homo sapiens mRNA; cDNA DKFZp586I1524 (f | 5.1 |
| | 414696 | AF002020 | Hs.76918 | Niemann-Pick disease, type C1 | 5.1 |
| | 426822 | W78950 | Hs.220823 | ESTs | 5.1 |
| | 444269 | AI590346 | Hs.146220 | ESTs | 5.1 |
| 30 | 437204 | AL110216 | Hs.12285 | ESTs | 5.1 |
| | 443180 | R15875 | Hs.70945 | ESTs | 5.1 |
| | 431510 | AA580082 | Hs.112264 | ESTs | 5.0 |
| | 446312 | BE087853 | | gb:QV1-BT0681-290400-181-h05 BT0681 Homo | 5.0 |
| | 449870 | AI672487 | Hs.15423 | hypothetical protein HDCMCD4P | 5.0 |
| 35 | 430462 | AI584156 | Hs.105640 | ESTs | 5.0 |
| | 457452 | AW972675 | | gb:EST384766 MAGE resequences, MAGL Homo | 5.0 |
| | 420397 | NM_007018 | Hs.97437 | centrosomal protein 1 | 5.0 |
| | 408750 | BE294069 | Hs.93581 | hypothetical protein FLJ10512 | 5.0 |
| | 426874 | N67325 | Hs.247132 | ESTs | 5.0 |
| 40 | 419746 | AW867943 | Hs.127216 | Homo sapiens cDNA FLJ13485 fis, clone PL | 5.0 |
| | 434237 | AF119908 | Hs.235516 | hypothetical protein PRO2955 | 5.0 |
| | 410274 | AA381807 | Hs.61762 | hypoxia-inducible protein 2 | 5.0 |

TABLE 35B:

| | | |
|----|-------------|---------------------------------------|
| 45 | Pkey: | Unique Eos probeset identifier number |
| | CAT number: | Gene cluster number |
| | Accession: | Genbank accession numbers |

| | | | |
|----|--------|------------|---|
| 50 | Pkey | CAT number | Accession |
| | 411937 | 1266219_1 | AW876626 AW876622 AW876624 |
| | 413497 | 1373771_1 | BE177661 H06215 BE144709 BE144829 |
| | 420825 | 196769_1 | AI656727 AI697887 AI802122 AA910877 Z28718 T16711 AA651731 AL047264 BE000621 R68736 AW992695 AI768764 AW271284 AW974653 AI308951 AW055146 R93609 AW467031 AI096866 AI371871 AI126182 AI564756 AI361460 AI358914 AI419231 AW439733 R87059 AA628064 AW088970 AW008695 R68682 AI719136 R97752 AW196262 |
| 55 | 425331 | 250199_1 | AW962128 AA355353 AA427363 |
| | 437205 | 43463_1 | AL110232 N94765 |
| | 438966 | 467436_1 | AW979074 AA834841 AA828650 |
| | 442438 | 542469_1 | AA995998 AI916584 R61781 T77332 F07756 F08149 F07647 |
| | 443161 | 561305_1 | AI038316 AI344631 AI261653 |
| 60 | 446312 | 671114_1 | BE087853 AI286184 |
| | 447197 | 711623_1 | R36075 AI366546 R36167 |
| | 447974 | 745643_1 | R76886 AI453674 R77049 |
| | 448212 | 755099_1 | AI475858 AW969013 |
| | 451818 | 887271_1 | AI819018 R05492 W27615 |
| 65 | 453013 | 94390_1 | AA031407 N85751 AW974119 AA031408 AA572965 |
| | 455716 | 1352695_1 | BE070263 BE070195 BE070265 BE070202 BE070233 BE070399 BE070203 |
| | 457452 | 339381_1 | AW972675 AA541366 AA523039 |
| | 407305 | 312657 | AA715284 |

TABLE 35C:

| | | |
|----|--------------|---|
| 70 | Pkey: | Unique number corresponding to an Eos probeset |
| | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. |
| | Strand: | Indicates DNA strand from which exons were predicted. |
| 75 | NL_position: | Indicates nucleotide positions of predicted exons. |

| | | | | |
|----|--------|---------|--------|-------------------------------------|
| 80 | Pkey | Ref | Strand | NL_position |
| | 401539 | 8072433 | Minus | 62028-62608 |
| | 402474 | 7547175 | Minus | 53526-53628,55755-55920,57530-57757 |
| | 403549 | 8081591 | Minus | 137150-137362 |
| | 403713 | 6573831 | Minus | 152769-153155 |
| | 403790 | 8084957 | Minus | 87826-87947,89835-90002 |
| | 404176 | 9931122 | Plus | 52685-52800 |
| | 405257 | 7329310 | Plus | 73121-73273 |

405475 1931025 Plus 1548-1702

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TABLE 36A: ABOUT 169 GENES UP-REGULATED IN KIDNEY CANCER

Table 36A lists about 169 genes up-regulated in kidney cancer compared to normal kidney that are likely to be extracellular or cell-surface proteins. These were selected as for Table 35A and the predicted protein contained a structural domain that is indicative of surface or extracellular localization (e.g. ig, fn3, egf, 7tm domains). Predicted protein domains are noted.

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Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 PSDomain: Protein Structural Domain
 R1: Ratio of tumor to normal tissue

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| Pkey | ExAccn | UnigeneID | Unigene Title | PSDomain | R1 |
|--------|-----------|-----------|-----------------|---|------|
| 424704 | AI263293 | Hs.152096 | cytochrome P450 | SS,p450 | 40.9 |
| 426559 | AB001914 | Hs.170414 | paired basic am | TM,Peptidase_S8,P | 35.6 |
| 458079 | AI796870 | Hs.54277 | ESTs | TM | 34.6 |
| 446921 | AB012113 | Hs.16530 | small inducible | SS,IL8 | 25.9 |
| 452401 | NM_007115 | Hs.29352 | tumor necrosis | TM,SS,Xlink,CUB | 24.8 |
| 414821 | M63835 | Hs.77424 | Fc fragment of | TM,SS,ig | 23.4 |
| 414812 | X72755 | Hs.77367 | monokine induce | SS,IL8 | 22.1 |
| 426471 | M22440 | Hs.170009 | transforming gr | TM,SS,EGF | 21.3 |
| 449523 | NM_000579 | Hs.54443 | chemokine (C-C | TM,7tm_1 | 20.7 |
| 428227 | AA321649 | Hs.2248 | small inducible | IL8 | 19.5 |
| 456804 | AI421645 | Hs.139851 | caveolin 2 | TM,Caveolin | 17.8 |
| 411642 | NM_014932 | Hs.71132 | neurodin 1 | TM,SS,COesterase | 16.2 |
| 427581 | NM_014788 | Hs.179703 | KIAA0129 gene p | TM | 15.6 |
| 448520 | AB002367 | Hs.21355 | doublecortin an | TM,kinase | 14.8 |
| 417308 | H60720 | Hs.81892 | KIAA0101 gene p | TM | 14.8 |
| 421566 | NM_000399 | Hs.1395 | early growth re | TM,zf-C2H2 | 14.6 |
| 422603 | BE242587 | Hs.118651 | hematopoietical | TM,SS,homeobox | 14.4 |
| 425984 | AW836277 | Hs.165636 | hypothetical pr | TM | 14.2 |
| 432606 | NM_002104 | Hs.3066 | granzyme K (ser | TM,SS,trypsin | 14.1 |
| 458809 | AW972512 | Hs.20985 | sin3-associated | SS | 13.7 |
| 446627 | AI973016 | Hs.15725 | hypothetical pr | TM | 13.6 |
| 452960 | AK001335 | Hs.31137 | Homo sapiens cD | TM,Y_phosphatase | 13.3 |
| 420552 | AK000492 | Hs.98806 | hypothetical pr | TM,SS | 13.0 |
| 425188 | AK002052 | Hs.155071 | hypothetical pr | TM | 12.6 |
| 419034 | NM_002110 | Hs.89555 | hemopoietic cel | TM,kinase,SH2,SH3 | 12.3 |
| 442932 | AA457211 | Hs.8858 | bromodomain adj | TM,bromodomain,PHD | 12.3 |
| 434398 | AA121098 | Hs.3838 | serum-inducible | TM,kinase,POLO_box | 12.2 |
| 450506 | NM_004460 | Hs.418 | fibroblast acti | SS,DPPIV_N_term,Peptidase_S9 | 12.1 |
| 425782 | U66468 | Hs.159525 | cell growth reg | SS | 12.0 |
| 426108 | AA622037 | Hs.166468 | programmed cell | TM,DUF122 | 11.9 |
| 450236 | AW162998 | Hs.24684 | KIAA1376 protei | TM,SS | 11.7 |
| 452838 | U65011 | Hs.30743 | preferentially | TM | 11.2 |
| 426780 | BE242284 | Hs.172199 | adenylate cycla | TM,guanylate_cyc | 11.1 |
| 415323 | BE269352 | Hs.949 | neutrophil cyto | TM,SH3,TPR | 11.0 |
| 423508 | AW604297 | Hs.129711 | hepatitis A vir | TM,SS,ig | 11.0 |
| 408380 | AF123050 | Hs.44532 | diubiquitin | TM,ubiquitin,7tm_3,ANF_receptor,sushi,7tm_1 | 11.0 |
| 448410 | AK000227 | Hs.21126 | hypothetical pr | TM | 11.0 |
| 451277 | AK001123 | Hs.26176 | hypothetical pr | TM | 10.8 |
| 453165 | S74727 | Hs.32042 | aspartoacylase | TM | 10.8 |
| 418036 | Z37976 | Hs.83337 | latent transfor | SS,TB,EGF | 10.5 |
| 431512 | BE270734 | Hs.2795 | lactate dehydro | TM,ldh | 10.3 |
| 433862 | D86960 | Hs.3610 | KIAA0205 gene p | TM,SS | 10.3 |
| 431211 | M86849 | Hs.5566 | gap junction pr | TM,connexin | 10.2 |
| 432579 | AF043244 | Hs.278439 | nucleolar prote | TM | 10.0 |
| 439653 | AW021103 | Hs.6631 | hypothetical pr | TM,SS | 9.9 |
| 428862 | NM_000346 | Hs.2316 | SRY (sex-determ | TM,HMG_box | 9.8 |
| 410762 | AF226053 | Hs.66170 | HSKM-B protein | SS,zf-MYND | 9.8 |
| 452431 | U88879 | Hs.29499 | tol-like recep | TM,SS,TIR,LRRC | 9.5 |
| 405121 | AB028989 | Hs.88500 | mitogen-activat | SS,vwa,vwd,TIL_Cys_knot,vwc | 9.5 |
| 449625 | NM_014253 | Hs.23796 | odc (odd Oz/ten | SH2,EGF | 9.4 |
| 421659 | NM_014459 | Hs.106511 | protocadherin 1 | TM,SS,cadherin | 9.2 |
| 427283 | AL119796 | Hs.174185 | ectonucleotide | TM,SS,Phosphodiester,Somatostatin_B | 9.1 |
| 407975 | X89426 | Hs.41716 | endothelial cel | SS,IGFBP | 8.9 |
| 413554 | AA319146 | Hs.75426 | secretogranin I | TM,SS,Granin | 8.6 |
| 418693 | AI750878 | Hs.87409 | thrombospondin | EGF,TSPN_tsp_1,tsp_3,vwc | 8.6 |
| 437672 | AW748265 | Hs.5741 | flavohemoprotei | TM,heme_1,oxidoreductase | 8.6 |
| 430268 | AK000737 | Hs.237480 | hypothetical pr | TM,SS | 8.5 |
| 447850 | AB018298 | Hs.19822 | SEC24 (S. cerev | TM | 8.4 |
| 435717 | AF227905 | Hs.105794 | UDP-glucose:gly | TM,Glyco_transf_8 | 8.3 |
| 433376 | AI249361 | Hs.74122 | caspase 4, apop | TM,JICE_p20,JICE_p10,CARD | 8.2 |
| 419490 | NM_006144 | Hs.90708 | granzyme A (gra | TM,SS,trypsin | 8.2 |
| 453033 | AA325869 | Hs.31463 | KIAA0281 gene p | TM | 8.2 |
| 432328 | AI572739 | Hs.195471 | 6-phosphofructo | TM,6PF2K,PGAM | 7.9 |
| 413719 | BE439580 | Hs.75438 | small inducible | SS,IL8 | 7.9 |
| 412448 | L12964 | Hs.73895 | tumor necrosis | TM,SS,TNFR_c6 | 7.9 |
| 424247 | X14008 | Hs.234734 | lysozyme (renal | SS,lvs | 7.8 |
| 421991 | NM_014918 | Hs.110488 | KIAA0990 protei | SS | 7.8 |
| 400793 | AA635062 | Hs.50094 | Homo sapiens mR | TM,BIR,CARD,zf-C3HC4 | 7.7 |

| | | | | | | |
|----|--------|-----------|-----------|------------------|--|-----|
| | 414646 | AA353776 | Hs.901 | CD48 antigen (B | TM,lg | 7.6 |
| | 418372 | AA311833 | Hs.84318 | replication pro | TM | 7.6 |
| | 408418 | AW963897 | Hs.44743 | KIAA1435 protei | TM,WD40,FYVE | 7.6 |
| 5 | 425354 | U62027 | Hs.155935 | complement comp | TM,7tm_1 | 7.5 |
| | 432753 | NM_014075 | Hs.278915 | PRO0593 protein | TM,ptkinase | 7.4 |
| | 447046 | AA326187 | Hs.17170 | G protein-coupl | TM,7tm_1 | 7.4 |
| | 410577 | X91911 | Hs.64639 | glioma pathogen | TM,SCP | 7.4 |
| | 422631 | BE218919 | Hs.118793 | hypothetical pr | TM | 7.3 |
| 10 | 417022 | NM_014737 | Hs.80905 | Ras association | TM,RA | 7.2 |
| | 430105 | X70297 | Hs.2540 | cholinergic rec | TM,neur_chan | 7.2 |
| | 451621 | AI879148 | Hs.26770 | fatty acid bind | TM,SS,lipocatin | 7.2 |
| | 415138 | C18356 | Hs.78045 | tissue factor p | Kunitz_BPTI,G-gamma | 7.2 |
| | 426028 | NM_001110 | Hs.172028 | a disintegrin a | TM,SS,disintegrin,Repolysin | 7.2 |
| 15 | 434096 | AW662958 | Hs.75825 | pleiomorphic ad | TM,zf-C2H2 | 7.1 |
| | 426423 | NM_012446 | Hs.169833 | single-stranded | TM | 7.1 |
| | 412783 | BE276738 | Hs.74578 | DEAD/H (Asp-Glu | TM,dsm,helicase_C | 7.1 |
| | 431556 | AF016028 | Hs.260039 | sarcospan (Kras | TM | 6.9 |
| | 420018 | U56387 | Hs.94376 | proprotein conv | TM,SS,Peptidase_S8,P | 6.9 |
| 20 | 444042 | NM_004915 | Hs.10237 | ATP-binding cas | TM,ABC_tran | 6.9 |
| | 432656 | NM_000246 | Hs.3076 | MHC class II tr | TM,LRR | 6.9 |
| | 430066 | AF929659 | Hs.237825 | signal recognit | TM,TPR | 6.9 |
| | 401539 | | | | TM,SS,zf-B_box,zf-C3HC4,Lysyl_oxidase | 6.8 |
| | 416058 | L08895 | Hs.78995 | MADS box transc | TM,SRF-TF | 6.8 |
| 25 | 413249 | AF167160 | Hs.75251 | DEAD/H (Asp-Glu | TM,SAP | 6.7 |
| | 424063 | NM_002019 | Hs.138671 | fms-related tyr | TM,SS,ptkinase,lg | 6.7 |
| | 418026 | BE379727 | Hs.83213 | fatty acid bind | TM,SS,lipocatin | 6.6 |
| | 438619 | AB032773 | Hs.6341 | TU12B1-TY prote | TM | 6.6 |
| | 408741 | M73720 | Hs.646 | carboxypeptidas | SS,Zn_carbOpept,Propep_M14 | 6.6 |
| 30 | 403549 | | | | TM,ptkinase | 6.6 |
| | 435798 | BE395289 | Hs.12720 | elF4E-transport | TM | 6.6 |
| | 453070 | AK001465 | Hs.31575 | SEC63, endoplas | TM,SS,DnaJ | 6.6 |
| | 452092 | BE245374 | Hs.27842 | hypothetical pr | TM,SS,Acyltransferase | 6.5 |
| | 437396 | BE140396 | Hs.21621 | hypothetical pr | TM | 6.4 |
| | 402474 | | | | TM,Peptidase_C1 | 6.4 |
| 35 | 401600 | BE247275 | Hs.151787 | U5 snRNP-specif | TM,SS,HECT | 6.4 |
| | 415076 | NM_000857 | Hs.77890 | guanylate cycla | TM,guanylate_cyc | 6.4 |
| | 430335 | D80007 | Hs.239499 | KIAA0185 protei | TM,S1 | 6.3 |
| | 434203 | BE262677 | Hs.283558 | hypothetical pr | TM | 6.2 |
| 40 | 430287 | AW182459 | Hs.125759 | ESTs, Weakly si | TM,SS | 6.2 |
| | 417259 | AW903838 | Hs.81800 | chondroitin sul | TM,Xlink,lectin_c,sushi,EGF,lg | 6.1 |
| | 421202 | AF193339 | Hs.102506 | eukaryotic tran | TM,SS | 6.1 |
| | 452235 | AL039743 | Hs.28514 | Homo sapiens mR | TM | 6.0 |
| | 429653 | NM_005955 | Hs.211581 | metal-regulator | TM,zf-C2H2 | 6.0 |
| 45 | 444484 | AK002126 | Hs.11260 | hypothetical pr | TM | 5.9 |
| | 410193 | AJ132592 | Hs.59757 | zinc finger pro | TM,zf-C2H2 | 5.9 |
| | 425361 | AA355933 | Hs.132221 | Homo sapiens cD | TM | 5.9 |
| | 410361 | BE391804 | Hs.62661 | guanylate bindi | TM,SS,GBP | 5.8 |
| | 415714 | NM_002290 | Hs.78672 | laminin, alpha | TM,SS,laminin_G,laminin_EGF | 5.8 |
| 50 | 421689 | N87820 | Hs.106826 | hypothetical pr | TM,SS,PHD | 5.8 |
| | 443837 | AI984625 | Hs.9884 | spindle pole bo | SS | 5.8 |
| | 422544 | AB018259 | Hs.118140 | KIAA0716 gene p | TM | 5.7 |
| | 412584 | X54870 | Hs.74085 | DNA segment on | TM,lectin_c | 5.7 |
| | 410425 | BE278367 | Hs.63510 | KIAA0141 gene p | TM | 5.7 |
| 55 | 426283 | NM_003937 | Hs.169139 | kynureninase (L | TM | 5.7 |
| | 430440 | X52599 | Hs.2561 | nerve growth fa | TM,SS,NGF | 5.7 |
| | 413551 | BE242639 | Hs.75425 | ubiquitin assoc | TM,SS,UBA | 5.7 |
| | 418250 | U29926 | Hs.83918 | adenosine monoph | TM,A_deaminase | 5.6 |
| | 419839 | U24577 | Hs.93304 | phospholipase A | SS | 5.6 |
| 60 | 430253 | AK001514 | Hs.236844 | hypothetical pr | TM | 5.6 |
| | 450447 | AF212223 | Hs.25010 | hypothetical pr | TM,ANF_receptor,guanylate_cyc,ptkinase | 5.6 |
| | 414020 | NM_002984 | Hs.75703 | small inducible | SS,IL8 | 5.6 |
| | 414844 | AA296874 | Hs.77494 | deoxyguanosine | SS,dNK | 5.6 |
| | 416498 | U33632 | Hs.79351 | potassium chann | TM | 5.6 |
| 65 | 430512 | AF182294 | Hs.241578 | U6 snRNA-associ | SS | 5.6 |
| | 419929 | U90268 | Hs.93810 | cerebral cavern | SS,ank,Band_41 | 5.5 |
| | 407094 | AF000574 | Hs.22405 | leukocyte immun | TM,SS,lg | 5.5 |
| | 411653 | AF070578 | Hs.71168 | Homo sapiens cl | TM,SS,Aa_trans | 5.5 |
| | 452355 | N54926 | Hs.29202 | G protein-coupl | TM,7tm_1 | 5.5 |
| 70 | 440486 | BE243513 | Hs.7212 | hypothetical pr | TM | 5.5 |
| | 444825 | AW167613 | Hs.248 | mitogen-activat | TM,SS,ptkinase | 5.5 |
| | 447072 | D61594 | Hs.17279 | tyrosylprotein | SS | 5.4 |
| | 453392 | U23752 | Hs.32964 | SRY (sex determ | TM,HMG_box | 5.4 |
| | 411213 | AA676939 | Hs.69285 | neuropilin 1 | TM,CUB,F5_F8_type_C,MAM | 5.4 |
| 75 | 429688 | BE245169 | Hs.211610 | CUG triplet rep | TM,rm | 5.4 |
| | 405257 | | | | TM | 5.4 |
| | 414911 | NM_000107 | Hs.77602 | damage-specific | TM,WD40 | 5.3 |
| | 430598 | AK001764 | Hs.247112 | hypothetical pr | TM | 5.3 |
| | 428753 | AW939252 | Hs.192927 | hypothetical pr | TM,SS | 5.3 |
| 80 | 406625 | Y13647 | Hs.119597 | stearyl-CoA de | TM,Desaturase | 5.3 |
| | 405475 | | | | TM,sugar_tr | 5.3 |
| | 430180 | AA331406 | Hs.75456 | A kinase (PRKA) | TM | 5.3 |
| | 417381 | AF164142 | Hs.82042 | solute carrier | TM,xan_ur_permease | 5.3 |
| | 433029 | NM_014322 | Hs.279926 | opsin 3 (enceph | TM,7tm_1 | 5.3 |

| | | | | | | |
|----|---|---|-------------------|--|--------------------------------|-----|
| | 417355 | D13168 | Hs.82002 | endothelin rece | TM,SS,7tm_1,zf-C3HC4 | 5.3 |
| | 412420 | AL035668 | Hs.73853 | bone morphogene | SS,TGFb_propeptide,TGF-beta | 5.2 |
| | 416975 | NM_004131 | Hs.1051 | granzyme B (gra | SS,trypsin | 5.2 |
| 5 | 451418 | BE387790 | Hs.26369 | hypothetical pr | TM | 5.2 |
| | 425322 | U63630 | Hs.155637 | protein kinase, | TM,MCM,FAT,FATC,PI3_P14_kinase | 5.2 |
| | 415910 | U20350 | Hs.78913 | chemokine (C-X3 | TM,7tm_1 | 5.2 |
| | 428593 | AW207440 | Hs.185973 | degenerative sp | TM | 5.2 |
| | 417696 | BE241624 | Hs.82401 | CD69 antigen (p | TM,lectin_c | 5.2 |
| 10 | 442991 | BE281238 | Hs.8886 | hypothetical pr | TM | 5.2 |
| | 420567 | AK000812 | Hs.98874 | similar to prol | TM | 5.2 |
| | 412676 | NM_000165 | Hs.74471 | gap junction pr | TM,connexin | 5.1 |
| | 423430 | AF112481 | Hs.128501 | RAD54, S. cerev | TM,SNF2_N,helicase_C | 5.1 |
| | 421633 | AF121860 | Hs.106260 | sorting nexin 1 | TM,PX | 5.1 |
| 15 | 436943 | AA773838 | Hs.5353 | caspase 10, apo | TM,ICE_p10,ICE_p20,DED | 5.1 |
| | 414696 | AF002020 | Hs.76918 | Niemann-Pick di | TM,SS,Patched | 5.1 |
| | 446312 | BE087853 | | gb:QV1-8T0681-2 | TM | 5.1 |
| | 420397 | NM_007018 | Hs.97437 | centrosomal pro | TM | 5.0 |
| | 410274 | AA381807 | Hs.61762 | hypoxia-inducib | SS | 5.0 |
| 20 | TABLE 36B* | | | | | |
| | Pkey: | Unique Eos probeset identifier number | | | | |
| | CAT number: | Gene cluster number | | | | |
| | Accession: | Genbank accession numbers | | | | |
| 25 | Pkey | CAT number | Accession | | | |
| | 446312 | 671114_1 | BE087853 AI286184 | | | |
| | TABLE 36C: | | | | | |
| 30 | Pkey: | Unique number corresponding to an Eos probeset | | | | |
| | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. | | | | |
| | Strand: | Indicates DNA strand from which exons were predicted. | | | | |
| | Nt_position: | Indicates nucleotide positions of predicted exons. | | | | |
| 35 | Pkey | Ref | Strand | Nt_position | | |
| | 401539 | 8072433 | Minus | 62028-62608 | | |
| | 402474 | 7547175 | Minus | 53526-53628,55755-55920,57530-57757 | | |
| | 403549 | 8081591 | Minus | 137150-137362 | | |
| 40 | 405257 | 7329310 | Plus | 73121-73273 | | |
| | 405475 | 1931025 | Plus | 1548-1702 | | |
| | TABLE 37A: ABOUT 280 GENES DOWN-REGULATED IN KIDNEY CANCER | | | | | |
| 45 | Table 37A lists about 280 genes significantly down-regulated in kidney cancer compared to normal kidney. These were selected as for Table 35A, except that the numerator and denominator were switched. | | | | | |
| | Pkey: | Unique Eos probeset identifier number | | | | |
| | ExAccon: | Exemplar Accession number, Genbank accession number | | | | |
| | UnigeneID: | Unigene number | | | | |
| 50 | Unigene Title: | Unigene gene title | | | | |
| | R1: | Ratio of normal to tumor tissue | | | | |
| | Pkey | ExAccon | UnigeneID | UnigeneTitle | R1 | |
| 55 | 425260 | L47726 | Hs.1870 | phenylalanine hydroxylase | 50.20 | |
| | 445635 | AI769774 | Hs.209831 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 48.14 | |
| | 440243 | BE301029 | Hs.226422 | ESTs | 42.54 | |
| | 431657 | AI345227 | Hs.105448 | ESTs, Weakly similar to B34087 hypotheti | 40.14 | |
| | 441120 | AI632015 | Hs.164492 | ESTs | 34.56 | |
| | 432488 | AA551010 | Hs.216640 | ESTs | 33.16 | |
| 60 | 416854 | H40164 | Hs.80296 | Purkinje cell protein 4 | 32.06 | |
| | 438452 | AI220911 | Hs.288959 | Homo sapiens cDNA: FLJ20920 fis, clone A | 29.54 | |
| | 414523 | AU076633 | Hs.76353 | serine (or cysteine) proteinase inhibito | 28.26 | |
| | 430250 | NM_016929 | Hs.283021 | chloride intracellular channel 5 | 28.16 | |
| | 446795 | AI797713 | Hs.156471 | ESTs | 27.23 | |
| 65 | 451949 | U03884 | Hs.463 | potassium inwardly-rectifying channel, s | 26.98 | |
| | 432128 | AA127221 | Hs.117037 | ESTs | 26.54 | |
| | 448178 | AI479482 | Hs.170789 | ESTs | 25.42 | |
| | 436639 | D14838 | Hs.111 | fibroblast growth factor 9 (glia-activat | 23.99 | |
| | 426770 | AI948618 | Hs.150178 | ESTs | 23.78 | |
| 70 | 428839 | AI767756 | Hs.82302 | ESTs | 23.04 | |
| | 431124 | AF284221 | Hs.59506 | doublesex and mab-3 related transcriptio | 22.38 | |
| | 413333 | M74028 | Hs.75297 | fibroblast growth factor 1 (acidic) | 22.28 | |
| | 437575 | AW954355 | Hs.36529 | ESTs | 22.14 | |
| | 451062 | AL110125 | Hs.25910 | Homo sapiens mRNA; cDNA DKFZp564C1416 (f | 22.12 | |
| 75 | 447350 | AI375572 | Hs.172634 | ESTs | 20.40 | |
| | 425920 | AL049977 | Hs.162209 | claudin 8 | 20.30 | |
| | 446293 | AI420213 | Hs.149722 | ESTs | 19.48 | |
| | 425075 | AA506324 | Hs.1852 | acid phosphatase, prostate | 19.10 | |
| | 418318 | U47732 | Hs.84072 | transmembrane 4 superfamily member 3 | 18.74 | |
| 80 | 430130 | AL137311 | Hs.234074 | Homo sapiens mRNA; cDNA DKFZp761G02121 (| 18.56 | |
| | 441560 | F13386 | Hs.7888 | Homo sapiens clone 23736 mRNA sequence | 17.40 | |
| | 434880 | U02388 | Hs.101 | cytochrome P450, subfamily IVF, polypept | 17.30 | |
| | 406667 | M12523 | Hs.75442 | albumin | 17.06 | |
| | 414602 | AW630088 | Hs.76550 | Homo sapiens mRNA; cDNA DKFZp564B1264 (f | 16.54 | |

| | | | | | |
|----|--------|-----------|-----------|---|-------|
| | 418021 | M15881 | Hs.1137 | uromodulin (uromucoid, Tamm-Horsfall gly | 16.11 |
| | 410681 | AW246890 | Hs.65425 | calbindin 1, (28kD) | 15.84 |
| | 443324 | R44013 | Hs.164225 | ESTs | 15.68 |
| 5 | 421285 | NM_000102 | Hs.1363 | cytochrome P450, subfamily XVII (steroid | 15.46 |
| | 436637 | A1783629 | Hs.26766 | ESTs | 15.18 |
| | 448406 | AW772298 | Hs.21103 | Homo sapiens mRNA; cDNA DKFZp564B076 (tr | 14.52 |
| | 434874 | N62448 | Hs.135906 | ESTs | 14.46 |
| | 407744 | AB020629 | Hs.38095 | ATP-binding cassette, sub-family A (ABC1 | 13.84 |
| 10 | 453685 | AL110309 | | gb:DKFZp564L0278_r1 564 (synonym: hfor2) | 13.48 |
| | 451939 | U80456 | Hs.27311 | single-minded (Drosophila) homolog 2 | 13.24 |
| | 436624 | T64297 | Hs.5241 | fatty acid binding protein 1, liver | 13.05 |
| | 428931 | AA994979 | Hs.98967 | ATPase, H(+) -transporting, lysosomal, no | 12.97 |
| | 424823 | NM_006226 | Hs.153322 | phosphatase C, epsilon | 12.66 |
| 15 | 431713 | AK000388 | Hs.267997 | EHM2 gene | 12.66 |
| | 436679 | A127483 | Hs.120451 | ESTs, Weakly similar to unnamed protein | 12.36 |
| | 413859 | AW992356 | Hs.8364 | pyruvate dehydrogenase kinase, isoenzyme | 12.32 |
| | 425707 | AF115402 | Hs.11713 | ET4-like factor 5 (ets domain transcript) | 11.92 |
| | 440504 | A1948966 | Hs.130017 | ESTs, Weakly similar to VATX_HUMAN VACUO | 11.66 |
| 20 | 417275 | X63578 | Hs.81849 | parvalbumin | 11.48 |
| | 410929 | H47233 | Hs.30643 | ESTs | 11.40 |
| | 427167 | A1239607 | Hs.99196 | ESTs | 11.34 |
| | 445591 | A1471866 | Hs.149095 | ESTs | 11.30 |
| | 443622 | A1911527 | Hs.11805 | ESTs | 11.23 |
| 25 | 438935 | H40665 | Hs.31564 | ESTs | 11.16 |
| | 438461 | AW075485 | Hs.286049 | phosphoserine aminotransferase | 11.00 |
| | 415539 | A1733881 | Hs.72472 | ESTs | 10.84 |
| | 438081 | H49546 | Hs.298964 | ESTs | 9.76 |
| | 421688 | AK000307 | Hs.106825 | hypothetical protein FLJ20300 | 9.74 |
| 30 | 407280 | A1241296 | Hs.145609 | ESTs | 9.71 |
| | 427969 | NM_001963 | Hs.2230 | epidermal growth factor (beta-urogastron | 9.61 |
| | 442448 | A1733144 | Hs.129611 | ESTs | 9.52 |
| | 442308 | AA989402 | Hs.45194 | ESTs | 9.51 |
| | 410467 | AF102546 | Hs.63931 | dachshund (Drosophila) homolog | 9.35 |
| 35 | 429469 | M64590 | Hs.27 | glycine dehydrogenase (decarboxylating; | 9.32 |
| | 418068 | AW971155 | Hs.293902 | ESTs, Weakly similar to prolyl 4-hydroxy | 9.31 |
| | 459247 | N46243 | Hs.110373 | ESTs | 9.20 |
| | 423629 | AW021173 | Hs.18612 | Homo sapiens cDNA: FLJ21909 fis, clone H | 9.16 |
| | 410247 | AF181721 | Hs.61345 | RU2S | 9.10 |
| 40 | 430573 | AA744550 | Hs.136345 | ESTs | 9.08 |
| | 457411 | AW085961 | Hs.130093 | ESTs | 8.99 |
| | 443790 | NM_003500 | Hs.9795 | acyl-Coenzyme A oxidase 2, branched chain | 8.92 |
| | 435024 | A1863518 | Hs.127743 | ESTs, Weakly similar to V-ATPase G-subun | 8.76 |
| | 435056 | AW023337 | Hs.5422 | glycoprotein M6B | 8.74 |
| 45 | 426451 | A1908165 | Hs.169946 | GATA-binding protein 3 | 8.50 |
| | 450648 | A1703366 | Hs.26766 | ESTs | 8.38 |
| | 426255 | BE262530 | Hs.2006 | glutathione S-transferase M3 (brain) | 8.31 |
| | 431820 | AW410408 | Hs.271167 | L-pipecolic acid oxidase | 8.28 |
| | 451027 | AW519204 | Hs.40808 | ESTs | 8.10 |
| 50 | 435823 | R07856 | Hs.16355 | ESTs | 8.06 |
| | 429269 | AA449013 | Hs.99203 | ESTs | 8.02 |
| | 438199 | AW016531 | Hs.122147 | ESTs | 7.94 |
| | 442176 | AA983764 | Hs.128910 | ESTs | 7.94 |
| | 450164 | A1239923 | Hs.30098 | ESTs | 7.86 |
| 55 | 445627 | AW818475 | Hs.7363 | ESTs | 7.85 |
| | 445779 | A1253104 | Hs.189267 | ESTs | 7.82 |
| | 407178 | AA195651 | Hs.104106 | ESTs | 7.68 |
| | 426966 | A1493134 | Hs.159125 | ESTs | 7.68 |
| | 445659 | AW300508 | Hs.149229 | ESTs | 7.50 |
| 60 | 403204 | | | | 7.46 |
| | 448037 | AW195634 | Hs.170401 | ESTs | 7.30 |
| | 413589 | AW452631 | Hs.258811 | coatomer protein complex, subunit gamma | 7.26 |
| | 446063 | A1720140 | Hs.151079 | ESTs | 7.26 |
| | 424626 | AA344308 | Hs.128427 | ESTs | 7.25 |
| 65 | 403381 | | | | 7.16 |
| | 414807 | A1738616 | Hs.77348 | hydroxyprostaglandin dehydrogenase 15-(N | 7.12 |
| | 432102 | AW015506 | Hs.130730 | ESTs | 7.12 |
| | 442315 | AA173992 | Hs.7956 | ESTs | 7.10 |
| | 453698 | AA037615 | Hs.42746 | ESTs | 7.02 |
| 70 | 415003 | M11437 | Hs.77741 | kininogen | 6.95 |
| | 426418 | M90464 | Hs.169825 | collagen, type IV, alpha 5 (Alport syndr | 6.92 |
| | 452883 | X80031 | Hs.150318 | ESTs | 6.88 |
| | 408621 | A1970672 | Hs.46638 | chromosome 11 open reading frame 8 | 6.76 |
| | 410781 | A1375672 | Hs.165028 | ESTs | 6.74 |
| 75 | 424596 | AB020639 | Hs.151017 | estrogen-related receptor gamma | 6.66 |
| | 441031 | A1110684 | Hs.7645 | fibrinogen, B beta polypeptide | 6.66 |
| | 451099 | R52795 | Hs.25954 | interleukin 13 receptor, alpha 2 | 6.64 |
| | 437553 | A1829935 | Hs.130497 | ESTs, Weakly similar to MAT8_HUMAN CHLOR | 6.63 |
| | 445286 | U03886 | Hs.264 | GS2 gene | 6.54 |
| 80 | 408427 | AW194270 | Hs.177236 | ESTs | 6.52 |
| | 410442 | X73424 | Hs.63788 | propionyl Coenzyme A carboxylase, beta p | 6.46 |
| | 457001 | J03258 | Hs.2062 | vitamin D (1,25-dihydroxyvitamin D3) re | 6.46 |
| | 420205 | AA256395 | Hs.88156 | ESTs | 6.42 |
| | 441364 | AW450466 | Hs.126830 | ESTs | 6.36 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 425649 | U30930 | Hs.158540 | UDP glycosyltransferase 8 (UDP-galactose | 6.34 |
| | 405373 | | | | |
| | 431322 | AW970622 | | gb:EST382704 MAGE resequences, MAGK Homo | 6.32 |
| 5 | 440094 | AI651558 | Hs.270372 | ESTs | 6.32 |
| | 442764 | AI762254 | Hs.131122 | ESTs | 6.27 |
| | 424433 | HO4607 | Hs.9218 | ESTs | 6.21 |
| | 415025 | AW207091 | Hs.72307 | ESTs | 6.20 |
| | 428927 | AA441837 | Hs.90250 | ESTs | 6.16 |
| 10 | 439145 | H67346 | Hs.269187 | ESTs | 6.16 |
| | 424683 | N87519 | Hs.27196 | ESTs | 6.06 |
| | 415314 | N88802 | Hs.5422 | glycoprotein M6B | 6.04 |
| | 424025 | AI701852 | Hs.301296 | ESTs | 5.94 |
| | 445911 | AI985987 | Hs.145645 | ESTs, Moderately similar to ALU1_HUMAN A | 5.90 |
| 15 | 417332 | AW972717 | Hs.288462 | Homo sapiens cDNA: FLJ21511 f5, clone C | 5.89 |
| | 440102 | AI672443 | Hs.131190 | ESTs | 5.86 |
| | 429609 | AF002246 | Hs.210863 | cell adhesion molecule with homology to | 5.84 |
| | 411666 | AF106564 | Hs.71346 | neurofilament 3 (150kD medium) | 5.82 |
| | 446224 | AW450551 | Hs.13308 | ESTs | 5.82 |
| 20 | 422305 | AI928242 | Hs.293438 | ESTs, Highly similar to AF198488 1 trans | 5.74 |
| | 436802 | N34486 | Hs.170504 | ESTs | 5.72 |
| | 412452 | AA215731 | Hs.283446 | ESTs, Weakly similar to ALAT_HUMAN ALANI | 5.72 |
| | 445611 | AW418497 | Hs.145583 | ESTs | 5.70 |
| | 440038 | AA861627 | Hs.143989 | ESTs | 5.66 |
| 25 | 424028 | AF055084 | Hs.153692 | KIAA0686 protein | 5.66 |
| | 410530 | M25809 | Hs.64173 | ESTs, Highly similar to VAB1_HUMAN VACUO | 5.61 |
| | 425907 | AA365752 | Hs.155965 | ESTs | 5.60 |
| | 428523 | AW974540 | Hs.98626 | ESTs | 5.60 |
| | 429918 | AW873986 | Hs.119383 | ESTs | 5.58 |
| 30 | 408369 | R38438 | Hs.182575 | solute carrier family 15 (H+/peptide tra | 5.58 |
| | 446163 | AA026880 | Hs.25252 | Homo sapiens cDNA FLJ13603 f5, clone PL | 5.56 |
| | 427398 | AW390020 | Hs.20415 | chromosome 21 open reading frame 11 | 5.56 |
| | 418504 | BE159718 | Hs.85335 | Homo sapiens mRNA: cDNA DKFZp564D1462 (f | 5.52 |
| | 440656 | AA902650 | Hs.192742 | Homo sapiens cDNA FLJ12785 f5, clone NT | 5.51 |
| 35 | 432286 | AW327432 | Hs.255843 | ESTs | 5.50 |
| | 451236 | AI767406 | Hs.207026 | ESTs, Weakly similar to B56205 transcrip | 5.48 |
| | 422746 | NM_004484 | Hs.119651 | glypican 3 | 5.46 |
| | 416426 | AA180256 | Hs.210473 | ESTs, Weakly similar to GELS_HUMAN GELSO | 5.43 |
| | 414449 | AA557660 | Hs.76152 | decorin | 5.37 |
| 40 | 445898 | AF070623 | Hs.13423 | Homo sapiens clone 24468 mRNA sequence | 5.36 |
| | 451835 | T63643 | Hs.209715 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 5.34 |
| | 424566 | M16801 | Hs.1790 | nuclear receptor subfamily 3, group C, m | 5.32 |
| | 408604 | D51408 | Hs.21925 | ESTs | 5.22 |
| | 456576 | AA287443 | | gb:zs52c10.r1 NCL_CGAP_GCB1 Homo sapiens | 5.18 |
| 45 | 433212 | BE218049 | Hs.121820 | ESTs | 5.18 |
| | 452114 | N22687 | Hs.8236 | ESTs | 5.16 |
| | 458072 | AI890347 | Hs.271923 | Homo sapiens cDNA: FLJ22785 f5, clone K | 5.14 |
| | 443005 | AI027184 | Hs.200918 | ESTs | 5.14 |
| | 408554 | AA836381 | Hs.7323 | ESTs | 5.14 |
| 50 | 438609 | T62870 | Hs.291991 | ESTs | 5.12 |
| | 429343 | AK000785 | Hs.199480 | epsin 3 | 5.10 |
| | 452223 | AA425467 | Hs.8035 | ESTs | 5.10 |
| | 446925 | AW974605 | Hs.176669 | ESTs | 5.10 |
| | 407664 | AW063476 | Hs.279080 | ESTs | 5.09 |
| 55 | 414664 | AA587775 | Hs.66295 | Homo sapiens HSPC311 mRNA, partial cds | 5.08 |
| | 407978 | AW385129 | Hs.41717 | phosphodiesterase 1A, calmodulin-depende | 5.06 |
| | 435343 | AW194962 | Hs.199028 | ESTs | 5.04 |
| | 419150 | T29618 | Hs.89640 | TEK tyrosine kinase, endothelial (venous | 5.04 |
| | 442317 | AI915599 | Hs.129225 | ESTs | 5.04 |
| 60 | 404319 | | | | 5.02 |
| | 433637 | AW024214 | Hs.135405 | ESTs | 5.02 |
| | 440205 | T86950 | Hs.188465 | ESTs | 4.92 |
| | 432029 | D31628 | Hs.2899 | 4-hydroxyphenylpyruvate dioxygenase | 4.84 |
| 65 | 453125 | AW779544 | Hs.115497 | Homo sapiens cDNA: FLJ22655 f5, clone H | 4.83 |
| | 407788 | BE514982 | Hs.38991 | S100 calcium-binding protein A2 | 4.80 |
| | 439750 | AL359053 | Hs.57664 | Homo sapiens mRNA full length insert cDN | 4.78 |
| | 443633 | AL031290 | Hs.9654 | similar to pregnancy-associated plasma p | 4.75 |
| | 449050 | AW302858 | Hs.187333 | ESTs | 4.74 |
| | 422237 | M13149 | Hs.1498 | histidine-rich glycoprotein | 4.69 |
| 70 | 442476 | AF069475 | | gb:AF069475 Homo sapiens astrocytoma lib | 4.67 |
| | 431130 | NM_006103 | Hs.2719 | epididymis-specific, whey-acidic protein | 4.64 |
| | 440624 | AF017987 | Hs.7306 | secreted fibrinogen-related protein 1 | 4.58 |
| | 403046 | | | | 4.58 |
| | 450838 | R65841 | Hs.28653 | ESTs | 4.51 |
| 75 | 455887 | BE154173 | | gb:PM1-HT0340-201299-004-f12 HT0340 Homo | 4.48 |
| | 453500 | AI478427 | Hs.43125 | ESTs | 4.47 |
| | 405701 | | | | 4.40 |
| | 426657 | NM_015865 | Hs.171731 | solute carrier family 14 (urea transport | 4.37 |
| 80 | 451032 | W03692 | Hs.25832 | Homo sapiens mRNA: cDNA DKFZp564P116 (fr | 4.37 |
| | 426200 | AA371876 | Hs.234786 | KIAA0707 protein | 4.37 |
| | 418836 | AI655499 | Hs.161712 | ESTs | 4.35 |
| | 447754 | AW073310 | Hs.163533 | Homo sapiens cDNA FLJ14142 f5, clone MA | 4.34 |
| | 438209 | AL120659 | Hs.6111 | KIAA0307 gene product | 4.32 |
| | 404559 | | | | 4.23 |
| | | | | | 4.22 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 413272 | AA127923 | Hs.293256 | ESTs | 4.21 |
| | 423068 | M25629 | Hs.123107 | kallikrein 1, renal/pancreas/salivary | 4.19 |
| | 416982 | J05401 | Hs.80691 | creatine kinase, mitochondrial 2 (sarcom | 4.18 |
| | 445512 | A1241246 | Hs.148903 | EST | 4.17 |
| 5 | 445177 | A1215070 | Hs.16135 | ESTs | 4.16 |
| | 448475 | BE613134 | Hs.247474 | Homo sapiens cDNA: FLJ21032 fis, clone C | 4.14 |
| | 402072 | | | | 4.09 |
| | 439285 | AL133916 | Hs.298998 | ESTs | 4.02 |
| | 429621 | A1823386 | Hs.130874 | Homo sapiens cDNA FLJ14181 fis, clone NT | 3.99 |
| 10 | 450273 | AW296454 | Hs.24743 | hypothetical protein FLJ20171 | 3.97 |
| | 453511 | AL031224 | Hs.33102 | transcription factor AP-2 beta (activati | 3.94 |
| | 452620 | AA436504 | Hs.119286 | ESTs | 3.92 |
| | 425642 | X91220 | Hs.158462 | solute carrier family 12 (sodium/chlorid | 3.91 |
| | 435884 | AA701443 | Hs.192868 | ESTs | 3.90 |
| 15 | 416889 | AW250318 | Hs.80395 | mal, T-cell differentiation protein | 3.89 |
| | 419677 | N77342 | Hs.21851 | Homo sapiens cDNA FLJ12900 fis, clone NT | 3.88 |
| | 431958 | X63629 | Hs.2877 | cadherin 3, type 1, P-cadherin (placenta | 3.84 |
| | 456844 | A1264155 | Hs.152981 | CDP-diacylglycerol synthase (phosphatida | 3.82 |
| | 442306 | A1820660 | Hs.129205 | ESTs | 3.82 |
| 20 | 438453 | D17056 | Hs.288959 | Homo sapiens cDNA: FLJ20920 fis, clone A | 3.81 |
| | 407198 | H91679 | | gb:yy04a07.s1 Soares fetal liver spleen | 3.80 |
| | 431441 | U81961 | Hs.2794 | sodium channel, nonvoltage-gated 1 alpha | 3.79 |
| | 413841 | M34276 | Hs.75576 | plasminogen | 3.77 |
| | 431161 | AA493591 | | gb:nh01a12.s1 NCI_CGAP_Thy1 Homo sapiens | 3.76 |
| 25 | 428544 | AA430034 | Hs.191611 | ESTs | 3.74 |
| | 453903 | AW299606 | Hs.232777 | ESTs | 3.74 |
| | 434051 | AW024973 | Hs.283675 | NPD009 protein | 3.73 |
| | 444805 | AB007899 | Hs.12017 | KIAA0439 protein; homolog of yeast ubiqu | 3.73 |
| | 440080 | AW051597 | Hs.143707 | ESTs | 3.71 |
| 30 | 440230 | A1732970 | Hs.126246 | ESTs | 3.70 |
| | 428735 | AJ279246 | Hs.192657 | NPHS2 gene (podocin) | 3.68 |
| | 421832 | NM_016098 | Hs.108725 | HSPC040 protein | 3.66 |
| | 430135 | NM_000035 | Hs.234234 | aldolase B, fructose-bisphosphate | 3.65 |
| | 453055 | AW291436 | Hs.31917 | ESTs | 3.65 |
| 35 | 450696 | A1654223 | Hs.16026 | Homo sapiens cDNA: FLJ23191 fis, clone L | 3.59 |
| | 440232 | A1766925 | Hs.112554 | ESTs | 3.57 |
| | 432099 | U20760 | Hs.272429 | calcium-sensing receptor (hypocalciuric | 3.57 |
| | 445924 | A1264671 | Hs.164166 | ESTs | 3.56 |
| 40 | 411356 | H45377 | | gb:yn95h03.r1 Soares adult brain N2bSHB5 | 3.56 |
| | 431103 | M57399 | Hs.44 | pleiotrophin (heparin binding growth fac | 3.55 |
| | 413752 | BE161807 | | gb:MR3-HT0446-300300-203-h01 HT0446 Homo | 3.53 |
| | 416298 | NM_003891 | Hs.1011 | protein Z, vitamin K-dependent plasma gl | 3.53 |
| | 423603 | AB007880 | Hs.129883 | KIAA0420 gene product | 3.53 |
| | 436610 | AW611912 | Hs.120414 | ESTs | 3.50 |
| 45 | 425905 | AB032959 | Hs.161700 | KIAA1133 protein | 3.48 |
| | 403625 | | | | 3.47 |
| | 425210 | AA054679 | Hs.155150 | ribonuclease P (14kD) | 3.45 |
| | 430168 | AW968343 | Hs.300896 | ESTs, Highly similar to AF128113 1 promi | 3.42 |
| 50 | 448877 | A1583696 | Hs.253313 | ESTs | 3.40 |
| | 456686 | A1554303 | Hs.35982 | Homo sapiens cDNA FLJ12776 fis, clone NT | 3.38 |
| | 414725 | AA769791 | Hs.120355 | Homo sapiens cDNA FLJ13148 fis, clone NT | 3.37 |
| | 453574 | A1767947 | Hs.50841 | ESTs, Weakly similar to tufelin [M.musc | 3.32 |
| | 438535 | L09078 | | gb:Homo sapiens mRNA fragment | 3.31 |
| 55 | 414040 | N58513 | Hs.32171 | ESTs | 3.30 |
| | 451416 | AW631469 | Hs.203213 | ESTs | 3.30 |
| | 444564 | A1167877 | Hs.143716 | ESTs | 3.29 |
| | 408001 | AA046458 | Hs.95296 | ESTs | 3.27 |
| | 406566 | V00495 | Hs.75442 | albumin | 3.24 |
| 60 | 421750 | AK000768 | Hs.107872 | hypothetical protein FLJ20761 | 3.24 |
| | 445337 | NM_013280 | Hs.12523 | fibronectin leucine rich transmembrane p | 3.23 |
| | 423968 | AF098277 | Hs.136529 | solute carrier family 23 (nucleobase tra | 3.21 |
| | 427209 | H06509 | Hs.92423 | KIAA1566 protein | 3.20 |
| | 403442 | | | | 3.20 |
| 65 | 419713 | AW968058 | Hs.92381 | nudix (nucleoside diphosphate linked moi | 3.19 |
| | 425548 | AA890023 | Hs.1906 | prolactin receptor | 3.17 |
| | 414502 | AL133721 | Hs.224680 | ESTs | 3.16 |
| | 427811 | M81057 | Hs.180884 | carboxypeptidase B1 (tissue)- | 3.14 |
| | 436330 | NM_004413 | Hs.109 | dipeptidase 1 (renal) | 3.11 |
| 70 | 433942 | AW272166 | Hs.123465 | ESTs | 3.11 |
| | 408692 | AL040127 | Hs.34074 | dipeptidylpeptidase VI | 3.10 |
| | 448819 | A1589190 | Hs.188372 | ESTs | 3.10 |
| | 423041 | BE170842 | Hs.123123 | chloride channel Ka | 3.10 |
| | 454554 | AW847505 | | gb:RC0-CT0210-280999-021-c10 CT0210 Homo | 3.10 |
| 75 | 405664 | L34041 | Hs.25478 | glycerol-3-phosphate dehydrogenase 1 (so | 3.10 |
| | 449850 | AW206292 | Hs.199751 | ESTs | 3.08 |
| | 427450 | AB014526 | Hs.178121 | KIAA0626 gene product | 3.08 |
| | 454788 | AW820691 | | gb:RC5-ST0300-300100-012-H05 ST0300 Homo | 3.06 |
| | 444895 | A1674383 | Hs.301192 | ESTs | 3.06 |
| | 457782 | N54493 | | gb:yy40g05.s1 Soares fetal liver spleen | 3.05 |
| 80 | 429023 | NM_000312 | Hs.2351 | protein C (inactivator of coagulation fa | 3.05 |
| | 427041 | A1693661 | Hs.97557 | ESTs | 3.01 |
| | 434788 | AF154121 | Hs.102867 | sodium-dependent high-affinity dicarboxy | 3.01 |
| | 419003 | T78640 | Hs.268595 | ESTs | 3.01 |

TABLE 37B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

| Pkey | CAT number | Accession |
|--------|------------|--|
| 411356 | 1240273_1 | H45377 H21137 AW838640 |
| 413752 | 1386338_1 | BE161807 BE161584 BE161700 BE161748 |
| 431161 | 328713_1 | AA493591 AA829120 AA533792 |
| 431322 | 331543_1 | AW970622 AA503009 AA502998 AA502989 AA502805 T92188 |
| 438535 | 45946_1 | L09078 L03145 L09094 L09098 L03165 L09102 |
| 442476 | 543547_1 | AF069475 AF069477 AF069476 |
| 453685 | 977734_1 | AL110309 AW088119 H22881 |
| 454554 | 1223842_1 | AW847505 AW811792 BE061442 BE061433 AW847506 AW806999 AW806996 BE061436 BE061430 BE142460 BE146499 AW806994 AW809156 |
| | | AW806991 AW814082 AW806992 BE061669 AW807002 BE146659 AW806995 AW807000 AW845743 AW845747 AW847504 BE142458 BE061431 |
| | | BE061435 AW847507 BE146650 BE142470 AW814096 AW807012 BE061438 AW807011 AW806993 BE142465 BE142459 BE142462 AW854330 |
| | | AW854331 BE061434 BE061731 BE142464 AW847501 AW807001 BE142463 AW811800 BE061437 AW811802 BE061440 AW806997 AW806998 |
| | | BE061745 BE061753 |
| 454788 | 1234694_1 | AW820691 |
| 455887 | 1380836_1 | BE154173 BE154098 BE154096 |
| 456576 | 201378_1 | AA287443 AA419385 BE084078 A1478347 |
| 457782 | 405265_1 | N54493 AA679039 N76605 |
| 407198 | | H91679 |

TABLE 37C:

Pkey: Unique Eos probeset identifier number
 Ref: reference gi ID
 Strand: strand identification
 Nt_position: chromosomal nucleotide position

| Pkey | Ref | Strand | Nt_position |
|--------|---------|--------|-------------------------|
| 402072 | 8117363 | Plus | 71983-72128 |
| 403046 | 3540153 | Minus | 55707-55859,56369-56511 |
| 403204 | 7622392 | Plus | 16214-16439 |
| 403381 | 9438267 | Minus | 26009-26178 |
| 403442 | 7210003 | Plus | 174560-175270 |
| 403625 | 8569879 | Plus | 6551-7111 |
| 404319 | 9211467 | Plus | 54436-54608 |
| 404559 | 8748893 | Minus | 73499-73651,89575-89739 |
| 405373 | 2076718 | Plus | 21294-21575 |
| 405701 | 4263751 | Plus | 93243-93364 |

TABLE 38A: ABOUT 860 GENES UP-REGULATED IN KIDNEY CANCER COMPARED TO NORMAL ADULT TISSUES

Table 38A lists about 860 genes up-regulated in kidney cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" kidney cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" kidney cancer level was set to the 90th percentile amongst various kidney cancers. The "average" normal adult tissue level was set to the 70th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal adult tissues

| Pkey | ExAccn | UnigenelD | Unigene Title | R1 |
|--------|-----------|-----------|---|-------|
| 435013 | H91923 | Hs.110024 | | 15.71 |
| 447768 | X86400 | Hs.19520 | Hs.19520:FXFD domain-containing ion tran | 14.07 |
| 445178 | A1792241 | Hs.129614 | Hs.129614:kidney-specific membrane prote | 12.56 |
| 432542 | AW083920 | Hs.16098 | Hs.16098:claudin 2 | 12.41 |
| 443595 | AF169312 | Hs.9613 | NM_016109:Homo sapiens angiotensin-like | 11.77 |
| 413719 | BE439580 | Hs.75498 | NM_004591:Homo sapiens small inducible c | 10.39 |
| 436878 | BE465204 | Hs.47448 | Hs.47448:ESTs | 10.18 |
| 440304 | BE159984 | Hs.125395 | Hs.125395:ESTs | 9.95 |
| 407065 | Y10141 | | | 9.58 |
| 413049 | NM_002151 | Hs.823 | NM_002151:Homo sapiens hepsin (transmembr | 9.51 |
| 425983 | AK000226 | Hs.165619 | Hs.165619:mucin and cadherin-like | 8.88 |
| 423161 | AL049227 | Hs.124776 | Hs.124776:Homo sapiens mR: cD DKFZp564N1 | 8.77 |
| 430569 | AF241254 | Hs.178098 | Hs.178098:angiotensin I converting enzyme | 8.45 |
| 416768 | AA363733 | Hs.1032 | NM_002909:Homo sapiens regenerating isle | 7.94 |
| 422357 | AF016272 | Hs.115418 | NM_004062:Homo sapiens cadherin 16, KSP. | 7.78 |
| 420737 | L08096 | Hs.99899 | NM_001252:Homo sapiens tumor necrosis fa | 7.78 |
| 409745 | AA077391 | | AA077391:7B14E12 Chromosome 7 Fetal Brai | 7.74 |
| 413336 | AF113676 | Hs.297681 | NM_000295:Homo sapiens serine (or cystei | 7.32 |
| 426682 | AV660038 | Hs.2056 | Hs.2056:UDP glycosyltransferase 1 family | 7.20 |
| 406851 | AA609784 | Hs.352392 | Hs.352392:major histocompatibility compl | 7.03 |
| 419508 | AW997938 | Hs.90786 | Hs.90786:ATP-binding cassette, sub-famil | 6.57 |
| 428953 | AA306610 | Hs.348183 | NM_003823:Homo sapiens tumor necrosis fa | 6.36 |
| 435895 | AF037335 | Hs.5338 | NM_001218:Homo sapiens carbonic anhydras | 6.31 |
| 431842 | NM_005764 | Hs.271473 | NM_005764:Homo sapiens epithelial protei | 6.20 |
| 430014 | H59354 | Hs.374303 | Hs.374303:hypothetical protein MGC20576 | 6.20 |
| 423803 | NM_005709 | Hs.132945 | NM_005709:Homo sapiens PDZ-73 protein (P | 6.19 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 434779 | AF153815 | Hs.50151 | Hs.50151:potassium inwardly-rectifying c | 6.11 |
| | 435767 | H73505 | Hs.117874 | Hs.117874:ESTs | 6.08 |
| | 422664 | AA315933 | Hs.120879 | Hs.120879:Homo sapiens, clone MGC:32871 | 6.02 |
| 5 | 425280 | U31519 | Hs.1872 | Hs.1872:phosphoenolpyruvate carboxykinase | 5.81 |
| | 426559 | AB001914 | Hs.170414 | NM_002570:Homo sapiens paired basic amin | 5.73 |
| | 451564 | AU076698 | Hs.132760 | NM_001467:Homo sapiens glucose-6-phospha | 5.69 |
| | 418526 | BE019020 | Hs.85838 | NM_004207:Homo sapiens solute carrier fa | 5.68 |
| | 444151 | AW972917 | Hs.128749 | Hs.128749:alpha-methylacyl-CoA racemase | 5.66 |
| | 426471 | M22440 | Hs.170009 | NM_003236:Homo sapiens transforming grow | 5.48 |
| 10 | 432579 | AF043244 | Hs.278439 | NM_003946:Homo sapiens nucleolar protein | 5.45 |
| | 448733 | NM_005629 | Hs.187958 | NM_005629:Homo sapiens solute carrier fa | 5.42 |
| | 446650 | AB016625 | Hs.15813 | NM_003060:Homo sapiens solute carrier fa | 5.36 |
| | 417089 | HS2280 | Hs.18612 | Hs.18612:Homo sapiens cD: FLJ21909 fis, | 5.35 |
| | 437848 | AI906419 | Hs.284380 | Hs.284380:gamma-glutamyltransferase 1 | 5.32 |
| 15 | 423081 | AF262992 | Hs.123159 | Hs.123159:sperm associated antigen 4 | 5.30 |
| | 421893 | NM_001078 | Hs.109225 | NM_001078:Homo sapiens vascular cell adh | 5.23 |
| | 435886 | BE265839 | Hs.12126 | Hs.12126:hepatocellular carcinoma-associ | 5.20 |
| | 410276 | AI554545 | Hs.359201 | Hs.359201:ESTs | 5.20 |
| | 429451 | BE409861 | Hs.202833 | NM_002133:Homo sapiens heme oxygase (dec | 5.14 |
| 20 | 446404 | AA019961 | Hs.26216 | Hs.26216:Homo sapiens cD: FLJ22811 fis, | 5.13 |
| | 423445 | NM_014324 | Hs.128749 | NM_014324:Homo sapiens alpha-methylacyl- | 5.09 |
| | 449444 | AW818436 | Hs.351306 | NM_004696:Homo sapiens solute carrier fa | 5.05 |
| | 438106 | BE245551 | Hs.6079 | NM_014863:Homo sapiens B cell RAG associ | 5.02 |
| | 400419 | AF084545 | | AF084545:Homo sapiens versican Vint iso | 5.01 |
| 25 | 453920 | AI133148 | Hs.36602 | NM_000204:Homo sapiens I factor (complem | 4.99 |
| | 447881 | BE620886 | Hs.355279 | Hs.355279:Homo sapiens cD FLJ23711 fis, | 4.97 |
| | 422253 | W81526 | Hs.113882 | NM_000815:Homo sapiens gamma-aminobutyri | 4.93 |
| | 439024 | R96696 | Hs.35598 | Hs.35598:ESTs | 4.88 |
| | 414799 | AI752416 | Hs.77326 | NM_000598:Homo sapiens insulin-like grow | 4.80 |
| 30 | 426530 | U24578 | Hs.278625 | NM_000592:Homo sapiens complement compon | 4.77 |
| | 410055 | AJ250839 | Hs.58241 | Hs.58241:gene for serine/threonine prote | 4.72 |
| | 404240 | | | | 4.71 |
| | 414617 | AI339520 | Hs.288817 | Hs.288817:hypothetical protein FLJ22761 | 4.68 |
| 35 | 448249 | AW855331 | Hs.337124 | Hs.337124:ESTs | 4.67 |
| | 447818 | W79940 | Hs.21906 | Hs.21906:Homo sapiens clone 24670 mR seq | 4.66 |
| | 449057 | AB037784 | Hs.22941 | Hs.22941:KIAA1363 protein | 4.66 |
| | 422424 | AI186431 | Hs.296638 | NM_004864:Homo sapiens prostate differen | 4.62 |
| | 417335 | R70429 | Hs.81988 | NM_001343:Homo sapiens disabled homolog | 4.62 |
| 40 | 425873 | NM_013390 | Hs.160417 | NM_013390:Homo sapiens transmembrane pro | 4.58 |
| | 444700 | NM_003645 | Hs.11729 | NM_003645:Homo sapiens fatty-acid-Coenzy | 4.58 |
| | 414998 | NM_002543 | Hs.77729 | NM_002543:Homo sapiens oxidised low dens | 4.56 |
| | 414763 | U97276 | Hs.77266 | NM_002626:Homo sapiens quiescin Q6 (QSCN | 4.48 |
| | 443358 | H65417 | Hs.17757 | Hs.17757:pleckstrin homology domain-cont | 4.45 |
| | 440091 | AI767388 | Hs.37890 | Hs.37890:Homo sapiens, clone IMAGE:48275 | 4.43 |
| 45 | 447131 | NM_004585 | Hs.17466 | NM_004585:Homo sapiens retinoic acid rec | 4.43 |
| | 406973 | M34996 | Hs.198253 | Hs.198253:major histocompatibility compl | 4.42 |
| | 427740 | BE242604 | Hs.180616 | NM_005505:Homo sapiens CD36 antigen (col | 4.40 |
| | 436258 | AW867491 | Hs.107125 | Hs.107125:plasmalemma vesicle associated | 4.38 |
| | 452884 | C05964 | Hs.31841 | Hs.31841:ESTs | 4.37 |
| 50 | 444006 | BE395085 | Hs.10086 | NM_016639:Homo sapiens type I transmembr | 4.36 |
| | 422627 | BE336857 | Hs.118787 | NM_000358:Homo sapiens transforming grow | 4.35 |
| | 418054 | NM_002318 | Hs.83354 | NM_002318:Homo sapiens lysyl oxidase-lik | 4.34 |
| | 419011 | H56244 | Hs.89552 | NM_000846:Homo sapiens glutathione S-tra | 4.34 |
| | 404277 | | | | 4.33 |
| 55 | 435563 | AF210317 | Hs.95497 | Hs.95497:solute carrier family 2 (facili | 4.30 |
| | 431779 | AW971178 | Hs.268571 | NM_001645:Homo sapiens apolipoprotein C- | 4.29 |
| | 406645 | M57466 | Hs.814 | Hs.814:major histocompatibility complex, | 4.28 |
| | 421485 | AA243499 | Hs.104800 | Hs.104800:hypothetical protein FLJ10134 | 4.26 |
| 60 | 426812 | AF105365 | Hs.172613 | NM_005598:Homo sapiens solute carrier fa | 4.25 |
| | 407910 | AA650274 | Hs.41296 | NM_013281:Homo sapiens fibronectin leuci | 4.22 |
| | 438030 | X98427 | Hs.122634 | Hs.122634:ESTs | 4.22 |
| | 430661 | AC005551 | Hs.130714 | Hs.130714:ESTs, Moderately similar to AF | 4.21 |
| | 444381 | BE387335 | Hs.283713 | Hs.283713:hypothetical protein BC014245 | 4.20 |
| | 438203 | BE540090 | Hs.7345 | Hs.7345:MAD1 mitotic arrest deficient-I | 4.16 |
| 65 | 411358 | R47479 | Hs.94761 | Hs.94761:KIAA1691 protein | 4.15 |
| | 418323 | NM_002118 | Hs.1162 | NM_002118:Homo sapiens major histocompat | 4.12 |
| | 449853 | AF006823 | Hs.24040 | NM_002246:Homo sapiens potassium channel | 4.11 |
| | 415198 | AW009480 | Hs.943 | NM_004221:Homo sapiens tural killer cell | 4.11 |
| | 418751 | BE389014 | Hs.372548 | Hs.372548:phosphoinositide-3-kinase, regul | 4.09 |
| 70 | 414166 | AW888941 | Hs.75789 | NM_006096:Homo sapiens N-myc downstream | 4.07 |
| | 424125 | M31669 | Hs.1735 | Hs.1735:inhibin, beta B (activin AB beta | 4.00 |
| | 416926 | H03109 | Hs.263395 | Hs.263395:sema domain, transmembrane dom | 3.92 |
| | 419175 | AW270037 | Hs.362996 | Hs.362996:KIAA0779 protein | 3.92 |
| | 424218 | AF031824 | Hs.143212 | NM_003650:Homo sapiens cystatin F (leuko | 3.91 |
| 75 | 412870 | N22788 | Hs.82407 | Hs.82407:chemokine (C-X-C motif) ligand | 3.88 |
| | 452203 | X57522 | Hs.352018 | NM_000593:Homo sapiens transporter 1, AT | 3.87 |
| | 446872 | X97058 | Hs.16362 | NM_004154:Homo sapiens pyrimidinergic re | 3.87 |
| | 449961 | AW265634 | Hs.133100 | Hs.133100:ESTs | 3.87 |
| | 424517 | AI539443 | Hs.137447 | Hs.137447:Homo sapiens cD FLJ12169 fis, | 3.86 |
| 80 | 425262 | D87119 | Hs.155418 | Hs.155418:GS3955 protein | 3.83 |
| | 443639 | BE269042 | Hs.9661 | NM_002801:Homo sapiens proteasome (proso | 3.82 |
| | 448133 | AA723157 | Hs.73769 | NM_000802:Homo sapiens folate receptor 1 | 3.81 |
| | 418030 | BE207573 | Hs.83321 | Hs.83321:neuromedin B | 3.81 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| 5 | 412939 | AW411491 | Hs.75069 | NM_005412:Homo sapiens serine hydroxymet | 3.80 |
| | 409162 | H25530 | Hs.50868 | NM_002555:Homo sapiens solute carrier fa | 3.79 |
| | 427715 | BE245274 | Hs.180428 | Hs.180428:KIAA1181 protein | 3.78 |
| | 412006 | AW451618 | Hs.290216 | Hs.290216:ESTs | 3.77 |
| | 430413 | AW842182 | Hs.241392 | NM_002985:Homo sapiens small inducible c | 3.76 |
| | 422282 | AF019225 | Hs.114309 | Hs.114309:apolipoprotein L 1 | 3.76 |
| | 420747 | BE294407 | Hs.99910 | Hs.99910:phosphofructokinase, platelet | 3.76 |
| | 414875 | H42679 | Hs.77522 | NM_006120:Homo sapiens major histocompat | 3.75 |
| 10 | 418793 | AW382987 | Hs.88474 | Hs.88474:prostaglandin-endoperoxide synt | 3.74 |
| | 446291 | BE397753 | Hs.14623 | NM_006332:Homo sapiens interferon, gamma | 3.71 |
| | 417289 | D86962 | Hs.81875 | Hs.81875:growth factor receptor-bound pr | 3.69 |
| | 422672 | X12784 | Hs.119129 | NM_001845:Homo sapiens collagen, type IV | 3.68 |
| | 448569 | BE382657 | Hs.21486 | NM_007315:Homo sapiens sigl transducer a | 3.68 |
| 15 | 437270 | R18087 | Hs.323769 | Hs.323769:cisplatin resistance related p | 3.67 |
| | 408452 | AA054683 | Hs.192455 | Hs.192455:ESTs, Moderately similar to hy | 3.67 |
| | 443986 | AI381750 | Hs.283437 | Hs.283437:HT-GN29 protein | 3.66 |
| | 418869 | AW516565 | | AW516565:xq01d05.x1 Soares_NHCC_cervica | 3.65 |
| | 425998 | AU076629 | Hs.165950 | NM_002011:Homo sapiens fibroblast growth | 3.62 |
| 20 | 428699 | AW578252 | Hs.190161 | NM_014020:Homo sapiens LR8 protein (LR8) | 3.62 |
| | 418299 | AA279530 | Hs.83968 | NM_000211:Homo sapiens integrin, beta 2 | 3.61 |
| | 432593 | AW301003 | Hs.51483 | Hs.51483:Homo sapiens, Similar to RIKEN | 3.59 |
| | 415765 | NM_005424 | Hs.78824 | NM_005424:Homo sapiens tyrosine kinase wil | 3.58 |
| | 445985 | BE621800 | Hs.29444 | Hs.29444:putative small membrane protein | 3.57 |
| 25 | 424893 | AW295112 | Hs.153648 | Hs.153648:protein tyrosine phosphatase, | 3.57 |
| | 426046 | AA833655 | Hs.206868 | Hs.206868:Homo sapiens cD FLJ14056 fis, | 3.57 |
| | 424415 | NM_001975 | Hs.146580 | NM_001975:Homo sapiens enolase 2, (gamma | 3.57 |
| | 412612 | NM_000047 | Hs.74131 | NM_000047:Homo sapiens arylsulfatase E (| 3.56 |
| | 443834 | AI741510 | Hs.173548 | Hs.173548:ESTs | 3.54 |
| 30 | 431630 | NM_002204 | Hs.265829 | NM_002204:Homo sapiens integrin, alpha 3 | 3.53 |
| | 418371 | M13560 | Hs.84298 | Hs.84298:CD74 antigen (invariant polypep | 3.52 |
| | 444838 | AV651680 | Hs.208558 | Hs.208558:ESTs | 3.52 |
| | 449378 | AW664026 | Hs.59892 | Hs.59892:ESTs, Weakly similar to alpha 5 | 3.52 |
| | 411393 | AW797437 | Hs.69771 | NM_001710:Homo sapiens B-factor, properd | 3.50 |
| 35 | 414311 | AI693547 | Hs.71746 | Hs.71746:aminopeptidase-like 1 | 3.50 |
| | 415149 | X12451 | Hs.78056 | NM_001912:Homo sapiens cathepsin L (CTSL | 3.50 |
| | 424321 | W74048 | Hs.1765 | Hs.1765:lymphocyte-specific protein tyro | 3.49 |
| | 414825 | X06370 | Hs.77432 | NM_005228:Homo sapiens epidermal growth | 3.48 |
| | 408194 | AA601038 | Hs.191797 | Hs.191797:ESTs | 3.48 |
| 40 | 410600 | AW575742 | Hs.351676 | Hs.351676:ESTs, Weakly similar to T02670 | 3.47 |
| | 416899 | BE262645 | Hs.80420 | NM_002996:Homo sapiens small inducible c | 3.47 |
| | 436856 | AI469355 | Hs.127310 | Hs.127310:hypothetical protein BC014917 | 3.47 |
| | 419660 | BE280337 | Hs.194693 | NM_003982:Homo sapiens solute carrier fa | 3.47 |
| | 413566 | AW604451 | Hs.285814 | Hs.285814:growth factor receptor-bound p | 3.47 |
| 45 | 412104 | AW205197 | Hs.240951 | Hs.240951:ked cuticle homolog 2 (Drosoph | 3.46 |
| | 444488 | AW192879 | Hs.355660 | Hs.355660:peptide-histidine transporter | 3.46 |
| | 449475 | AI348027 | Hs.108557 | Hs.108557:hypothetical protein PP1057 | 3.46 |
| | 412276 | BE262621 | Hs.73798 | NM_002415:Homo sapiens macrophage migrat | 3.45 |
| | 449338 | H73444 | Hs.394 | NM_001124:Homo sapiens adrenomedullin (A | 3.44 |
| 50 | 430304 | AL122071 | Hs.238927 | Hs.238927:Homo sapiens mR; cD DKFZp434H1 | 3.43 |
| | 415388 | AF018081 | Hs.78409 | (locuslink)NM_030582:Homo sapiens collag | 3.43 |
| | 432210 | AI567421 | Hs.273330 | Hs.273330:agrin | 3.43 |
| | 418177 | N44967 | Hs.351554 | Hs.351554:Homo sapiens cD FLJ32092 fis, | 3.42 |
| | 414888 | AL039185 | Hs.77558 | Hs.77558:thyroid hormone receptor intera | 3.42 |
| 55 | 452445 | AB002438 | Hs.29596 | Hs.29596:Homo sapiens mR from chromosome | 3.41 |
| | 414803 | X03100 | Hs.914 | Hs.914:major histocompatibility complex, | 3.41 |
| | 419201 | M22324 | Hs.1239 | NM_001150:Homo sapiens alanyl (membrane) | 3.41 |
| | 445139 | AB037848 | Hs.12365 | Hs.12365:syptotagmin XIII | 3.41 |
| | 435021 | AA922192 | Hs.73962 | Hs.73962:EphA7 | 3.41 |
| 60 | 417259 | AW903838 | Hs.81800 | Hs.81800:chondroitin sulfate proteoglyca | 3.40 |
| | 439737 | AI751438 | Hs.41271 | Hs.41271:Homo sapiens mR full length ins | 3.39 |
| | 410636 | AA088177 | Hs.172870 | Hs.172870:KIAA1913 protein | 3.39 |
| | 431590 | AB037789 | Hs.263395 | Hs.263395:sema domain, transmembrane dom | 3.38 |
| | 415000 | AW025529 | Hs.239812 | Hs.239812:serologically defined breast c | 3.36 |
| 65 | 416700 | AW498958 | Hs.343475 | NM_001909:Homo sapiens cathepsin D (lyso | 3.36 |
| | 440516 | S42303 | Hs.161 | NM_001792:Homo sapiens cathepsin 2, type | 3.35 |
| | 423720 | AL044191 | Hs.23388 | Hs.23388:hypothetical protein DKFZp434F0 | 3.32 |
| | 421902 | BE392717 | | BE392717:601307571F1 NIH_MGC_44 Homo sap | 3.32 |
| | 409220 | BE243323 | Hs.51233 | Hs.51233:tumor necrosis factor receptor | 3.32 |
| 70 | 421502 | AF111856 | Hs.105039 | NM_006424:Homo sapiens solute carrier fa | 3.32 |
| | 416729 | U46165 | Hs.1027 | NM_004165:Homo sapiens Ras-related assoc | 3.30 |
| | 430302 | AL137502 | Hs.238679 | Hs.238679:Rag D protein | 3.30 |
| | 445084 | H38914 | Hs.250848 | Hs.250848:Homo sapiens cD FLJ14761 fis, | 3.29 |
| | 406825 | AI982529 | Hs.84298 | Hs.84298:CD74 antigen (invariant polypep | 3.29 |
| 75 | 446272 | BE268912 | Hs.14601 | NM_005335:Homo sapiens hematopoietic cel | 3.28 |
| | 437145 | AF007216 | Hs.5462 | NM_003759:Homo sapiens solute carrier fa | 3.27 |
| | 444071 | AI627808 | Hs.110524 | Hs.110524:ESTs | 3.27 |
| | 414662 | AL036058 | Hs.76807 | Hs.76807:major histocompatibility comple | 3.27 |
| | 436576 | AI458213 | Hs.77542 | Hs.77542:ESTs, Weakly similar to S26650 | 3.26 |
| 80 | 424675 | NM_005512 | Hs.151641 | NM_005512:Homo sapiens glycoprotein A re | 3.25 |
| | 437897 | AA770561 | Hs.146170 | Hs.146170:hypothetical protein FLJ22969 | 3.25 |
| | 449703 | H61001 | Hs.171802 | Hs.171802:Homo sapiens, clone IMAGE:3956 | 3.25 |
| | 414788 | X78342 | Hs.77313 | NM_003674:Homo sapiens cyclin-dependent | 3.25 |
| | 414249 | AI797994 | Hs.279929 | Hs.279929:gp25L2 protein | 3.24 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 430396 | D49742 | Hs.241363 | NM_004132:Homo sapiens hyaluron binding | 3.23 |
| | 424456 | AA341017 | Hs.25549 | Hs.25549:hypothetical protein FLJ20898 | 3.23 |
| | 452303 | R27257 | Hs.57734 | Hs.57734:G protein-coupled receptor kise | 3.22 |
| | 425390 | AJ092634 | Hs.156114 | NM_004648:Homo sapiens protein tyrosine | 3.21 |
| 5 | 416033 | NM_012201 | Hs.78979 | NM_012201:Homo sapiens golgi apparatus p | 3.19 |
| | 450931 | N25156 | Hs.25648 | Hs.25648:tumor necrosis factor receptor | 3.19 |
| | 428065 | AI634046 | Hs.157313 | Hs.157313:ESTs | 3.18 |
| | 422616 | BE300330 | Hs.118725 | NM_012248:Homo sapiens selenophosphate s | 3.18 |
| | 439318 | AW837046 | Hs.6527 | Hs.6527:G protein-coupled receptor 56 | 3.17 |
| 10 | 427640 | AF058293 | Hs.180015 | NM_001355:Homo sapiens D-dopachrome taut | 3.17 |
| | 409936 | AK001691 | Hs.57655 | Hs.57655:dudulin 2 | 3.16 |
| | 435001 | AW903849 | Hs.173840 | Hs.173840:similar to endothelial cell-se | 3.16 |
| | 451154 | AA015879 | Hs.33536 | Hs.33536:ESTs | 3.16 |
| | 420256 | U84722 | Hs.76206 | NM_001795:Homo sapiens cadherin 5, type | 3.16 |
| 15 | 407584 | W25945 | Hs.8173 | Hs.8173:hypothetical protein FLJ10803 | 3.15 |
| | 428593 | AW207440 | Hs.185973 | NM_003676:Homo sapiens degenerative sper | 3.15 |
| | 410026 | AI912061 | Hs.55016 | Hs.55016:EPS8-related protein 2 | 3.15 |
| | 445333 | BE537641 | Hs.44278 | Hs.44278:RAB17, member RAS oncogene fami | 3.14 |
| | 448143 | AF039704 | Hs.20478 | NM_000391:Homo sapiens ceroid-lipofuscin | 3.14 |
| 20 | 423007 | AA320134 | Hs.196029 | Hs.196029:Homo sapiens mR for KIAA1657 p | 3.14 |
| | 416511 | NM_006762 | Hs.79356 | NM_006762:Homo sapiens Lysosomal-associa | 3.14 |
| | 439237 | AW408158 | Hs.318893 | Hs.318893:ESTs, Weakly similar to Z195_H | 3.13 |
| | 446899 | NM_005397 | Hs.16426 | NM_005397:Homo sapiens podocalyxin-like | 3.13 |
| 25 | 413916 | N49813 | Hs.75615 | NM_000483:Homo sapiens apolipoprotein C- | 3.13 |
| | 434398 | AA121098 | Hs.3838 | NM_006622:Homo sapiens serum-inducible k | 3.12 |
| | 441283 | AA927670 | Hs.131704 | Hs.131704:ESTs | 3.12 |
| | 418945 | BE246762 | Hs.89499 | NM_000698:Homo sapiens arachidole 5-lipo | 3.12 |
| | 418458 | AA332941 | Hs.85226 | NM_000235:Homo sapiens lipase A, lysosom | 3.12 |
| 30 | 408989 | AW361666 | Hs.49500 | Hs.49500:KIAA0746 protein | 3.11 |
| | 436906 | H95990 | Hs.181244 | Hs.181244:major histocompatibility compl | 3.11 |
| | 411089 | AA456454 | Hs.355702 | Hs.355702:ESTs, Weakly similar to AC0048 | 3.11 |
| | 432990 | AL036071 | Hs.273899 | NM_003820:Homo sapiens tumor necrosis fa | 3.11 |
| | 425009 | X58288 | Hs.154151 | NM_002845:Homo sapiens protein tyrosine | 3.10 |
| 35 | 443601 | AI078554 | Hs.42658 | Hs.42658:Homo sapiens cD FLJ30167 fis, c | 3.10 |
| | 430603 | AA148164 | Hs.247280 | Hs.247280:chromosome 20 open reading fra | 3.10 |
| | 413672 | BE156536 | Hs.353632 | Hs.353632:ESTs, Moderately similar to hy | 3.09 |
| | 407786 | AA687538 | Hs.38972 | NM_005727:Homo sapiens tetraspan 1 (TSPA | 3.09 |
| | 414586 | AA306160 | Hs.16488 | NM_002298:Homo sapiens lymphocyte cytosol | 3.08 |
| 40 | 423712 | W46802 | Hs.81988 | Hs.81988:disabled homolog 2, mitogen-res | 3.08 |
| | 438552 | AJ245820 | Hs.6314 | NM_012410:Homo sapiens type I transmembr | 3.06 |
| | 448364 | T08958 | Hs.297214 | Hs.297214:HSPC141 protein | 3.06 |
| | 426437 | BE076537 | Hs.169895 | NM_004223:Homo sapiens ubiquitin-conjuga | 3.06 |
| | 437679 | NM_014214 | Hs.5753 | NM_014214:Homo sapiens inositol(myo)-1(o | 3.06 |
| 45 | 422262 | AL022315 | Hs.113987 | NM_006498:Homo sapiens lectin, galactosi | 3.06 |
| | 410480 | R97457 | Hs.63984 | NM_001257:Homo sapiens cadherin 13, H-ca | 3.05 |
| | 435818 | AA700553 | Hs.368614 | Hs.368614:ESTs | 3.05 |
| | 418883 | BE387036 | Hs.1211 | NM_001611:Homo sapiens acid phosphatase | 3.05 |
| | 453613 | F06838 | Hs.374476 | Hs.374476:ESTs | 3.05 |
| 50 | 408051 | AI623351 | Hs.172148 | Hs.172148:ESTs | 3.05 |
| | 432278 | AL137506 | Hs.274256 | Hs.274256:hypothetical protein FLJ23563 | 3.04 |
| | 407949 | W21874 | Hs.247057 | Hs.247057:ESTs, Weakly similar to 210926 | 3.04 |
| | 418090 | U57059 | Hs.83429 | NM_003810:Homo sapiens tumor necrosis fa | 3.04 |
| | 433165 | AA578904 | Hs.292437 | Hs.292437:ESTs | 3.03 |
| 55 | 425809 | AA370362 | Hs.57958 | Hs.57958:EGF-TM7-latrophilin-related pro | 3.03 |
| | 443884 | N20617 | Hs.194397 | Hs.194397:ESTs, Moderately similar to 22 | 3.03 |
| | 447831 | AI433293 | Hs.164115 | Hs.164115:ESTs | 3.02 |
| | 413278 | BE563085 | Hs.833 | NM_005101:Homo sapiens interferon-stimul | 3.01 |
| | 418870 | AF147204 | Hs.89414 | Hs.89414:chemokine (C-X-C motif), recept | 3.00 |
| 60 | 456376 | AA663904 | Hs.89862 | Hs.89862:TNFRSF1A-associated via death d | 3.00 |
| | 439738 | BE246502 | Hs.9598 | Hs.9598:sema domain, immunoglobulin doma | 3.00 |
| | 444416 | AW288085 | Hs.11156 | NM_016494:Homo sapiens hypothetical prot | 3.00 |
| | 406656 | M16714 | Hs.89643 | Hs.89643:transketolase (Wernicke-Korsako | 3.00 |
| | 406826 | AW516005 | Hs.84298 | Hs.84298:CD74 antigen (invariant polypep | 2.99 |
| 65 | 418707 | U97502 | Hs.87497 | Hs.87497:butyrophilin, subfamily 3, memb | 2.99 |
| | 421742 | AW970004 | Hs.107528 | NM_016108:Homo sapiens androgen induced | 2.99 |
| | 406824 | AW515961 | Hs.84298 | Hs.84298:CD74 antigen (invariant polypep | 2.99 |
| | 435605 | AF151815 | Hs.4973 | NM_015680:Homo sapiens hypothetical prot | 2.98 |
| | 410491 | AA465131 | Hs.64001 | Hs.64001:Homo sapiens clone 25218 mR seq | 2.98 |
| 70 | 427648 | AI376722 | Hs.180062 | NM_004159:Homo sapiens proteasome (proso | 2.98 |
| | 411125 | AA151647 | Hs.68877 | NM_000101:Homo sapiens cytochrome b-245, | 2.98 |
| | 435550 | AJ224456 | Hs.324507 | Hs.324507:hypothetical protein FLJ20986 | 2.98 |
| | 429373 | NM_014694 | Hs.200594 | NM_014694:Homo sapiens KIAA0605 gene pro | 2.98 |
| | 445701 | AF055581 | Hs.13131 | NM_005475:Homo sapiens lymphocyte adapt | 2.97 |
| 75 | 414649 | AI672727 | Hs.76753 | NM_000118:Homo sapiens endoglin (Osler-R | 2.97 |
| | 444207 | AI565004 | Hs.374415 | Hs.374415:ESTs | 2.97 |
| | 423225 | AA852604 | Hs.125359 | NM_006288:Homo sapiens Thy-1 cell surfac | 2.97 |
| | 407792 | AI077715 | Hs.39384 | NM_014344:Homo sapiens four jointed box | 2.97 |
| | 445707 | AJ248720 | Hs.114390 | Hs.114390:ESTs | 2.96 |
| 80 | 452888 | AW955454 | Hs.30942 | NM_004093:Homo sapiens ephrin-B2 (EFNB2) | 2.96 |
| | 418478 | U38945 | Hs.1174 | Hs.1174:cyclin-dependent kinase inhibitor | 2.95 |
| | 411441 | AL042355 | Hs.70202 | Hs.70202:WD repeat domain 10 | 2.95 |
| | 443426 | AF098158 | Hs.9329 | Hs.9329:chromosome 20 open reading frame | 2.94 |
| | 450876 | AF189062 | Hs.285976 | Hs.285976:LAG1 longevity assurance homol | 2.94 |

| | | | | |
|--------|-----------|-----------|---|------|
| 426359 | AA376409 | Hs.10862 | Hs.10862:Homo sapiens cD: FLJ23313 fis, | 2.94 |
| 425421 | L11669 | Hs.157145 | NM_001120:Homo sapiens tetracycline tran | 2.93 |
| 449879 | H03573 | Hs.287830 | Hs.287830:Homo sapiens mR: cD DKFZp434E1 | 2.93 |
| 454075 | R43826 | Hs.16313 | Hs.16313:Kruppel-like zinc finger protei | 2.93 |
| 421595 | AB014520 | Hs.301685 | Hs.301685:KIAA0620 protein | 2.93 |
| 457949 | W69171 | Hs.334814 | Hs.334814:hypothetical protein FLJ14868 | 2.92 |
| 443987 | AW163123 | Hs.10071 | NM_016551:Homo sapiens seven transmembra | 2.92 |
| 430259 | BE550182 | Hs.375142 | Hs.375142:RalGEF-like protein 3, mouse h | 2.92 |
| 415906 | AJ751357 | Hs.288741 | Hs.288741:Homo sapiens cD: FLJ22256 fis, | 2.91 |
| 429762 | A1346255 | Hs.216354 | NM_006913:Homo sapiens ring finger prote | 2.91 |
| 451527 | AF022813 | Hs.26518 | NM_003271:Homo sapiens transmembrane 4 s | 2.91 |
| 425356 | BE244879 | Hs.155939 | NM_005541:Homo sapiens inositol polyphos | 2.91 |
| 427080 | AW068287 | Hs.301175 | NM_002872:Homo sapiens ras-related C3 bo | 2.91 |
| 426432 | AF001601 | Hs.169857 | NM_000305:Homo sapiens paraoxase 2 (PON2 | 2.90 |
| 431476 | BE612705 | Hs.256697 | Hs.256697:histidine triad nucleotide bin | 2.89 |
| 406659 | AA663985 | Hs.277477 | Hs.277477:major histocompatibility compl | 2.89 |
| 451144 | AW956103 | Hs.61712 | Hs.61712:Homo sapiens cD FLJ31548 fis, c | 2.89 |
| 456362 | AW973003 | Hs.179909 | Hs.179909:nuclear receptor coactivator 6 | 2.88 |
| 426440 | BE382756 | Hs.169902 | NM_006516:Homo sapiens solute carrier fa | 2.88 |
| 456974 | M12529 | Hs.169401 | NM_000041:Homo sapiens apolipoprotein E | 2.88 |
| 418174 | L20688 | Hs.83656 | Hs.83656:Rho GDP dissociation inhibitor | 2.88 |
| 446055 | AJ815981 | Hs.12909 | Hs.12909:mucolipin 1 | 2.88 |
| 423184 | NM_004428 | Hs.1624 | NM_004428:Homo sapiens ephrin-A1 (EF1), | 2.87 |
| 427700 | AA262294 | Hs.180383 | NM_001946:Homo sapiens dual specificity | 2.87 |
| 410668 | BE379794 | Hs.159651 | NM_016629:Homo sapiens hypothetical prot | 2.87 |
| 444143 | AW747996 | Hs.160999 | Hs.160999:ESTs, Weakly similar to 17885 | 2.87 |
| 407151 | H25836 | Hs.301527 | Hs.301527:ESTs, Moderately similar to un | 2.86 |
| 449349 | AJ825386 | Hs.352579 | Hs.352579:Homo sapiens, chromosome 20 op | 2.86 |
| 436997 | AA741151 | Hs.137323 | Hs.137323:ESTs | 2.86 |
| 446143 | BE245342 | Hs.306079 | NM_013336:Homo sapiens protein transport | 2.86 |
| 417355 | D13168 | Hs.82002 | Hs.82002:endothelin receptor type B | 2.86 |
| 431685 | AW296135 | Hs.267659 | NM_006113:Homo sapiens vav 3 oncogene (V | 2.86 |
| 408877 | AA479033 | Hs.130315 | Hs.130315:ESTs | 2.85 |
| 429615 | AF258627 | Hs.211562 | NM_005502:Homo sapiens ATP-binding casse | 2.85 |
| 412014 | AJ620650 | Hs.43761 | Hs.43761:gap junction protein, alpha 7, | 2.84 |
| 436749 | AA584890 | Hs.5302 | NM_006149:Homo sapiens lectin, galactosi | 2.84 |
| 419625 | U91616 | Hs.182885 | NM_004556:Homo sapiens nuclear factor of | 2.84 |
| 439941 | AJ392640 | Hs.18272 | Hs.18272:solute carrier family 38, membe | 2.84 |
| 436496 | AA281959 | Hs.5210 | NM_004877:Homo sapiens glia maturation I | 2.84 |
| 422100 | AJ096988 | Hs.111554 | NM_005737:Homo sapiens ADP-ribosylation | 2.83 |
| 439730 | AF035292 | Hs.6654 | Hs.6654:KIAA0657 protein | 2.83 |
| 447217 | BE465754 | Hs.17778 | NM_003872:Homo sapiens neuropilin 2 (NRP | 2.83 |
| 428343 | AL043021 | Hs.12705 | Hs.12705:similar to HYPOTHETICAL 43.1 KO | 2.82 |
| 440524 | R71264 | Hs.16798 | Hs.16798:Homo sapiens mR: cD DKFZp564O24 | 2.82 |
| 415523 | AL042003 | Hs.296847 | NM_003119:Homo sapiens spastic paraplegi | 2.81 |
| 439668 | AJ091277 | Hs.302634 | Hs.302634:frizzled homolog 8 (Drosophila | 2.81 |
| 414570 | Y00285 | Hs.76473 | NM_000876:Homo sapiens insulin-like grow | 2.80 |
| 426535 | AJ077012 | Hs.288582 | NM_006287:Homo sapiens tissue factor pat | 2.80 |
| 409649 | AA159216 | Hs.55505 | Hs.55505:hypothetical protein FLJ20442 | 2.80 |
| 406655 | M21533 | Hs.277477 | Hs.277477:major histocompatibility compl | 2.79 |
| 415323 | BE269352 | Hs.949 | NM_000433:Homo sapiens neutrophil cytosol | 2.79 |
| 443195 | BE148235 | Hs.193063 | Hs.193063:Homo sapiens cD FLJ14201 fis, | 2.78 |
| 451356 | AA748418 | Hs.164577 | Hs.164577:ESTs | 2.78 |
| 450708 | AA376654 | Hs.350065 | Hs.350065:Homo sapiens cD FLJ30634 fis, | 2.78 |
| 433681 | AJ004377 | Hs.200360 | Hs.200360:Homo sapiens cD FLJ13027 fis, | 2.77 |
| 442599 | AF078037 | Hs.324051 | NM_006663:Homo sapiens RalA-associated i | 2.76 |
| 414509 | AW161311 | Hs.76294 | NM_001780:Homo sapiens CD63 antigen (mel | 2.76 |
| 431394 | AK000692 | Hs.252351 | Hs.252351:HERV-H LTR-associating 2 | 2.76 |
| 417331 | AW411297 | Hs.81972 | Hs.81972:SHC (Src homology 2 domain cont | 2.76 |
| 415995 | NM_004573 | Hs.355888 | NM_004573:Homo sapiens phosphotipase C, | 2.75 |
| 414911 | NM_000107 | Hs.77602 | NM_000107:Homo sapiens damage-specific D | 2.75 |
| 425976 | C75094 | Hs.334514 | Hs.334514:chromosome 6 open reading fram | 2.75 |
| 407893 | BE408359 | Hs.43621 | Hs.43621:hypothetical protein MBC3205 | 2.75 |
| 407903 | AJ287341 | Hs.154029 | Hs.154029:bHLH factor Hes4 | 2.75 |
| 416062 | AA724811 | Hs.334791 | Hs.334791:similar to neurol tetraspanin | 2.75 |
| 428494 | AA233439 | Hs.184634 | Hs.184634:hypothetical protein FLJ20005 | 2.75 |
| 421506 | BE302796 | Hs.105097 | NM_003258:Homo sapiens thymidine kise 1, | 2.74 |
| 427581 | NM_014768 | Hs.179703 | NM_014768:Homo sapiens tripartite motif, | 2.74 |
| 424527 | AW138558 | Hs.334873 | Hs.334873:carboxypeptidase M | 2.74 |
| 439578 | AW263124 | Hs.350547 | Hs.350547:nuclear receptor co-repressor/ | 2.74 |
| 425188 | AK002052 | Hs.155071 | Hs.155071:chromosome 20 open reading fra | 2.74 |
| 428013 | AF151020 | Hs.181444 | NM_016456:Homo sapiens hypothetical prot | 2.73 |
| 439333 | AW384710 | Hs.132986 | Hs.132986:Homo sapiens cD FLJ31588 fis, | 2.73 |
| 450935 | BE514743 | Hs.355753 | NM_005851:Homo sapiens tumor suppressor | 2.73 |
| 421532 | AW138207 | Hs.146170 | Hs.146170:hypothetical protein FLJ22969 | 2.73 |
| 440502 | AJ824113 | Hs.78281 | Hs.78281:regulator of G-protein siglting | 2.73 |
| 444981 | AW855398 | Hs.12210 | Hs.12210:tumor endothelial marker 6 | 2.72 |
| 439219 | N33883 | Hs.41322 | Hs.41322:ESTs | 2.72 |
| 416847 | L43821 | Hs.80261 | NM_006403:Homo sapiens enhancer of filam | 2.72 |
| 433179 | AW362945 | Hs.162459 | Hs.162459:ESTs | 2.72 |
| 424528 | AW073971 | Hs.238954 | Hs.238954:ESTs, Weakly similar to putati | 2.71 |
| 411213 | AA676939 | Hs.69285 | NM_003873:Homo sapiens neuropilin 1 (NRP | 2.70 |
| 433012 | NM_004045 | Hs.279910 | NM_004045:Homo sapiens ATX1 antioxidant | 2.70 |

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|----|--------|-----------|-----------|--|------|
| | 425345 | AU077297 | Hs.155894 | NM_002827:Homo sapiens protein tyrosine | 2.69 |
| | 428923 | BE047698 | Hs.188785 | Hs.188785:ESTs | 2.69 |
| | 427923 | AW274357 | Hs.301406 | Hs.301406:hypothetical protein PP3501 | 2.69 |
| | 446644 | NM_003272 | Hs.15791 | NM_003272:Homo sapiens transmembrane 7 s | 2.69 |
| 5 | 421743 | T35958 | Hs.107614 | Hs.107614:OKFZP56411171 protein | 2.68 |
| | 416207 | NM_014745 | Hs.79077 | NM_014745:Homo sapiens KIAA0233 gene pro | 2.68 |
| | 420372 | AW960049 | Hs.293660 | Hs.293660:gene overexpressed in astrocyt | 2.68 |
| | 420542 | NM_000505 | Hs.1321 | NM_000505:Homo sapiens coagulation facto | 2.67 |
| | 425069 | AA687465 | Hs.298184 | Hs.298184:potassium voltage-gated channe | 2.67 |
| 10 | 418558 | AW082266 | Hs.86131 | NM_003824:Homo sapiens Fas (TNFRSF6)-ass | 2.67 |
| | 426251 | M24283 | Hs.168383 | NM_000201:Homo sapiens intercellular adh | 2.66 |
| | 406701 | AA780613 | Hs.62954 | Hs.62954:ferritin, heavy polypeptide 1 | 2.66 |
| | 431681 | AK000378 | Hs.267566 | Hs.267566:hypothetical protein FLJ20371 | 2.66 |
| | 412833 | AW960547 | Hs.298262 | Hs.298262:ribosomal protein S19 | 2.66 |
| 15 | 433101 | AW572317 | Hs.12082 | Hs.12082:TIGA1 | 2.66 |
| | 414774 | X02419 | Hs.77274 | NM_002658:Homo sapiens plasminogen activ | 2.66 |
| | 427868 | AI360119 | Hs.181013 | NM_002629:Homo sapiens phosphoglycerate | 2.66 |
| | 413929 | BE501689 | Hs.75617 | Hs.75617:collagen, type IV, alpha 2 | 2.66 |
| | 424762 | AL119442 | Hs.183684 | Hs.183684:eukaryotic translation initiat | 2.66 |
| 20 | 422048 | NM_012445 | Hs.288126 | NM_012445:Homo sapiens spondin 2, extrac | 2.65 |
| | 431350 | AI192528 | Hs.164537 | Hs.164537:ESTs | 2.65 |
| | 450184 | W31096 | Hs.237617 | Hs.237617:dipeptidylpeptidase 9 | 2.65 |
| | 419285 | D31887 | Hs.89868 | Hs.89868:KIAA0062 protein | 2.65 |
| | 414217 | AI309298 | Hs.279898 | Hs.279898:Homo sapiens cD: FLJ23165 fis, | 2.64 |
| 25 | 451253 | H48299 | Hs.26126 | NM_005984:Homo sapiens claudin 10 (CLDN1 | 2.64 |
| | 435905 | AW997484 | Hs.5003 | Hs.5003:SLIT-ROBO Rho GTPase-activating | 2.64 |
| | 432581 | AU076465 | Hs.278441 | NM_014634:Homo sapiens KIAA0015 gene pro | 2.63 |
| | 415782 | AA169345 | Hs.123177 | Hs.123177:hypothetical protein BC011406 | 2.63 |
| | 430223 | NM_002514 | Hs.235935 | NM_002514:Homo sapiens neuroblastoma ov | 2.63 |
| 30 | 417526 | AA568906 | Hs.82240 | NM_004177:Homo sapiens syntaxin 3A (STX3 | 2.63 |
| | 409956 | AW103364 | Hs.727 | NM_002192:Homo sapiens inhibin, beta A (| 2.63 |
| | 449843 | R85337 | Hs.24030 | NM_001860:Homo sapiens solute carrier fa | 2.62 |
| | 417389 | BE260964 | Hs.82045 | NM_002391:Homo sapiens midkine (neurite | 2.62 |
| | 446312 | BE087853 | Hs.171802 | Hs.171802:Homo sapiens, clone IMAGE:3956 | 2.62 |
| 35 | 435099 | AC004770 | Hs.4756 | Hs.4756:flap structure-specific endonucle | 2.62 |
| | 417920 | S47833 | Hs.82927 | NM_004037:Homo sapiens adenosine monopho | 2.62 |
| | 435702 | AI033647 | Hs.121001 | Hs.121001:Homo sapiens, clone MGC:45521 | 2.62 |
| | 422959 | AV647015 | Hs.349256 | Hs.349256:paired immunoglobulin-like rec | 2.62 |
| | 419938 | AU076772 | Hs.1279 | NM_001733:Homo sapiens complement compon | 2.62 |
| 40 | 450954 | AI904740 | Hs.25691 | NM_005856:Homo sapiens receptor (calcito | 2.61 |
| | 421753 | BE314828 | Hs.107911 | Hs.107911:ATP-binding cassette, sub-fami | 2.61 |
| | 443577 | AI078033 | Hs.177170 | Hs.177170:ESTs, Weakly similar to ALU8_H | 2.61 |
| | 453886 | R66282 | Hs.20247 | Hs.20247:ESTs | 2.61 |
| | 421883 | X55079 | Hs.1437 | NM_000152:Homo sapiens glucosidase, alph | 2.60 |
| 45 | 440457 | BE387593 | Hs.21321 | Hs.21321:granule cell differentiation pr | 2.60 |
| | 410295 | AA741357 | Hs.356624 | Hs.356624:ESTs | 2.59 |
| | 420679 | X57152 | Hs.99853 | NM_001436:Homo sapiens fibrillarin (FBL) | 2.59 |
| | 451558 | NM_001089 | Hs.26630 | NM_001089:Homo sapiens ATP-binding casse | 2.59 |
| | 444672 | Z95636 | Hs.11669 | Hs.11669:laminin, alpha 5 | 2.59 |
| 50 | 408669 | AI493591 | Hs.78146 | Hs.78146:platelet/endothelial cell adhes | 2.59 |
| | 426194 | T50872 | Hs.2001 | Hs.2001:thromboxane A synthase 1 (platelet | 2.59 |
| | 421814 | L12350 | Hs.108623 | NM_003247:Homo sapiens thrombospondin 2 | 2.59 |
| | 456371 | S76825 | Hs.89695 | Hs.89695:insulin receptor | 2.59 |
| 55 | 429098 | AF030249 | Hs.196176 | NM_001398:Homo sapiens enoyl Coenzyme A | 2.59 |
| | 414443 | AU077268 | Hs.76144 | NM_002609:Homo sapiens platelet-derived | 2.59 |
| | 428484 | AF104032 | Hs.184501 | NM_003486:Homo sapiens solute carrier fa | 2.59 |
| | 453309 | AI791809 | Hs.32949 | NM_005218:Homo sapiens defensin, beta 1 | 2.59 |
| | 412867 | AU076861 | Hs.74637 | NM_003217:Homo sapiens testis enhanced g | 2.58 |
| 60 | 432827 | Z58128 | Hs.3109 | Hs.3109:Rho GTPase activating protein 4 | 2.58 |
| | 412669 | AW880841 | Hs.96908 | NM_006034:Homo sapiens p53-induced prote | 2.58 |
| | 412115 | AK001763 | Hs.73239 | Hs.73239:hypothetical protein FLJ10901 | 2.58 |
| | 452866 | R26969 | Hs.268016 | Hs.268016:Homo sapiens cD: FLJ21243 fis, | 2.58 |
| | 435129 | AI381659 | Hs.267086 | Hs.267086:ESTs | 2.57 |
| | 424482 | BE268621 | Hs.149155 | NM_003374:Homo sapiens voltage-dependent | 2.57 |
| 65 | 410494 | M36564 | Hs.64016 | NM_000313:Homo sapiens protein S (alpha) | 2.56 |
| | 433895 | AI287912 | Hs.3628 | NM_004834:Homo sapiens mitogen-activated | 2.56 |
| | 442566 | R37337 | Hs.12111 | Hs.12111:ESTs | 2.56 |
| | 417640 | D30857 | Hs.82353 | NM_006404:Homo sapiens protein C recepto | 2.56 |
| | 442622 | NM_000435 | Hs.8546 | NM_000435:Homo sapiens Notch homolog 3 (| 2.56 |
| 70 | 430346 | AK000331 | Hs.297641 | Hs.297641:retinoblastoma-associated fact | 2.55 |
| | 419344 | U94905 | Hs.277445 | Hs.277445:diacylglycerol kinase, zeta (104 | 2.55 |
| | 426500 | NM_014638 | Hs.170156 | NM_014638:Homo sapiens KIAA0450 gene pro | 2.55 |
| | 408048 | NM_007203 | Hs.42322 | NM_007203:Homo sapiens A kinase (PRKA) anc | 2.55 |
| | 450700 | AW732799 | Hs.25348 | NM_005860:Homo sapiens follistatin-like | 2.54 |
| 75 | 417018 | M16038 | Hs.80887 | NM_002350:Homo sapiens v-yes-1 Yamaguchi | 2.54 |
| | 419378 | R24922 | Hs.90078 | Hs.90078:nucleotide-sugar transporter si | 2.54 |
| | 422451 | AA310753 | Hs.42491 | Hs.42491:ESTs, Moderately similar to hyp | 2.53 |
| | 435906 | AI686379 | Hs.110796 | Hs.110796:SAR1 protein | 2.53 |
| | 400231 | | | | 2.53 |
| 80 | 417849 | AW291587 | Hs.82733 | NM_007361:Homo sapiens nidogen 2 (NID2), | 2.53 |
| | 427380 | NM_005534 | Hs.177559 | NM_005534:Homo sapiens interferon gamma | 2.52 |
| | 428385 | AF112213 | Hs.184062 | Hs.184062:chromosome 20 open reading tra | 2.52 |
| | 438000 | AI825880 | Hs.5985 | Hs.5985:non-kinase Cdc42 effector protein | 2.52 |

| | | | | |
|--------|-----------|-----------|---|------|
| 448719 | AA033627 | Hs.21858 | Hs.21858:serine (or cysteine) protease i | 2.52 |
| 422396 | W21872 | Hs.7907 | Hs.7907:L-fucose kase | 2.52 |
| 420787 | AA564248 | Hs.351292 | Hs.351292:Homo sapiens cD FLJ32605 fis, | 2.51 |
| 430590 | AW383947 | Hs.246381 | NM_001251:Homo sapiens CD68 antigen (CD6 | 2.51 |
| 447026 | BE313144 | Hs.324844 | Hs.324844:hypothetical protein IMAGE3455 | 2.51 |
| 439223 | AW238299 | Hs.250618 | Hs.250618:UL16 binding protein 2 | 2.50 |
| 435151 | AA348482 | Hs.4788 | Hs.4788:nicastatin | 2.50 |
| 448202 | AB002292 | Hs.20695 | NM_014629:Homo sapiens Rho guanine nucle | 2.50 |
| 449943 | AF104266 | Hs.24212 | Hs.24212:latrophilin | 2.50 |
| 425743 | BE396495 | Hs.159428 | Hs.159428:BCL2-associated X protein | 2.50 |
| 444681 | AJ243937 | Hs.288316 | Hs.288316:chromosome 6 open reading fram | 2.50 |
| 421643 | BE281170 | Hs.106357 | NM_007126:Homo sapiens valosin-containin | 2.50 |
| 426865 | D63476 | Hs.172813 | NM_003899:Homo sapiens Rho guanine nucle | 2.50 |
| 432306 | Y18207 | Hs.303090 | NM_005398:Homo sapiens protein phosphata | 2.49 |
| 421846 | AA017707 | Hs.1432 | NM_002743:Homo sapiens protein kase C su | 2.49 |
| 421905 | AJ660247 | Hs.32699 | Hs.32699:Homo sapiens, Similar to RIKEN | 2.49 |
| 419493 | AF001212 | Hs.90744 | NM_002815:Homo sapiens proteasome (proso | 2.49 |
| 422530 | AW972300 | Hs.118110 | NM_004335:Homo sapiens bone marrow strom | 2.48 |
| 442821 | BE391929 | Hs.8752 | NM_014255:Homo sapiens transmembrane pro | 2.48 |
| 416919 | T97839 | Hs.80464 | NM_006402:Homo sapiens hepatitis B virus | 2.48 |
| 443105 | X96753 | Hs.9004 | NM_001897:Homo sapiens chondroitin sulfat | 2.48 |
| 430040 | AW503115 | Hs.227823 | NM_014287:Homo sapiens pMS protein (PM5) | 2.48 |
| 428028 | U52112 | Hs.182018 | NM_001569:Homo sapiens interleukin-1 rec | 2.47 |
| 424307 | AW293399 | Hs.356377 | Hs.356377:Homo sapiens, clone IMAGE:3633 | 2.46 |
| 434511 | R28982 | Hs.18106 | Hs.18106:ESTs, Weakly similar to T06291 | 2.46 |
| 454390 | AB020713 | Hs.56966 | Hs.56966:KIAA0906 protein | 2.46 |
| 417785 | X59812 | Hs.82568 | NM_000784:Homo sapiens cytochrome P450, | 2.46 |
| 424573 | AA345051 | Hs.294092 | Hs.294092:Homo sapiens mR full length in | 2.46 |
| 422003 | AA361760 | Hs.296326 | Hs.296326:ESTs, Weakly similar to A33533 | 2.46 |
| 432126 | AA865239 | Hs.37196 | Hs.37196:putative G protein coupled rece | 2.46 |
| 445937 | AJ452943 | Hs.321231 | NM_003779:Homo sapiens UDP-GalbetaGlc | 2.46 |
| 409354 | N68188 | Hs.159472 | Hs.159472:Homo sapiens cD: FLJ22224 fis, | 2.46 |
| 401179 | | | | 2.46 |
| 418151 | AA864238 | Hs.83583 | NM_005731:Homo sapiens actin related pro | 2.45 |
| 422648 | D86983 | Hs.118893 | Hs.118893:Melanoma associated gene | 2.45 |
| 427759 | BE245578 | Hs.2200 | NM_005041:Homo sapiens perforin 1 (prelo | 2.45 |
| 431222 | X56777 | Hs.273790 | NM_007155:Homo sapiens zo pellucida glyc | 2.45 |
| 411529 | AA430348 | Hs.317596 | Hs.317596:Homo sapiens cD FLJ12927 fis, | 2.45 |
| 426825 | AL133415 | Hs.297753 | NM_003380:Homo sapiens vimentin (VIM), m | 2.45 |
| 422242 | AJ251760 | Hs.273385 | NM_016592:Homo sapiens GS complex locus | 2.45 |
| 408105 | AW152207 | Hs.270977 | Hs.270977:ESTs | 2.44 |
| 426410 | BE298446 | Hs.305890 | Hs.305890:BCL2-like 1 | 2.44 |
| 421064 | AJ245432 | Hs.101382 | NM_006291:Homo sapiens tumor necrosis fa | 2.44 |
| 428157 | AJ738719 | Hs.198427 | NM_000189:Homo sapiens hexokase 2 (HK2), | 2.44 |
| 424398 | BE397787 | Hs.146393 | NM_014685:Homo sapiens homocysteine-indu | 2.44 |
| 424825 | AF207069 | Hs.153357 | NM_001084:Homo sapiens procollagen-lysin | 2.44 |
| 426031 | AA295251 | Hs.166066 | Hs.166066:cisplatin resistance associate | 2.43 |
| 409817 | BE295464 | Hs.56607 | Hs.56607:Williams-Beuren syndrome chromo | 2.43 |
| 429359 | W00482 | Hs.2399 | NM_004995:Homo sapiens matrix metallopro | 2.43 |
| 426761 | AJ015709 | Hs.172089 | Hs.172089:pro-oncosis receptor inducing | 2.43 |
| 429332 | AF030403 | Hs.199263 | NM_013233:Homo sapiens serine threonine | 2.43 |
| 425923 | NM_005026 | Hs.162808 | NM_005026:Homo sapiens phosphoinositide- | 2.43 |
| 432211 | BE274530 | Hs.273333 | Hs.273333:hypothetical protein FLJ10986 | 2.43 |
| 433339 | AF019226 | Hs.8036 | Hs.8036:RAB3D, member RAS oncogene famil | 2.42 |
| 420539 | AA282735 | Hs.44004 | Hs.44004:AD031 protein | 2.42 |
| 413243 | AA769266 | Hs.193657 | Hs.193657:ESTs | 2.42 |
| 435029 | AF167706 | Hs.19280 | Hs.19280:cysteine-rich motor neuron 1 | 2.42 |
| 422374 | AW732869 | Hs.1519 | Hs.1519:protein kase, cAMP-dependent, re | 2.42 |
| 444501 | AW247624 | Hs.11342 | NM_004148:Homo sapiens ninjurin 1 (NINJ1 | 2.42 |
| 414919 | AW087337 | Hs.194461 | Hs.194461:ESTs | 2.42 |
| 419355 | AA428520 | Hs.90061 | NM_006667:Homo sapiens progesterone rece | 2.42 |
| 436042 | AF284422 | Hs.119178 | Hs.119178:cation-chloride cotransporter- | 2.42 |
| 418245 | AA088767 | Hs.83883 | Hs.83883:transmembrane, prostate androge | 2.42 |
| 444215 | AB033075 | Hs.10669 | Hs.10669:development and differentiation | 2.41 |
| 408683 | R58665 | Hs.46847 | NM_016614:Homo sapiens TRAF and TNF rece | 2.41 |
| 423701 | AA329856 | Hs.143022 | Hs.143022:ESTs | 2.41 |
| 441783 | BE313412 | Hs.7961 | Hs.7961:Homo sapiens clone 25012 mR sequ | 2.41 |
| 428072 | BE258602 | Hs.182366 | NM_016292:Homo sapiens heat shock protei | 2.41 |
| 434599 | AB002313 | Hs.3989 | Hs.3989:plexin B2 | 2.40 |
| 442351 | W52642 | Hs.8261 | Hs.8261:SPRY domain-containing SOCS box | 2.40 |
| 407894 | AJ278313 | Hs.41143 | Hs.41143:phospholipase C, beta 1 (phosph | 2.40 |
| 453449 | W16752 | Hs.32981 | Hs.32981:sema domain, immunoglobulin dom | 2.40 |
| 408688 | AJ634522 | Hs.152925 | Hs.152925:KIAA1268 protein | 2.40 |
| 422448 | AW372922 | Hs.116774 | Hs.116774:integrin, alpha 1 | 2.39 |
| 416269 | AA177138 | Hs.161671 | Hs.161671:ESTs | 2.39 |
| 452679 | Z42387 | Hs.83883 | Hs.83883:transmembrane, prostate androge | 2.38 |
| 432981 | NM_002733 | Hs.3136 | NM_002733:Homo sapiens protein kase, AMP | 2.38 |
| 419846 | NM_015977 | Hs.285681 | Hs.285681:Williams Beuren syndrome chrom | 2.38 |
| 422110 | AJ376736 | Hs.111779 | Hs.111779:secreted protein, acidic, cyst | 2.38 |
| 413092 | AA126856 | Hs.118665 | Hs.118665:ESTs | 2.38 |
| 433969 | AW207279 | Hs.271786 | Hs.271786:ESTs, Weakly similar to PC4395 | 2.37 |
| 451267 | AJ033894 | Hs.117865 | Hs.117865:solute carrier family 17 (anion | 2.37 |
| 447526 | AL048753 | Hs.303649 | NM_002982:Homo sapiens small inducible c | 2.37 |

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|----|--------|-----------|-----------|--|------|
| 5 | 441623 | AA315805 | Hs.348710 | Hs.348710:Homo sapiens, clone IMAGE:4242 | 2.37 |
| | 420255 | NM_007289 | Hs.1298 | NM_007289:Homo sapiens membrane metallo- | 2.37 |
| | 409274 | NM_003930 | Hs.52644 | NM_003930:Homo sapiens src family associ | 2.36 |
| | 422801 | AF125672 | Hs.287994 | Hs.287994:nuclear receptor co-repressor | 2.36 |
| | 407887 | AA579668 | Hs.41072 | Hs.41072:serine (or cysteine) protease i | 2.36 |
| | 408212 | AA297567 | Hs.43728 | NM_015696:Homo sapiens weakly similar to | 2.36 |
| | 430478 | NM_014349 | Hs.241535 | NM_014349:Homo sapiens apolipoprotein L, | 2.36 |
| | 405102 | | | | 2.35 |
| 10 | 423583 | AL122055 | Hs.129836 | Hs.129836:KIAA1028 protein | 2.35 |
| | 426125 | X87241 | Hs.166994 | NM_005245:Homo sapiens FAT tumor suppres | 2.35 |
| | 425204 | NM_002436 | Hs.1861 | NM_002436:Homo sapiens membrane protein, | 2.35 |
| | 420676 | AI434780 | Hs.4248 | Hs.4248:Homo sapiens PP3781 mR, complete | 2.35 |
| | 421079 | AW404994 | Hs.101695 | Hs.101695:NCK adaptor protein 2 | 2.35 |
| | 410039 | AF207989 | Hs.58014 | Hs.58014:G protein-coupled receptor, fam | 2.34 |
| 15 | 412958 | BE391579 | Hs.75087 | NM_006712:Homo sapiens FAST kise (FASTK) | 2.34 |
| | 430363 | M28713 | Hs.274464 | NM_000398:Homo sapiens diaphorase (DH) (| 2.34 |
| | 425397 | J04088 | Hs.156346 | NM_001067:Homo sapiens topoisomerase (D) | 2.34 |
| | 451035 | AU076785 | Hs.430 | NM_002670:Homo sapiens plastin 1 (I iso) | 2.34 |
| 20 | 449027 | AJ271216 | Hs.22880 | Hs.22880:dipeptidylpeptidase III | 2.34 |
| | 429457 | BE243065 | Hs.202955 | Hs.202955:hypothetical protein FLJ20507 | 2.34 |
| | 417709 | D87434 | Hs.82426 | NM_014734:Homo sapiens KIAA0247 gene pro | 2.34 |
| | 412805 | AW954569 | Hs.278675 | Hs.278675:bromodomain-containing 4 | 2.34 |
| | 427647 | W19744 | Hs.180059 | Hs.180059:Homo sapiens cD FLJ31360 fis, | 2.34 |
| 25 | 430702 | U56979 | Hs.278568 | NM_000186:Homo sapiens H factor 1 (compl | 2.33 |
| | 456804 | AJ421645 | Hs.139851 | NM_001233:Homo sapiens caveolin 2 (CAV2) | 2.33 |
| | 453648 | W21493 | Hs.28329 | Hs.28329:protein phosphatase 1, regulato | 2.33 |
| | 450812 | AB002360 | Hs.25515 | Hs.25515:MCF.2 cell line derived translo | 2.33 |
| | 402575 | | | | 2.33 |
| 30 | 424670 | W61215 | Hs.116651 | NM_005797:Homo sapiens epithelial V-like | 2.32 |
| | 452960 | AK001335 | Hs.31137 | NM_006504:Homo sapiens protein tyrosine | 2.32 |
| | 442968 | AK000606 | Hs.8868 | NM_004871:Homo sapiens golgi SP receptor | 2.32 |
| | 410639 | BE269047 | Hs.65234 | Hs.65234:DEAD/H (Asp-Glu-Ala-Asp/His) bo | 2.32 |
| | 415169 | W42913 | Hs.78089 | NM_004231:Homo sapiens ATPase, H+ transp | 2.32 |
| 35 | 450160 | BE048099 | Hs.183738 | Hs.183738:FERM, RhoGEF (ARHGEF) and plec | 2.32 |
| | 407223 | H96850 | | H96850:yo03b12.s1 Soares melanocyte 2NbH | 2.32 |
| | 426780 | BE242284 | Hs.172199 | NM_001114:Homo sapiens adenylate cyclase | 2.32 |
| | 434987 | AW975114 | Hs.371677 | Hs.371677:ESTs | 2.32 |
| | 416354 | NM_000633 | Hs.79241 | NM_000633:Homo sapiens B-cell CLL/lympho | 2.31 |
| 40 | 453107 | NM_016113 | Hs.279746 | NM_016113:Homo sapiens transient recepto | 2.31 |
| | 422963 | M79141 | Hs.13234 | Hs.13234:ESTs, Weakly similar to hypothe | 2.31 |
| | 433618 | AA602539 | Hs.345494 | Hs.345494:ESTs, Moderately similar to ZN | 2.31 |
| | 438584 | AA811347 | | AA811347:xb81h06.s1 NCI_CGAP_GCB1 Homo s | 2.31 |
| | 446126 | AW085909 | Hs.356618 | Hs.356618:ESTs, Weakly similar to PC4259 | 2.31 |
| 45 | 408716 | AI567839 | Hs.151714 | Hs.151714:peroxisomal proliferator-activ | 2.30 |
| | 433230 | AW136134 | Hs.220277 | Hs.220277:ESTs, Weakly similar to expres | 2.30 |
| | 410168 | AW834050 | Hs.351432 | Hs.351432:tensin | 2.30 |
| | 446342 | BE298665 | Hs.14846 | Hs.14846:Homo sapiens mR; cD DKFZp564D01 | 2.30 |
| | 418452 | BE379749 | Hs.85201 | NM_005127:Homo sapiens C-type (calcium d | 2.30 |
| 50 | 453175 | NM_006834 | Hs.32217 | NM_006834:Homo sapiens RAB32, member RAS | 2.29 |
| | 409012 | AL117435 | Hs.49725 | Hs.49725:DKFZP434I216 protein | 2.29 |
| | 452848 | AJ417193 | Hs.288912 | Hs.288912:BBP-like protein 2 | 2.29 |
| | 418838 | AW385224 | Hs.35198 | Hs.35198:ectonucleotide pyrophosphatase/ | 2.29 |
| 55 | 422562 | AI962060 | Hs.118397 | NM_001129:Homo sapiens AE binding protei | 2.28 |
| | 432828 | AB042326 | Hs.287402 | Hs.287402:chondroitin 4-sulfotransferase | 2.28 |
| | 412948 | BE243313 | Hs.334851 | NM_006148:Homo sapiens LIM and SH3 prote | 2.28 |
| | 426068 | AF029778 | Hs.166154 | NM_002226:Homo sapiens jagged 2 (JAG2), | 2.28 |
| | 456919 | NM_003900 | Hs.182248 | NM_003900:Homo sapiens sequestosome 1 (S | 2.28 |
| | 452806 | AW014549 | Hs.58373 | Hs.58373:ESTs | 2.28 |
| 60 | 453983 | H94997 | Hs.16450 | Hs.16450:ESTs | 2.28 |
| | 407736 | N41744 | Hs.349326 | Hs.349326:Homo sapiens cD FLJ30677 fis, | 2.28 |
| | 413211 | AW967107 | Hs.109274 | Hs.109274:hypothetical protein MGCA365 | 2.28 |
| | 422051 | AW327546 | Hs.111024 | Hs.111024:solute carrier family 25 (mito | 2.27 |
| | 438438 | AA257992 | Hs.50651 | Hs.50651:Janus Kise 1 (a protein tyrosin | 2.27 |
| 65 | 436278 | BE396290 | Hs.5097 | NM_004710:Homo sapiens syptogyrin 2 (SYN | 2.27 |
| | 454080 | AI199711 | Hs.576 | NM_000147:Homo sapiens fucosidase, alpha | 2.27 |
| | 426542 | AF190746 | Hs.170310 | NM_017424:Homo sapiens cat eye syndrome | 2.27 |
| | 417115 | AW952792 | Hs.334612 | NM_003094:Homo sapiens small nuclear rib | 2.27 |
| | 402901 | | | | 2.26 |
| 70 | 412898 | AI129903 | Hs.74669 | NM_006634:Homo sapiens vesicle-associate | 2.26 |
| | 413020 | R98736 | | R98736:yr31h09.r1 Soares fetal liver spl | 2.26 |
| | 413939 | AL047051 | Hs.199961 | Hs.199961:ESTs, Weakly similar to hypo | 2.26 |
| | 408681 | AW953853 | Hs.281462 | Hs.281462:hypothetical protein FLJ14251 | 2.25 |
| | 412330 | NM_005100 | Hs.788 | NM_005100:Homo sapiens A kise (PRKA) anc | 2.25 |
| 75 | 442083 | R50192 | Hs.165062 | Hs.165062:ESTs | 2.25 |
| | 418271 | NM_000919 | Hs.83920 | NM_000919:Homo sapiens peptidylglycine a | 2.25 |
| | 433376 | AI249361 | Hs.74122 | NM_001225:Homo sapiens caspase 4, apopto | 2.25 |
| | 438562 | AI566826 | Hs.25890 | Hs.25890:ESTs, Weakly similar to transdu | 2.25 |
| | 443883 | AA114212 | Hs.9930 | NM_001235:Homo sapiens serine (or cystei | 2.25 |
| 80 | 416976 | BE243985 | Hs.80680 | Hs.80680:major vault protein | 2.24 |
| | 416914 | AA344481 | Hs.80426 | Hs.80426:brain and reproductive organ-ex | 2.24 |
| | 400288 | X06256 | Hs.149609 | NM_002205:Homo sapiens integrin, alpha 5 | 2.24 |
| | 407904 | W44735 | Hs.107260 | Hs.107260:putative UDP-Galc:polypeptide | 2.24 |
| | 429690 | AW956329 | Hs.23721 | Hs.23721:ESTs | 2.24 |

| | | | | |
|--------|-----------|-----------|---|------|
| 443813 | AA876372 | Hs.93961 | Hs.93961:Homo sapiens mR; cD DKFZp667D09 | 2.24 |
| 427458 | BE208364 | Hs.29283 | Hs.29283:ESTs, Weakly similar to LKHU pr | 2.24 |
| 454294 | AB000734 | Hs.50640 | NM_003745:Homo sapiens JAK binding prote | 2.24 |
| 407192 | AA609200 | Hs.366318 | Hs.366318:ESTs | 2.23 |
| 425751 | T19239 | Hs.1940 | NM_001885:Homo sapiens crystallin, alpha | 2.23 |
| 456437 | AI924228 | Hs.115185 | Hs.115185:ESTs | 2.23 |
| 413019 | BE281604 | Hs.75140 | NM_002337:Homo sapiens low density lipop | 2.23 |
| 418852 | BE550964 | Hs.89399 | Hs.89399:ATP synthase, H+ transporting, | 2.23 |
| 435284 | AA879470 | Hs.96849 | Hs.96849:Homo sapiens cD FLJ11492 fis, c | 2.23 |
| 429630 | M85289 | Hs.211573 | NM_005529:Homo sapiens heparan sulfate p | 2.23 |
| 427609 | AK000436 | Hs.179791 | Hs.179791:RAB20, member RAS oncogene fam | 2.23 |
| 421917 | AB028943 | Hs.109445 | Hs.109445:hypermethylated in cancer 2 | 2.23 |
| 446616 | R65964 | Hs.334873 | Hs.334873:carboxypeptidase M | 2.23 |
| 407232 | X04526 | | X04526:Human liver mR for beta-subunit s | 2.23 |
| 423798 | AF047033 | Hs.132904 | Hs.132904:solute carrier family 4, sodiu | 2.23 |
| 446755 | AW451473 | Hs.16134 | NM_005990:Homo sapiens serine/threonine | 2.22 |
| 452865 | AI924046 | Hs.119567 | Hs.119567:ESTs, Weakly similar to ALU1_H | 2.22 |
| 431393 | AW971493 | Hs.134269 | Hs.134269:ESTs, Weakly similar to 200439 | 2.22 |
| 431890 | X17033 | Hs.271986 | NM_002203:Homo sapiens integrin, alpha 2 | 2.22 |
| 428782 | X12830 | Hs.193400 | NM_000665:Homo sapiens interleukin 6 rec | 2.22 |
| 446006 | NM_004403 | Hs.13530 | NM_004403:Homo sapiens deafness, autosom | 2.22 |
| 436418 | AJ245874 | Hs.4245 | Hs.4245:chromosome 11 hypothetical prote | 2.22 |
| 423869 | BE409301 | Hs.134012 | NM_006688:Homo sapiens C1q-related facto | 2.21 |
| 437730 | AW071087 | Hs.239176 | Hs.239176:insulin-like growth factor 1 r | 2.21 |
| 444020 | R92962 | Hs.35052 | Hs.35052:ESTs | 2.21 |
| 413882 | AA132973 | Hs.184492 | Hs.184492:Homo sapiens mR; cD DKFZp667B0 | 2.21 |
| 412654 | AI093480 | Hs.374319 | Hs.374319:ESTs | 2.21 |
| 448988 | Y09763 | Hs.22785 | NM_004961:Homo sapiens gamma-aminobutyri | 2.21 |
| 426841 | AI052358 | Hs.131741 | Hs.131741:ESTs | 2.21 |
| 408196 | AL034548 | Hs.43627 | NM_006943:Homo sapiens SRY (sex determin | 2.21 |
| 451711 | AK000461 | Hs.26890 | Hs.26890:cat eye syndrome chromosome reg | 2.20 |
| 414325 | AA251929 | Hs.355341 | Hs.355341:Homo sapiens, clone IMAGE:3536 | 2.20 |
| 424512 | X53002 | Hs.149846 | NM_002213:Homo sapiens integrin, beta 5 | 2.20 |
| 448883 | BE614989 | Hs.7503 | Hs.7503:hypothetical protein FLJ14153 | 2.20 |
| 411296 | BE207307 | Hs.10114 | Hs.10114:growth suppressor 1 | 2.20 |
| 452268 | NM_003512 | Hs.28777 | NM_003512:Homo sapiens H2A histone fami | 2.20 |
| 416810 | AF035606 | Hs.80019 | NM_013232:Homo sapiens programmed cell d | 2.20 |
| 441415 | H21497 | Hs.7471 | Hs.7471:BBP-like protein 1 | 2.20 |
| 444212 | AW503976 | Hs.10649 | NM_004848:Homo sapiens basement membrane | 2.19 |
| 428044 | AA093322 | Hs.301404 | NM_006743:Homo sapiens R binding motif p | 2.19 |
| 430017 | AA263172 | Hs.35 | NM_002832:Homo sapiens protein tyrosine | 2.19 |
| 424490 | AJ278016 | Hs.55565 | Hs.55565:ankyrin repeat domain 3 | 2.19 |
| 431193 | AW749505 | Hs.296770 | Hs.296770:KIAA1719 protein | 2.19 |
| 453686 | AL110326 | Hs.304679 | Hs.304679:ESTs, Weakly similar to Z195_H | 2.19 |
| 448262 | AW880830 | Hs.186273 | Hs.186273:ESTs | 2.19 |
| 416065 | BE267931 | Hs.78996 | NM_002592:Homo sapiens proliferating cel | 2.19 |
| 442045 | C05768 | Hs.8078 | Hs.8078:Homo sapiens clone FBD3 Cri-du-c | 2.19 |
| 423804 | AW403448 | Hs.1706 | NM_006084:Homo sapiens interferon-stimul | 2.19 |
| 428024 | Z29067 | Hs.2236 | Hs.2236:NIMA (never in mitosis gene a)-r | 2.19 |
| 424503 | NM_002205 | Hs.149609 | NM_002205:Homo sapiens integrin, alpha 5 | 2.19 |
| 437696 | Z83844 | Hs.5790 | Hs.5790:hypothetical protein dJ37E16.5 | 2.18 |
| 405204 | | | | 2.18 |
| 426158 | NM_001982 | Hs.199067 | NM_001982:Homo sapiens v-erb-b2 erythro | 2.18 |
| 417418 | NM_002468 | Hs.82116 | NM_002468:Homo sapiens myeloid different | 2.18 |
| 412773 | H15785 | Hs.74573 | NM_012268:Homo sapiens similar to vaccin | 2.18 |
| 409402 | AF208234 | Hs.695 | NM_000100:Homo sapiens cystatin B (stefi | 2.18 |
| 443791 | N64458 | Hs.143345 | Hs.143345:ESTs | 2.18 |
| 435049 | AL122067 | Hs.4746 | Hs.4746:hypothetical protein FLJ21324 | 2.18 |
| 418389 | AA830613 | Hs.293849 | Hs.293849:ESTs | 2.18 |
| 450712 | AI732130 | Hs.270496 | Hs.270496:ESTs, Weakly similar to ALUB_H | 2.18 |
| 422007 | AI739435 | Hs.39168 | Hs.39168:ESTs, Weakly similar to T17340 | 2.18 |
| 453676 | AW853745 | Hs.286035 | Hs.286035:hypothetical protein FLJ22686 | 2.18 |
| 415718 | F30631 | Hs.200237 | Hs.200237:ESTs | 2.18 |
| 452688 | AA721140 | Hs.49930 | Hs.49930:ESTs, Weakly similar to B34087 | 2.18 |
| 415988 | BE407713 | Hs.78943 | NM_000386:Homo sapiens bleomycin hydrola | 2.18 |
| 409453 | AI885516 | Hs.95612 | Hs.95612:ESTs | 2.17 |
| 417512 | X76534 | Hs.82226 | NM_002510:Homo sapiens glycoprotein (tra | 2.17 |
| 427202 | BE272922 | Hs.173936 | NM_000628:Homo sapiens interleukin 10 re | 2.17 |
| 440983 | M20681 | Hs.7594 | NM_006931:Homo sapiens solute carrier fa | 2.17 |
| 416084 | L16991 | Hs.79006 | NM_012145:Homo sapiens deoxythymidylate | 2.17 |
| 429642 | X68264 | Hs.211579 | NM_006500:Homo sapiens melanoma adhesion | 2.17 |
| 427213 | AW007211 | Hs.348389 | Hs.348389:hypothetical protein FLJ12876 | 2.17 |
| 437763 | AA469369 | Hs.5831 | NM_003254:Homo sapiens tissue inhibitor | 2.17 |
| 454000 | AA040620 | Hs.5672 | Hs.5672:golgi membrane protein SB140 | 2.17 |
| 424247 | X14008 | Hs.234734 | NM_000239:Homo sapiens lysozyme (rel amy | 2.16 |
| 403857 | | | | 2.16 |
| 406648 | AA563730 | Hs.277477 | Hs.277477:major histocompatibility compl | 2.16 |
| 400265 | | | | 2.16 |
| 442379 | NM_004613 | Hs.8265 | NM_004613:Homo sapiens transglutaminase 2 | 2.16 |
| 441892 | AB028981 | Hs.8021 | Hs.8021:KIAA1058 protein | 2.16 |
| 417446 | AL118671 | Hs.82163 | NM_000898:Homo sapiens monoamine oxidase | 2.16 |
| 418386 | AA361739 | Hs.84549 | NM_002494:Homo sapiens DH dehydrogense (u | 2.16 |
| 414053 | BE391635 | Hs.75725 | NM_003564:Homo sapiens transgelin 2 (TAG | 2.16 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 440906 | AW161556 | Hs.240170 | Hs.240170:hypothetical protein MGC2731 | 2.16 |
| | 447650 | AW160386 | Hs.163667 | Hs.163667:ESTs, Weakly similar to CA1H_H | 2.16 |
| | 408279 | AF216965 | Hs.44095 | Hs.44095:cyclin M3 | 2.16 |
| 5 | 426152 | BE299190 | Hs.167246 | Hs.167246:P450 (cytochrome) oxidoreducta | 2.16 |
| | 437952 | D63209 | Hs.5944 | NM_014585:Homo sapiens solute carrier fa | 2.16 |
| | 415651 | AF057307 | Hs.78575 | Hs.78575:prosaposin (variant Gaucher dis | 2.15 |
| | 425302 | U79115 | Hs.155566 | NM_003805:Homo sapiens CASP2 and RIPK1 d | 2.15 |
| | 425996 | W67330 | Hs.374451 | Hs.374451:ESTs | 2.15 |
| 10 | 413745 | AW247252 | Hs.75514 | NM_000270:Homo sapiens nucleoside phosph | 2.15 |
| | 422070 | AF149785 | Hs.111126 | Hs.111126:pituitary tumor-transforming 1 | 2.15 |
| | 448424 | AW009892 | Hs.31924 | Hs.31924:ESTs | 2.15 |
| | 430035 | NM_003463 | Hs.227777 | NM_003463:Homo sapiens protein tyrosine | 2.15 |
| | 438407 | AI457122 | Hs.129673 | Hs.129673:eukaryotic translation initial | 2.15 |
| | 435551 | AF212365 | Hs.5470 | Hs.5470:interleukin 17B receptor | 2.15 |
| 15 | 437741 | BE561610 | Hs.5809 | Hs.5809:putative transmembrane protein; | 2.15 |
| | 441192 | AA526626 | Hs.7736 | NM_016504:Homo sapiens mitochondrial rib | 2.15 |
| | 435750 | AB029012 | Hs.4990 | Hs.4990:KIAA1089 protein | 2.15 |
| | 411165 | NM_000169 | Hs.69089 | NM_000169:Homo sapiens galactosidase, al | 2.14 |
| 20 | 425252 | AW391162 | Hs.349306 | Hs.349306:hypothetical protein FLJ31951 | 2.14 |
| | 427600 | AW630918 | Hs.179774 | NM_002818:Homo sapiens proteasome (proso | 2.14 |
| | 426818 | AA554827 | Hs.292936 | Hs.292936:postmeiotic segregation increa | 2.14 |
| | 442110 | AF113008 | Hs.8102 | NM_001023:Homo sapiens ribosomal protein | 2.14 |
| | 407797 | AK000524 | Hs.39850 | Hs.39850:uridine kise-like 1 | 2.14 |
| 25 | 443044 | N28522 | Hs.8935 | NM_014298:Homo sapiens quindite phospho | 2.14 |
| | 437103 | AW139408 | Hs.152940 | Hs.152940:ESTs | 2.14 |
| | 442069 | AW664144 | Hs.297007 | Hs.297007:Homo sapiens cD FLJ32174 fis, | 2.14 |
| | 424954 | NM_000546 | Hs.1846 | NM_000546:Homo sapiens tumor protein p53 | 2.14 |
| | 458097 | AW341135 | Hs.58104 | Hs.58104:Homo sapiens, clone IMAGE:47309 | 2.14 |
| 30 | 411925 | AW014588 | Hs.72925 | NM_003475:Homo sapiens chromosome 11 ope | 2.14 |
| | 449644 | AW960707 | Hs.148324 | Hs.148324:ESTs | 2.14 |
| | 422675 | BE018517 | Hs.119140 | NM_001970:Homo sapiens eukaryotic transl | 2.14 |
| | 428586 | M36712 | Hs.2299 | Hs.2299:CD8 antigen, beta polypeptide 1 | 2.14 |
| | 429379 | NM_014840 | Hs.200598 | NM_014840:Homo sapiens KIAA0537 gene pro | 2.13 |
| 35 | 410290 | AA402307 | Hs.322844 | Hs.322844:hypothetical protein DKFZp564A | 2.13 |
| | 443895 | AW979048 | Hs.292566 | Hs.292566:YEA4 protein | 2.13 |
| | 428145 | BE243327 | Hs.182626 | NM_012264:Homo sapiens chromosome 22 ope | 2.13 |
| | 453518 | AW503205 | Hs.27268 | Hs.27268:Homo sapiens cD: FLJ21933 fis, | 2.13 |
| | 456534 | X91195 | Hs.100623 | Hs.100623:protein phosphatase 1, regulat | 2.13 |
| 40 | 419972 | AL041465 | Hs.182982 | Hs.182982:gdlin-67 | 2.13 |
| | 424950 | AA602917 | Hs.156974 | Hs.156974:ESTs | 2.13 |
| | 427557 | NM_002659 | Hs.179657 | NM_002659:Homo sapiens plasminogen activ | 2.13 |
| | 431449 | M55994 | Hs.256278 | NM_001066:Homo sapiens tumor necrosis fa | 2.13 |
| | 418758 | AW959311 | Hs.172012 | Hs.172012:hypothetical protein DKFZp434J | 2.13 |
| 45 | 434202 | BE382411 | Hs.3764 | NM_000858:Homo sapiens guanylate kise 1 | 2.13 |
| | 433233 | AB040927 | Hs.301804 | Hs.301804:KIAA1494 protein | 2.12 |
| | 452700 | AI859390 | Hs.288940 | Hs.288940:transmembrane protein B (five | 2.12 |
| | 438033 | T26483 | Hs.6059 | NM_016938:Homo sapiens EGF-containing fi | 2.12 |
| | 400847 | | | | 2.12 |
| 50 | 447547 | NM_007229 | Hs.18842 | NM_007229:Homo sapiens protein kise C an | 2.12 |
| | 417052 | NM_000712 | Hs.81029 | NM_000712:Homo sapiens biliverdin reduct | 2.12 |
| | 413284 | AU077055 | Hs.289107 | NM_001166:Homo sapiens baculoviral IAP r | 2.11 |
| | 434558 | AW264102 | Hs.39168 | Hs.39168:ESTs, Weakly similar to T17340 | 2.11 |
| | 404030 | | | | 2.11 |
| 55 | 410801 | BE275469 | Hs.66493 | Hs.66493:Down syndrome critical region g | 2.11 |
| | 418613 | AA744529 | Hs.86575 | Hs.86575:mitogen-activated protein kise | 2.11 |
| | 447087 | AW403870 | Hs.301872 | Hs.301872:hypothetical protein MGC4840 | 2.11 |
| | 433026 | AW160616 | Hs.279921 | NM_016127:Homo sapiens hypothetical prot | 2.11 |
| | 426433 | L38969 | Hs.169875 | NM_007112:Homo sapiens thrombospondin 3 | 2.11 |
| 60 | 442439 | UD9759 | Hs.246857 | NM_002752:Homo sapiens mitogen-activated | 2.11 |
| | 437379 | AL359575 | Hs.23765 | Hs.23765:membrane metallo-endorpeptidase- | 2.11 |
| | 400208 | | | | 2.11 |
| | 455705 | AW161061 | Hs.356580 | Hs.356580:ESTs, Weakly similar to zinc I | 2.11 |
| 65 | 417599 | AA204688 | Hs.62954 | Hs.62954:ferritin, heavy polypeptide 1 | 2.10 |
| | 416728 | AB024597 | Hs.79658 | NM_001894:Homo sapiens casein kise 1, ep | 2.10 |
| | 439920 | H05430 | Hs.288433 | Hs.288433:neurotrimin | 2.10 |
| | 422309 | U79745 | Hs.114924 | NM_004694:Homo sapiens solute carrier fa | 2.10 |
| | 436114 | AA778232 | Hs.19515 | Hs.19515:ESTs, Highly similar to NRG3_HU | 2.10 |
| | 405517 | | | | 2.10 |
| 70 | 421872 | AA369753 | Hs.22824 | Hs.22824:MYB binding protein (P160) 1a | 2.10 |
| | 437712 | X04588 | Hs.85844 | Hs.85844:neurotrophic tyrosine kise, rec | 2.10 |
| | 431214 | AA294921 | Hs.348024 | NM_002881:Homo sapiens v-ral simian leuk | 2.10 |
| | 412856 | BE386745 | Hs.74631 | NM_001728:Homo sapiens basigin (BSG), mR | 2.10 |
| | 442064 | AI422867 | Hs.88594 | Hs.88594:Homo sapiens, clone IMAGE:43329 | 2.10 |
| | 434845 | BE267057 | Hs.325321 | Hs.325321:WD repeat domain 18 | 2.10 |
| 75 | 426728 | NM_007118 | Hs.367689 | NM_007118:Homo sapiens triple functio d | 2.10 |
| | 419596 | BE379320 | Hs.91448 | NM_007026:Homo sapiens dual specificity | 2.09 |
| | 448913 | AA194422 | Hs.22564 | NM_004999:Homo sapiens myosin VI (MYO6), | 2.09 |
| | 414721 | X90392 | Hs.77091 | NM_006730:Homo sapiens deoxyribonuclease | 2.09 |
| 80 | 424658 | NM_002406 | Hs.151513 | NM_002406:Homo sapiens mannosyl (alpha-1 | 2.09 |
| | 432805 | X94630 | Hs.3107 | Hs.3107:CD97 antigen | 2.09 |
| | 447032 | AK000310 | Hs.17138 | Hs.17138:hypothetical protein FLJ20303 | 2.09 |
| | 447484 | AA464839 | Hs.292566 | Hs.292566:YEA4 protein | 2.09 |
| | 440188 | AK001812 | Hs.7036 | Hs.7036:N-acetylglucosamine kise | 2.09 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 445584 | AF217518 | Hs.8360 | Hs.8360:PTD012 protein | 2.09 |
| | 402559 | | | | 2.09 |
| 5 | 418043 | AW377752 | Hs.83341 | Hs.83341:AXL receptor tyrosine kise | 2.09 |
| | 448888 | AW196663 | Hs.200242 | Hs.200242:caspase recruitment domain fam | 2.09 |
| | 436910 | AA926944 | Hs.261587 | Hs.261587:GCN2 eIF2alpha kise | 2.09 |
| | 422573 | AW297985 | Hs.295726 | Hs.295726:integrin, alpha V (vitronectin | 2.08 |
| | 415448 | L13210 | Hs.79339 | NM_005567:Homo sapiens lectin, galactosi | 2.08 |
| | 428727 | AF078847 | Hs.191356 | NM_001515:Homo sapiens general transcrip | 2.08 |
| 10 | 410301 | AW502935 | Hs.740 | Hs.740:PTK2 protein tyrosine kise 2 | 2.08 |
| | 449538 | AI559444 | Hs.104679 | Hs.104679:Homo sapiens, clone MGC:18216 | 2.08 |
| | 421205 | AL137540 | Hs.102541 | Hs.102541:netrin 4 | 2.08 |
| | 411779 | AA292811 | Hs.72050 | NM_003551:Homo sapiens non-metastatic ce | 2.08 |
| | 427704 | AW971063 | Hs.292882 | Hs.292882:ESTs | 2.07 |
| 15 | 413518 | BE149455 | Hs.75415 | NM_004048:Homo sapiens beta-2-microglobu | 2.07 |
| | 447345 | BE247767 | Hs.18166 | Hs.18166:KIAA0870 protein | 2.07 |
| | 407143 | C14076 | Hs.332329 | Hs.332329:EST | 2.07 |
| | 448431 | BE613061 | Hs.337772 | Hs.337772:hypothetical protein BC009331 | 2.07 |
| | 412760 | AW379030 | Hs.41324 | Hs.41324:ESTs | 2.07 |
| 20 | 446859 | AI494299 | Hs.16297 | NM_005694:Homo sapiens COX17 homolog, cy | 2.07 |
| | 403966 | | | | 2.07 |
| | 409115 | AI223335 | Hs.50651 | NM_002227:Homo sapiens Janus kise 1 (a p | 2.07 |
| | 436823 | AW749865 | Hs.117077 | Hs.117077:zinc finger protein 264 | 2.07 |
| | 414045 | NM_002951 | Hs.75722 | NM_002951:Homo sapiens ribophorin II (RP | 2.06 |
| 25 | 413980 | NM_002437 | Hs.75659 | NM_002437:Homo sapiens Mpv17 transgene, | 2.06 |
| | 439414 | NM_001183 | Hs.6551 | NM_001183:Homo sapiens ATPase, H+ transp | 2.06 |
| | 426059 | BE292842 | Hs.166120 | NM_001572:Homo sapiens interferon regula | 2.06 |
| | 429849 | U33053 | Hs.2499 | NM_002741:Homo sapiens protein kise C-6 | 2.06 |
| | 402424 | | | | 2.06 |
| 30 | 406626 | X04526 | Hs.215595 | Hs.215595:guanine nucleotide binding pro | 2.06 |
| | 458911 | AA373131 | Hs.24322 | Hs.24322:ATPase, H+ transporting, lysoso | 2.05 |
| | 426086 | T94907 | Hs.188572 | Hs.188572:ESTs | 2.05 |
| | 419726 | U50330 | Hs.1274 | NM_006129:Homo sapiens bone morphogeneti | 2.05 |
| | 452344 | AI264357 | Hs.55405 | Hs.55405:hypothetical protein MGC16212 | 2.05 |
| 35 | 442498 | U54617 | Hs.8364 | NM_002612:Homo sapiens pyruvate dehydrog | 2.05 |
| | 422114 | AW194851 | Hs.111801 | NM_015908:Homo sapiens arsene resistance | 2.05 |
| | 413420 | AW410235 | Hs.75348 | NM_006263:Homo sapiens proteasome (proso | 2.05 |
| | 409430 | R21945 | Hs.346735 | Hs.346735:Homo sapiens, clone IMAGE:3881 | 2.05 |
| | 409932 | AI376750 | Hs.57600 | Hs.57600:adaptor-related protein complex | 2.05 |
| 40 | 434848 | BE256304 | Hs.32148 | Hs.32148:AD-015 protein | 2.04 |
| | 453852 | AW961818 | Hs.374424 | Hs.374424:ESTs | 2.04 |
| | 427637 | AK000816 | Hs.179986 | NM_005803:Homo sapiens flotillin 1 (FLOT | 2.04 |
| | 400264 | | | | 2.04 |
| | 430016 | NM_004736 | Hs.227656 | NM_004736:Homo sapiens xenotropic and po | 2.04 |
| 45 | 410134 | U68140 | Hs.58927 | Hs.58927:nuclear VCP-like | 2.04 |
| | 440975 | AW499914 | Hs.7579 | Hs.7579:importin 9 | 2.04 |
| | 432280 | BE440142 | Hs.2943 | NM_003135:Homo sapiens sigl recognition | 2.04 |
| | 409504 | AA304961 | Hs.699 | NM_000942:Homo sapiens peptidylprolyl is | 2.04 |
| | 412146 | M92444 | Hs.73722 | NM_001641:Homo sapiens APEX nuclease (mu | 2.04 |
| 50 | 434203 | BE262677 | Hs.283558 | Hs.283558:hypothetical protein PRO1855 | 2.04 |
| | 422754 | AA316476 | Hs.171811 | Hs.171811:adenylate kise 2 | 2.04 |
| | 406729 | AA069711 | | AA069711:zm52b11.s1 Stratagene fibroblas | 2.04 |
| | 413086 | AA126841 | Hs.183834 | Hs.183834:ESTs | 2.03 |
| | 424340 | AA339036 | Hs.7033 | Hs.7033:ESTs | 2.03 |
| 55 | 450440 | AB024334 | Hs.25001 | NM_012479:Homo sapiens tyrosine 3-monoox | 2.03 |
| | 424682 | NM_002870 | Hs.151536 | NM_002870:Homo sapiens RAB13, member RAS | 2.03 |
| | 415740 | N80486 | Hs.39911 | Hs.39911:Homo sapiens mR for FLJ00089 pr | 2.03 |
| | 412749 | AA378417 | Hs.74564 | NM_003145:Homo sapiens sigl sequence rec | 2.03 |
| | 408393 | AW015318 | Hs.23165 | Hs.23165:ESTs | 2.03 |
| 60 | 421295 | AW081061 | Hs.103180 | Hs.103180:DC2 protein | 2.03 |
| | 445417 | AK001058 | Hs.12680 | Hs.12680:Homo sapiens cD FLJ10196 fis, c | 2.03 |
| | 414883 | AA926960 | Hs.348669 | NM_001826:Homo sapiens CDC28 protein kis | 2.03 |
| | 447298 | BE617527 | Hs.239818 | Hs.239818:phosphoinositide-3-kise, catal | 2.02 |
| | 459580 | AA022888 | Hs.176065 | Hs.176065:ESTs | 2.02 |
| 65 | 422785 | AI824114 | Hs.289088 | Hs.289088:heat shock 90kD protein 1, alp | 2.02 |
| | 452696 | AI826645 | Hs.211534 | Hs.211534:Homo sapiens cD FLJ31665 fis, | 2.02 |
| | 452056 | AW955065 | Hs.101150 | Hs.101150:KIAA1949 protein | 2.02 |
| | 450690 | AA296696 | Hs.333418 | NM_014164:Homo sapiens FXYD domain-conta | 2.02 |
| | 423527 | AI206965 | Hs.105861 | Hs.105861:engulfment and cell motility 3 | 2.01 |
| 70 | 429545 | AI824164 | Hs.356130 | Hs.356130:ESTs | 2.01 |
| | 439180 | AI393742 | Hs.199067 | Hs.199067:v-erb-b2 erythroblastic leukem | 2.01 |
| | 437193 | BE259190 | Hs.289721 | Hs.289721:growth arrest-specific 5 | 2.01 |
| | 436014 | AF281134 | Hs.283741 | Hs.283741:exosome component Rrp46 | 2.01 |
| | 453329 | T97205 | Hs.193400 | Hs.193400:interleukin 1 receptor | 2.01 |
| 75 | 407347 | AA829847 | | TZ3514:seq3329 1-NIB Homo sapiens cD clo | 2.01 |
| | 435370 | AI964074 | Hs.225838 | Hs.225838:ESTs | 2.01 |
| | 430657 | AA482910 | Hs.370602 | Hs.370602:ESTs. Weakly similar to hypoth | 2.01 |
| | 427157 | U51166 | Hs.173824 | NM_003211:Homo sapiens thymine-D glycosy | 2.01 |
| | 424833 | NM_003894 | Hs.153405 | NM_003894:Homo sapiens period homolog 2 | 2.01 |
| 80 | 440086 | NM_005402 | Hs.6906 | NM_005402:Homo sapiens v-ral simian leuk | 2.01 |
| | 438543 | AA810141 | Hs.192182 | Hs.192182:ESTs | 2.01 |
| | 417426 | NM_002291 | Hs.82124 | NM_002291:Homo sapiens laminin, beta 1 (| 2.01 |
| | 412790 | NM_014767 | Hs.74583 | NM_014767:Homo sapiens KIAA0275 gene pro | 2.01 |
| | 445892 | AV655500 | Hs.93961 | Hs.93961:Homo sapiens mR, cD DKFZp667D09 | 2.01 |

TABLE 38B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

| Pkey | CAT Number | Accession |
|--------|------------|--|
| 409745 | MH1944_5 | B1030997 AA921874 AW188822 B1027862 AJ347618 AJ361453 AJ088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 B1007625 B1027864 B1009100 B1006275 B1006270 B1031000 B1029864 B1006277 B1007627 B1006266 B1006991 B1006990 B1007763 B1007762 BG997377 AA150780 B1033518 B1027818 BG015789 B1033807 AA341445 N64410 AA248866 AA248779 W02010 AL390180 AA359908 BE177778 BE177779 AW893733 BF756318 AA229762 AA230035 AA677593 AA618150 AA557952 BG171436 BE079601 BE079534 AA299964 BE392717 BE883402 BE079532 BE018148 BF889427 W00396 B1030997 AA921874 AW188822 B1027862 AJ347618 AJ361453 AJ088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 B1007625 B1027864 B1009100 B1006275 B1006270 B1031000 B1029864 B1006277 B1007627 B1006266 B1006991 B1006990 B1007763 B1007762 BG997377 AA150780 B1033518 B1027818 BG015789 B1033807 AA341445 AW173494 AJ804346 AA669490 AW837178 T77002 F13038 T63141 AJ821021 BF370092 BF370127 BF370060 T62998 BC006097 X03066 NM_002120 M26040 AW469119 AW469127 AJ299772 AW518149 AJ144456 AW628070 AJ629032 AJ358810 AJ880433 AJ1440472 AJ357070 AJ865365 AW014799 AJ767973 AW518041 AA909398 AW768606 AF086037 H89360 H89546 AW936378 AW936544 AW813513 AW934714 AW749864 AW749902 BE162498 BE161005 BE162499 BE161006 AA190449 AW513465 BE162500 BE161007 AW974073 T56957 |

TABLE 38C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

| Pkey | Ref | Strand | NL_position |
|--------|---------|--------|-------------------------------------|
| 403346 | 8569726 | Plus | 92752-93015 |
| 401621 | 8570184 | Minus | 193-608 |
| 403344 | 8569726 | Plus | 70823-70990 |
| 404240 | 5002624 | Minus | 116132-116407,116653-116922 |
| 401964 | 3126781 | Minus | 13510-13725,13847-14015 |
| 404277 | 1834458 | Minus | 91665-91946 |
| 405121 | 8102330 | Minus | 35816-36004,36587-36684 |
| 402493 | 9797670 | Minus | 205146-205240,205428-205542 |
| 402121 | 9188523 | Plus | 25692-25895 |
| 402474 | 7547175 | Minus | 53526-53628,55755-55920,57530-57757 |
| 403887 | 7710553 | Minus | 69533-69868 |
| 403328 | 8469086 | Minus | 120428-120703 |
| 401241 | 4827300 | Minus | 30503-30844,31056-31248 |
| 401736 | 3219338 | Plus | 1771-1894 |
| 405029 | 7533975 | Minus | 37929-38224 |
| 404171 | 9930793 | Plus | 173667-173783,176876-177055 |
| 401797 | 6730720 | Plus | 6973-7118 |
| 401234 | 9929642 | Plus | 120173-120337 |
| 404170 | 9930793 | Plus | 168836-169248 |
| 406122 | 9144087 | Minus | 30940-31386 |

TABLE 39A: 856 GENES UP-REGULATED IN RENAL CANCER COMPARED TO NORMAL ADULT TISSUES AND TO NON-MALIGNANT RENAL TISSUES THAT ARE LIKELY TO ENCODE PROTEINS AMENABLE TO MODULATION BY SMALL MOLECULES, PEPTIDES, OR ANTIBODIES

Table 39A lists about 856 genes up-regulated in renal cancer compared to normal adult tissues and to non-malignant renal tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These were selected from the starting collection of 59680 probesets on the Affymetrix/Eos-Hu03 GeneChip® array as follows: the ratio of "average" renal cancer to "average" normal adult tissues was greater than or equal to 2.0, the ratio of "average" renal cancer to "average" non-malignant renal tissues was greater than or equal to 2.0, the "average" renal cancer level was set to the 90th percentile value amongst various renal specimens, the "average" normal adult tissue level was set to the 70th percentile value amongst various non-malignant tissues, the "average" non-malignant renal tissues level was set to the 50th percentile value amongst various non-malignant renal tissues, the "average" renal cancer value was greater than or equal to 50 units, and the predicted protein contained a structural domain that is indicative of having an oncogenic function or of transducing an intracellular signal, or of being modifiable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion_transporter).

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal adult tissues

| Pkey | ExAccn | UnigenelD | Unigene Title | R1 |
|--------|----------|-----------|--|-------|
| 435013 | H91923 | Hs.110024 | | 15.71 |
| 447768 | X86400 | Hs.19520 | Hs.19520:FXFD domain-containing ion tran | 14.07 |
| 445178 | AJ792241 | Hs.129614 | Hs.129614:kidney-specific membrane prote | 12.56 |
| 432542 | AW083920 | Hs.16098 | Hs.16098:claudin 2 | 12.41 |
| 443595 | AF169312 | Hs.9613 | NM_016109:Homo sapiens angiopoietin-like | 11.77 |
| 413719 | BE439580 | Hs.75498 | NM_004591:Homo sapiens small inducible c | 10.39 |
| 435878 | BE465204 | Hs.47448 | Hs.47448:ESTs | 10.18 |
| 440304 | BE159984 | Hs.125395 | Hs.125395:ESTs | 9.95 |
| 407065 | Y10141 | | | 9.58 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| 5 | 413049 | NM_002151 | Hs.823 | NM_002151:Homo sapiens hepsin (transmembr | 9.51 |
| | 425983 | AK000226 | Hs.165619 | Hs.165619:mucin and cadherin-like | 8.88 |
| | 423161 | AL049227 | Hs.124776 | Hs.124776:Homo sapiens mR; cD DKFZp564N1 | 8.77 |
| | 430569 | AF241254 | Hs.178098 | Hs.178098:angiotensin I converting enzyme | 8.45 |
| | 415768 | AA363733 | Hs.1032 | NM_002909:Homo sapiens regenerating isle | 7.94 |
| | 422357 | AF016272 | Hs.115418 | NM_004062:Homo sapiens cadherin 16, KSP- | 7.78 |
| | 420737 | L08096 | Hs.99899 | NM_001252:Homo sapiens tumor necrosis fa | 7.78 |
| | 409745 | AA077391 | | AA077391:7B14E12 Chromosome 7 Fetal Brai | 7.74 |
| 10 | 413936 | AF113676 | Hs.297681 | NM_000295:Homo sapiens serine (or cystei | 7.32 |
| | 426682 | AV660038 | Hs.2056 | Hs.2056:UDP glycosyltransferase 1 family | 7.20 |
| | 406851 | AA609784 | Hs.352392 | Hs.352392:major histocompatibility compl | 7.03 |
| | 419508 | AW997938 | Hs.90786 | Hs.90786:ATP-binding cassette, sub-famil | 6.57 |
| | 428953 | AA306610 | Hs.348183 | NM_003823:Homo sapiens tumor necrosis fa | 6.36 |
| 15 | 436895 | AF037335 | Hs.5338 | NM_001218:Homo sapiens carbonic anhydras | 6.31 |
| | 431842 | NM_005764 | Hs.271473 | NM_005764:Homo sapiens epithelial protei | 6.20 |
| | 430014 | H59354 | Hs.374303 | Hs.374303:hypothetical protein MGC20576 | 6.20 |
| | 423803 | NM_005709 | Hs.132945 | NM_005709:Homo sapiens PDZ-73 protein (P | 6.19 |
| | 434779 | AF153815 | Hs.50151 | Hs.50151:potassium inwardly-rectifying c | 6.11 |
| 20 | 435767 | H73505 | Hs.117874 | Hs.117874:ESTs | 6.08 |
| | 422664 | AA315933 | Hs.120879 | Hs.120879:Homo sapiens, clone MGC:32871 | 6.02 |
| | 425280 | U31519 | Hs.1872 | Hs.1872:phosphoenolpyruvate carboxylase | 5.81 |
| | 426559 | AB001914 | Hs.170414 | NM_002570:Homo sapiens paired basic amin | 5.73 |
| 25 | 451564 | AU076698 | Hs.132760 | NM_001467:Homo sapiens glucose-6-phospha | 5.69 |
| | 418526 | BE019020 | Hs.85838 | NM_004207:Homo sapiens solute carrier fa | 5.68 |
| | 444151 | AW972917 | Hs.128749 | Hs.128749:alpha-methylacyl-CoA racemase | 5.66 |
| | 426471 | M22440 | Hs.170009 | NM_003236:Homo sapiens transforming grow | 5.48 |
| | 432579 | AF043244 | Hs.278439 | NM_003946:Homo sapiens nucleolar protein | 5.45 |
| 30 | 448733 | NM_005629 | Hs.187958 | NM_005629:Homo sapiens solute carrier fa | 5.42 |
| | 446650 | AB016625 | Hs.15813 | NM_003060:Homo sapiens solute carrier fa | 5.36 |
| | 417089 | H52280 | Hs.18612 | Hs.18612:Homo sapiens cD: FLJ21909 fis, | 5.35 |
| | 437848 | A1906419 | Hs.284380 | Hs.284380:gamma-glutamyltransferase 1 | 5.32 |
| | 423081 | AF262992 | Hs.123159 | Hs.123159:sperm associated antigen 4 | 5.30 |
| | 421893 | NM_001078 | Hs.109225 | NM_001078:Homo sapiens vascular cell adh | 5.23 |
| 35 | 435886 | BE265839 | Hs.12126 | Hs.12126:hepatocellular carcinoma-associ | 5.20 |
| | 410276 | A1554545 | Hs.359201 | Hs.359201:ESTs | 5.20 |
| | 429451 | BE409861 | Hs.202833 | NM_002133:Homo sapiens heme oxygensa (dec | 5.14 |
| | 446404 | AA019961 | Hs.26216 | Hs.26216:Homo sapiens cD: FLJ22811 fis, | 5.13 |
| 40 | 423445 | NM_014324 | Hs.128749 | NM_014324:Homo sapiens alpha-methylacyl- | 5.09 |
| | 449444 | AWB18436 | Hs.351306 | NM_004696:Homo sapiens solute carrier fa | 5.05 |
| | 438106 | BE245551 | Hs.6079 | NM_014863:Homo sapiens B cell RAG associ | 5.02 |
| | 400419 | AF084545 | | AF084545:Homo sapiens versican Vint isoform | 5.01 |
| | 453920 | A1133148 | Hs.36602 | NM_000204:Homo sapiens I factor (complemen | 4.99 |
| 45 | 447881 | BE620886 | Hs.355279 | Hs.355279:Homo sapiens cD FLJ23711 fis, | 4.97 |
| | 422253 | W81526 | Hs.113882 | NM_000815:Homo sapiens gamma-aminobutyri | 4.93 |
| | 439024 | R96696 | Hs.35598 | Hs.35598:ESTs | 4.88 |
| | 414799 | A1752416 | Hs.77326 | NM_000598:Homo sapiens insulin-like grow | 4.80 |
| | 426530 | U24578 | Hs.278625 | NM_000592:Homo sapiens complement compon | 4.77 |
| | 410055 | AJ250839 | Hs.58241 | Hs.58241:gene for serine/threonine prote | 4.72 |
| 50 | 404240 | | | | 4.71 |
| | 414617 | A1339520 | Hs.288817 | Hs.288817:hypothetical protein FLJ22761 | 4.68 |
| | 448249 | AW855331 | Hs.337124 | Hs.337124:ESTs | 4.67 |
| | 447818 | W79940 | Hs.21906 | Hs.21906:Homo sapiens clone 24670 mR seq | 4.66 |
| 55 | 449057 | AB037784 | Hs.22941 | Hs.22941:KIAA1363 protein | 4.66 |
| | 422424 | A1185431 | Hs.296638 | NM_004864:Homo sapiens prostate differen | 4.62 |
| | 417336 | R70429 | Hs.81988 | NM_001343:Homo sapiens disabled homolog | 4.62 |
| | 425873 | NM_013390 | Hs.160417 | NM_013390:Homo sapiens transmembrane pro | 4.58 |
| | 444700 | NM_003645 | Hs.11729 | NM_003645:Homo sapiens fatty-acid-Coenzy | 4.58 |
| 60 | 414998 | NM_002543 | Hs.77729 | NM_002543:Homo sapiens oxidised low dens | 4.56 |
| | 414763 | U97276 | Hs.77266 | NM_002826:Homo sapiens quiescin Q6 (OSCN | 4.48 |
| | 443358 | H65417 | Hs.17757 | Hs.17757:pleckstrin homology domain-cont | 4.45 |
| | 440091 | A1767388 | Hs.37890 | Hs.37890:Homo sapiens, clone IMAGE:48275 | 4.43 |
| | 447131 | NM_004585 | Hs.17466 | NM_004585:Homo sapiens retinoic acid rec | 4.43 |
| 65 | 406973 | M34996 | Hs.198253 | Hs.198253:major histocompatibility compl | 4.42 |
| | 427740 | BE242604 | Hs.180616 | NM_005505:Homo sapiens CD36 antigen (col | 4.40 |
| | 435258 | AW867491 | Hs.107125 | Hs.107125:plasmalemma vesicle associated | 4.38 |
| | 452884 | C05964 | Hs.31841 | Hs.31841:ESTs | 4.37 |
| | 444006 | BE395085 | Hs.10086 | NM_016639:Homo sapiens type I transmembr | 4.36 |
| | 422627 | BE336857 | Hs.118787 | NM_000358:Homo sapiens transforming grow | 4.35 |
| 70 | 418054 | NM_002318 | Hs.83354 | NM_002318:Homo sapiens lysyl oxidase-lik | 4.34 |
| | 419011 | H56244 | Hs.89552 | NM_000846:Homo sapiens glutathione S-tra | 4.34 |
| | 404277 | | | | 4.33 |
| | 435563 | AF210317 | Hs.95497 | Hs.95497:solute carrier family 2 (facili | 4.30 |
| 75 | 431779 | AW971178 | Hs.268571 | NM_001645:Homo sapiens apolipoprotein C- | 4.29 |
| | 406645 | M57466 | Hs.814 | Hs.814:major histocompatibility complex, | 4.28 |
| | 421485 | AA243499 | Hs.104800 | Hs.104800:hypothetical protein FLJ10134 | 4.26 |
| | 426812 | AF105365 | Hs.172613 | NM_006598:Homo sapiens solute carrier fa | 4.25 |
| | 407910 | AA650274 | Hs.41296 | NM_013281:Homo sapiens fibronectin leuci | 4.22 |
| 80 | 438030 | X98427 | Hs.122634 | Hs.122634:ESTs | 4.22 |
| | 430661 | AC005551 | Hs.130714 | Hs.130714:ESTs, Moderately similar to AF | 4.21 |
| | 444381 | BE387335 | Hs.283713 | Hs.283713:hypothetical protein BC014245 | 4.20 |
| | 438203 | BE540090 | Hs.7345 | Hs.7345:MAD1 mitotic arrest deficient-I | 4.16 |
| | 411358 | R47479 | Hs.94761 | Hs.94761:KIAA1691 protein | 4.15 |
| | 418323 | NM_002118 | Hs.1162 | NM_002118:Homo sapiens major histocompat | 4.12 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| 5 | 449853 | AF006823 | Hs.24040 | NM_002246:Homo sapiens potassium channel | 4.11 |
| | 415198 | AW009480 | Hs.943 | NM_004221:Homo sapiens tural killer cell | 4.11 |
| | 418751 | BE389014 | Hs.372548 | Hs.372548:phosphoinositide-3-kinase, regul | 4.09 |
| | 414166 | AW888941 | Hs.75789 | NM_006096:Homo sapiens N-myc downstream | 4.07 |
| | 424125 | M31669 | Hs.1735 | Hs.1735:inhibin, beta B (activin AB beta | 4.00 |
| | 416926 | H03109 | Hs.263395 | Hs.263395:sema domain, transmembrane dom | 3.92 |
| | 419175 | AW270037 | Hs.362996 | Hs.362996:KIAA0779 protein | 3.92 |
| | 424218 | AF031824 | Hs.143212 | NM_003650:Homo sapiens cystatin F (leuko | 3.91 |
| 10 | 412870 | M22788 | Hs.82407 | Hs.82407:chemokine (C-X-C motif) ligand | 3.88 |
| | 452203 | X57522 | Hs.352018 | NM_000593:Homo sapiens transporter 1, AT | 3.87 |
| | 446872 | X97058 | Hs.16362 | NM_004154:Homo sapiens pyrimidinergic re | 3.87 |
| | 449961 | AW265634 | Hs.133100 | Hs.133100:ESTs | 3.87 |
| | 424517 | AI539443 | Hs.137447 | Hs.137447:Homo sapiens cD FLJ12169 fis, | 3.86 |
| 15 | 425262 | D87119 | Hs.155418 | Hs.155418:GSJ955 protein | 3.83 |
| | 443639 | BE269042 | Hs.9661 | NM_002801:Homo sapiens proteasome (proso | 3.82 |
| | 448133 | AA723157 | Hs.73769 | NM_000802:Homo sapiens folate receptor 1 | 3.81 |
| | 418030 | BE207573 | Hs.83321 | Hs.83321:neuromedin B | 3.81 |
| | 412939 | AW411491 | Hs.75069 | NM_005412:Homo sapiens serine hydroxymet | 3.80 |
| | 409162 | M25530 | Hs.50868 | NM_002555:Homo sapiens solute carrier fa | 3.79 |
| 20 | 427715 | BE245274 | Hs.180428 | Hs.180428:KIAA1181 protein | 3.78 |
| | 412006 | AW451618 | Hs.290216 | Hs.290216:ESTs | 3.77 |
| | 430413 | AW842182 | Hs.241392 | NM_002985:Homo sapiens small inducible c | 3.76 |
| | 422282 | AF019225 | Hs.114309 | Hs.114309:apolipoprotein L, 1 | 3.76 |
| | 420747 | BE294407 | Hs.99910 | Hs.99910:phosphofructokinase, platelet | 3.76 |
| 25 | 414875 | H42679 | Hs.77522 | NM_006120:Homo sapiens major histocompat | 3.75 |
| | 418793 | AW382987 | Hs.88474 | Hs.88474:prostaglandin-endoperoxide synt | 3.74 |
| | 446291 | BE397753 | Hs.14623 | NM_006332:Homo sapiens interferon, gamma | 3.71 |
| | 417289 | D86962 | Hs.81875 | Hs.81875:growth factor receptor-bound pr | 3.69 |
| 30 | 422672 | X12784 | Hs.119129 | NM_001845:Homo sapiens collagen, type IV | 3.68 |
| | 448569 | BE382657 | Hs.21486 | NM_007315:Homo sapiens sigl transducer a | 3.68 |
| | 437270 | R18087 | Hs.323769 | Hs.323769:cisplatin resistance related p | 3.67 |
| | 408452 | AA054683 | Hs.192455 | Hs.192455:ESTs, Moderately similar to hy | 3.67 |
| | 443986 | AI381750 | Hs.283437 | Hs.283437:HTGN29 protein | 3.66 |
| 35 | 418869 | AW516565 | | AW516565:xq01d05.x1 Soares_NHCeC_cervica | 3.65 |
| | 425998 | AU076629 | Hs.165950 | NM_002011:Homo sapiens fibroblast growth | 3.62 |
| | 428699 | AW578252 | Hs.190161 | NM_014020:Homo sapiens LR8 protein (LR8) | 3.62 |
| | 418299 | AA279530 | Hs.83968 | NM_000211:Homo sapiens integrin, beta 2 | 3.61 |
| | 432593 | AW301003 | Hs.51483 | Hs.51483:Homo sapiens, Similar to RIKEN | 3.59 |
| 40 | 415765 | NM_005424 | Hs.78824 | NM_005424:Homo sapiens tyrosine kinase wil | 3.58 |
| | 445985 | BE621800 | Hs.29444 | Hs.29444:putative small membrane protein | 3.57 |
| | 424893 | AW295112 | Hs.153648 | Hs.153648:protein tyrosine phosphatase, | 3.57 |
| | 426046 | AA833655 | Hs.208688 | Hs.208688:Homo sapiens cD FLJ14056 fis, | 3.57 |
| | 424415 | NM_001975 | Hs.146580 | NM_001975:Homo sapiens enolase 2, (gamma | 3.57 |
| 45 | 412612 | NM_000047 | Hs.74131 | NM_000047:Homo sapiens arylsulfatase E (| 3.56 |
| | 443834 | AI741510 | Hs.173548 | Hs.173548:ESTs | 3.54 |
| | 431630 | NM_002204 | Hs.265829 | NM_002204:Homo sapiens integrin, alpha 3 | 3.53 |
| | 418371 | M13560 | Hs.84298 | Hs.84298:CD74 antigen (invariant polypep | 3.52 |
| | 444838 | AV651680 | Hs.208558 | Hs.208558:ESTs | 3.52 |
| 50 | 449378 | AW664026 | Hs.59892 | Hs.59892:ESTs, Weakly similar to alpha 5 | 3.52 |
| | 411393 | AW797437 | Hs.69771 | NM_001710:Homo sapiens B-factor, properd | 3.50 |
| | 414311 | AI693547 | Hs.71746 | Hs.71746:aminopeptidase-like 1 | 3.50 |
| | 415149 | X12451 | Hs.78056 | NM_001912:Homo sapiens cathepsin L (CTSL | 3.50 |
| | 424321 | W74048 | Hs.1765 | Hs.1765:lymphocyte-specific protein tyro | 3.49 |
| 55 | 414825 | X06370 | Hs.77432 | NM_005228:Homo sapiens epidermal growth | 3.48 |
| | 408194 | AA601038 | Hs.191797 | Hs.191797:ESTs | 3.48 |
| | 410600 | AW575742 | Hs.351676 | Hs.351676:ESTs, Weakly similar to T02670 | 3.47 |
| | 416899 | BE262645 | Hs.80420 | NM_002996:Homo sapiens small inducible c | 3.47 |
| | 436856 | AI469355 | Hs.127310 | Hs.127310:hypothetical protein BC014917 | 3.47 |
| 60 | 419660 | BE280337 | Hs.194693 | NM_003982:Homo sapiens solute carrier fa | 3.47 |
| | 413566 | AW604451 | Hs.285814 | Hs.285814:growth factor receptor-bound p | 3.47 |
| | 412104 | AW205197 | Hs.240951 | Hs.240951:ked cuticle homolog 2 (Drosoph | 3.46 |
| | 444488 | AW192879 | Hs.355660 | Hs.355660:peptide-histidine transporter | 3.46 |
| | 449475 | AI348027 | Hs.108557 | Hs.108557:hypothetical protein PP1057 | 3.46 |
| 65 | 412276 | BE262621 | Hs.73798 | NM_002415:Homo sapiens macrophage migrat | 3.45 |
| | 449338 | H73444 | Hs.394 | NM_001124:Homo sapiens adrenomedullin (A | 3.44 |
| | 430304 | AL122071 | Hs.238927 | Hs.238927:Homo sapiens mR: cD DKFZp434H1 | 3.43 |
| | 415388 | AF018081 | Hs.78409 | (locuslink)NM_030582:Homo sapiens collag | 3.43 |
| | 432210 | AI567421 | Hs.273330 | Hs.273330:agrin | 3.43 |
| 70 | 418177 | N44967 | Hs.351554 | Hs.351554:Homo sapiens cD FLJ32092 fis, | 3.42 |
| | 414888 | AL039185 | Hs.77558 | Hs.77558:thyroid hormone receptor intera | 3.42 |
| | 452445 | AB002438 | Hs.29596 | Hs.29596:Homo sapiens mR from chromosome | 3.41 |
| | 414803 | X03100 | Hs.914 | Hs.914:major histocompatibility complex, | 3.41 |
| | 419201 | M22324 | Hs.1239 | NM_001150:Homo sapiens alanyl (membrane) | 3.41 |
| | 445139 | AB037848 | Hs.12365 | Hs.12365:syplotagrin XIII | 3.41 |
| 75 | 435021 | AA922192 | Hs.73962 | Hs.73962:EphA7 | 3.41 |
| | 417259 | AW903838 | Hs.81800 | Hs.81800:chondroitin sulfate proteoglyca | 3.40 |
| | 439737 | AI751438 | Hs.41271 | Hs.41271:Homo sapiens mR full length ins | 3.39 |
| | 410636 | AA088177 | Hs.172870 | Hs.172870:KIAA1913 protein | 3.39 |
| 80 | 431590 | AB037789 | Hs.263395 | Hs.263395:sema domain, transmembrane dom | 3.38 |
| | 415000 | AW025529 | Hs.239812 | Hs.239812:serologically defined breast c | 3.36 |
| | 416700 | AW498958 | Hs.343475 | NM_001909:Homo sapiens cathepsin D (lyso | 3.36 |
| | 440516 | S42303 | Hs.161 | NM_001792:Homo sapiens cadherin 2, type | 3.35 |
| | 423720 | AL044191 | Hs.23388 | Hs.23388:hypothetical protein DKFZp434F0 | 3.32 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 421902 | BE392717 | | BE392717:601307571F1 NIH_MGC_44 Homo sap | 3.32 |
| | 409220 | BE243323 | Hs.51233 | Hs.51233:tumor necrosis factor receptor | 3.32 |
| | 421502 | AF111856 | Hs.105039 | NM_006424:Homo sapiens solute carrier fa | 3.32 |
| 5 | 416729 | U46165 | Hs.1027 | NM_004165:Homo sapiens Ras-related assoc | 3.30 |
| | 430302 | AL137502 | Hs.238679 | Hs.238679:Rag D protein | 3.30 |
| | 445084 | H38914 | Hs.250848 | Hs.250848:Homo sapiens cD FLJ14761 fs, | 3.29 |
| | 406825 | AI982529 | Hs.84298 | Hs.84298:CD74 antigen (invariant polypep | 3.29 |
| | 446272 | BE268912 | Hs.14501 | NM_005335:Homo sapiens hematopoietic cel | 3.28 |
| 10 | 437145 | AF007216 | Hs.5462 | NM_003759:Homo sapiens solute carrier fa | 3.27 |
| | 444071 | AI627808 | Hs.110524 | Hs.110524:ESTs | 3.27 |
| | 414662 | AL036058 | Hs.76807 | Hs.76807:major histocompatibility comple | 3.27 |
| | 436576 | AI458213 | Hs.77542 | Hs.77542:ESTs, Weakly similar to S26650 | 3.26 |
| | 424675 | NM_005512 | Hs.151641 | NM_005512:Homo sapiens glycoprotein A re | 3.25 |
| 15 | 437897 | AA770561 | Hs.146170 | Hs.146170:hypothetical protein FLJ22969 | 3.25 |
| | 449703 | H61001 | Hs.171802 | Hs.171802:Homo sapiens, clone IMAGE:3956 | 3.25 |
| | 414788 | X78342 | Hs.77313 | NM_003674:Homo sapiens cyclin-dependent | 3.25 |
| | 414249 | AI797994 | Hs.279929 | Hs.279929:gp25L2 protein | 3.24 |
| | 430396 | D49742 | Hs.241363 | NM_004132:Homo sapiens hyaluron binding | 3.23 |
| 20 | 424456 | AA341017 | Hs.25549 | Hs.25549:hypothetical protein FLJ20898 | 3.23 |
| | 452303 | R27257 | Hs.57734 | Hs.57734:G protein-coupled receptor like | 3.22 |
| | 425390 | AI092634 | Hs.156114 | NM_004648:Homo sapiens protein tyrosine | 3.21 |
| | 416033 | NM_012201 | Hs.78979 | NM_012201:Homo sapiens golgi apparatus p | 3.19 |
| | 450931 | N25156 | Hs.25648 | Hs.25648:tumor necrosis factor receptor | 3.19 |
| 25 | 428065 | AI634046 | Hs.157313 | Hs.157313:ESTs | 3.18 |
| | 422616 | BE300330 | Hs.118725 | NM_012248:Homo sapiens selenophosphate s | 3.18 |
| | 439318 | AW837046 | Hs.6527 | Hs.6527:G protein-coupled receptor 56 | 3.17 |
| | 427640 | AF058293 | Hs.180015 | NM_001355:Homo sapiens D-dopachrome taut | 3.17 |
| | 409936 | AK001691 | Hs.57655 | Hs.57655:dudulin 2 | 3.16 |
| 30 | 436001 | AW903849 | Hs.173840 | Hs.173840:similar to endothelial cell-se | 3.16 |
| | 451154 | AA015879 | Hs.33536 | Hs.33536:ESTs | 3.16 |
| | 420256 | U84722 | Hs.76206 | NM_001795:Homo sapiens cadherin 5, type | 3.16 |
| | 407584 | W25945 | Hs.8173 | Hs.8173:hypothetical protein FLJ10803 | 3.15 |
| | 428593 | AW207440 | Hs.185973 | NM_003676:Homo sapiens degenerative sper | 3.15 |
| 35 | 410026 | AI912061 | Hs.55016 | Hs.55016:EPS8-related protein 2 | 3.15 |
| | 445333 | BE537641 | Hs.44278 | Hs.44278:RAB17, member RAS oncogene fami | 3.14 |
| | 448143 | AF039704 | Hs.20478 | NM_000391:Homo sapiens ceroid-lipofuscin | 3.14 |
| | 423007 | AA320134 | Hs.196029 | Hs.196029:Homo sapiens mR for KIAA1657 p | 3.14 |
| | 416511 | NM_006762 | Hs.79356 | NM_006762:Homo sapiens Lysosomal-associa | 3.14 |
| 40 | 439237 | AW408158 | Hs.318893 | Hs.318893:ESTs, Weakly similar to Z195_H | 3.13 |
| | 446899 | NM_005397 | Hs.16426 | NM_005397:Homo sapiens podocalyxin-like | 3.13 |
| | 413916 | N49813 | Hs.75615 | NM_000483:Homo sapiens apolipoprotein C- | 3.13 |
| | 434398 | AA121098 | Hs.3838 | NM_006622:Homo sapiens serum-inducible k | 3.12 |
| | 441283 | AA927670 | Hs.131704 | Hs.131704:ESTs | 3.12 |
| 45 | 418945 | BE246762 | Hs.89499 | NM_000698:Homo sapiens arachidate 5-lipo | 3.12 |
| | 418458 | AA332941 | Hs.85226 | NM_000235:Homo sapiens lipase A, lysosom | 3.12 |
| | 408989 | AW361666 | Hs.49500 | Hs.49500:KIAA0746 protein | 3.11 |
| | 436906 | H95990 | Hs.181244 | Hs.181244:major histocompatibility compl | 3.11 |
| 50 | 411089 | AA456454 | Hs.355702 | Hs.355702:ESTs, Weakly similar to AC0048 | 3.11 |
| | 432990 | AL036071 | Hs.279899 | NM_003820:Homo sapiens tumor necrosis fa | 3.11 |
| | 425009 | X58288 | Hs.154151 | NM_002845:Homo sapiens protein tyrosine | 3.10 |
| | 443601 | AI078554 | Hs.42658 | Hs.42658:Homo sapiens cD FLJ30167 fs, c | 3.10 |
| | 430603 | AA148164 | Hs.247280 | Hs.247280:chromosome 20 open reading fra | 3.10 |
| | 413672 | BE156536 | Hs.353632 | Hs.353632:ESTs, Moderately similar to hy | 3.09 |
| 55 | 407786 | AA687538 | Hs.38972 | NM_005727:Homo sapiens tetraspan 1 (TSPA | 3.09 |
| | 414586 | AA306160 | Hs.16488 | NM_007298:Homo sapiens lymphocyte cytosol | 3.08 |
| | 423712 | W46802 | Hs.81988 | Hs.81988:disabled homolog 2, mitogen-res | 3.08 |
| | 438552 | AJ245820 | Hs.6314 | NM_012410:Homo sapiens type I transmembr | 3.06 |
| | 448364 | T08958 | Hs.297214 | Hs.297214:HSPC141 protein | 3.06 |
| 60 | 426437 | BE076537 | Hs.169895 | NM_004223:Homo sapiens ubiquitin-conjuga | 3.06 |
| | 437679 | NM_014214 | Hs.5753 | NM_014214:Homo sapiens inositol(myo)-1(o | 3.06 |
| | 422262 | AL022315 | Hs.113987 | NM_006498:Homo sapiens lecltin, galactosi | 3.06 |
| | 410480 | R97457 | Hs.63384 | NM_001257:Homo sapiens cadherin 13, H-ca | 3.05 |
| | 435818 | AA700553 | Hs.368614 | Hs.368614:ESTs | 3.05 |
| 65 | 418883 | BE387036 | Hs.1211 | NM_001611:Homo sapiens acid phosphatase | 3.05 |
| | 453613 | F06838 | Hs.374476 | Hs.374476:ESTs | 3.05 |
| | 408051 | AI623351 | Hs.172148 | Hs.172148:ESTs | 3.05 |
| | 432278 | AL137506 | Hs.274256 | Hs.274256:hypothetical protein FLJ23563 | 3.04 |
| | 407949 | W21874 | Hs.247057 | Hs.247057:ESTs, Weakly similar to 210926 | 3.04 |
| 70 | 418090 | U57059 | Hs.83429 | NM_003810:Homo sapiens tumor necrosis fa | 3.04 |
| | 433165 | AA578904 | Hs.292437 | Hs.292437:ESTs | 3.03 |
| | 425809 | AA370362 | Hs.57958 | Hs.57958:EGF-TM7-tatrophilin-related pro | 3.03 |
| | 443884 | N20617 | Hs.194397 | Hs.194397:ESTs, Moderately similar to 22 | 3.03 |
| | 447831 | AI433293 | Hs.164115 | Hs.164115:ESTs | 3.02 |
| 75 | 413278 | BE563085 | Hs.833 | NM_005101:Homo sapiens interferon-stimul | 3.01 |
| | 418870 | AF147204 | Hs.89414 | Hs.89414:chemokine (C-X-C motif), recept | 3.00 |
| | 456376 | AA663904 | Hs.89862 | Hs.89862:TNFRSF1A-associated via death d | 3.00 |
| | 439738 | BE246502 | Hs.95598 | Hs.95598:sema domain, immunoglobulin doma | 3.00 |
| | 444416 | AW288085 | Hs.11156 | NM_016494:Homo sapiens hypothetical prot | 3.00 |
| 80 | 406656 | M16714 | Hs.89543 | Hs.89543:transketolase (Wernicke-Korsako | 3.00 |
| | 406826 | AW516005 | Hs.84298 | Hs.84298:CD74 antigen (invariant polypep | 2.99 |
| | 418707 | U97502 | Hs.87497 | Hs.87497:butyrophilin, subfamily 3, memb | 2.99 |
| | 421742 | AW970004 | Hs.107528 | NM_016108:Homo sapiens androgen induced | 2.99 |
| | 406824 | AW515961 | Hs.84298 | Hs.84298:CD74 antigen (invariant polypep | 2.99 |

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|----|--------|-----------|-----------|---|------|
| | 435605 | AF151815 | Hs.4973 | NM_015680:Homo sapiens hypothetical prot | 2.98 |
| | 410491 | AA465131 | Hs.64001 | Hs.64001:Homo sapiens clone 25218 mR seq | 2.98 |
| | 427648 | AI376722 | Hs.180062 | NM_004159:Homo sapiens proteasome (proso | 2.98 |
| | 411125 | AA151647 | Hs.68877 | NM_000101:Homo sapiens cytochrome b-245, | 2.98 |
| 5 | 435550 | AI224456 | Hs.324507 | Hs.324507:hypothetical protein FLJ20986 | 2.98 |
| | 429373 | NM_014694 | Hs.200594 | NM_014694:Homo sapiens KIAA0605 gene pro | 2.98 |
| | 445701 | AF055581 | Hs.13131 | NM_005475:Homo sapiens lymphocyte adapto | 2.97 |
| | 414649 | AI672727 | Hs.76753 | NM_000118:Homo sapiens endoglin (Osler-R | 2.97 |
| | 444207 | AI565004 | Hs.374415 | Hs.374415:ESTs | 2.97 |
| 10 | 423225 | AA852604 | Hs.125359 | NM_006288:Homo sapiens Thy-1 cell surfac | 2.97 |
| | 407792 | AI077715 | Hs.39384 | NM_014344:Homo sapiens four jointed box | 2.97 |
| | 445707 | AI248720 | Hs.114390 | Hs.114390:ESTs | 2.96 |
| | 452888 | AW955454 | Hs.30942 | NM_004093:Homo sapiens ephrin-B2 (EFNB2) | 2.96 |
| | 418478 | U38945 | Hs.1174 | Hs.1174:cyclin-dependent kinase inhibitor | 2.95 |
| 15 | 411441 | AL042355 | Hs.70202 | Hs.70202:WD repeat domain 10 | 2.95 |
| | 443426 | AF098158 | Hs.9329 | Hs.9329:chromosome 20 open reading frame | 2.94 |
| | 450876 | AF189062 | Hs.285976 | Hs.285976:LAG1 longevity assurance homol | 2.94 |
| | 426359 | AA376409 | Hs.10862 | Hs.10862:Homo sapiens cD: FLJ23313 fis, | 2.94 |
| | 425421 | L11669 | Hs.157145 | NM_001120:Homo sapiens tetracycline tran | 2.93 |
| 20 | 449879 | H03573 | Hs.287830 | Hs.287830:Homo sapiens mR: cD DKFZp434E1 | 2.93 |
| | 454075 | R43826 | Hs.16313 | Hs.16313:Krueppel-like zinc finger protea | 2.93 |
| | 421595 | AB014520 | Hs.301685 | Hs.301685:KIAA0620 protein | 2.93 |
| | 457949 | W69171 | Hs.334814 | Hs.334814:hypothetical protein FLJ14868 | 2.92 |
| | 443987 | AW163123 | Hs.10071 | NM_016551:Homo sapiens seven transmembra | 2.92 |
| 25 | 430259 | BE550182 | Hs.375142 | Hs.375142:RalGEF-like protein 3, mouse h | 2.92 |
| | 415906 | AI751357 | Hs.288741 | Hs.288741:Homo sapiens cD: FLJ22256 fis, | 2.91 |
| | 429762 | AI346255 | Hs.216354 | NM_006913:Homo sapiens ring finger prote | 2.91 |
| | 451527 | AF022813 | Hs.26518 | NM_003271:Homo sapiens transmembrane 4 s | 2.91 |
| 30 | 425356 | BE244879 | Hs.155939 | NM_005541:Homo sapiens inositol polyphos | 2.91 |
| | 427080 | AW068287 | Hs.301175 | NM_002872:Homo sapiens ras-related C3 bo | 2.91 |
| | 426432 | AF001601 | Hs.169857 | NM_000305:Homo sapiens paraoxase 2 (PON2 | 2.90 |
| | 431476 | BE612705 | Hs.256697 | Hs.256697:histidine triad nucleotide bin | 2.89 |
| | 406659 | AA663985 | Hs.277477 | Hs.277477:major histocompatibility compl | 2.89 |
| 35 | 451144 | AW956103 | Hs.61712 | Hs.61712:Homo sapiens cD FLJ31548 fis, c | 2.89 |
| | 456362 | AW973003 | Hs.179909 | Hs.179909:nuclear receptor coactivator 6 | 2.88 |
| | 426440 | BE382756 | Hs.169902 | NM_006516:Homo sapiens solute carrier fa | 2.88 |
| | 456974 | M12529 | Hs.169401 | NM_000041:Homo sapiens apolipoprotein E | 2.88 |
| | 418174 | L20688 | Hs.83656 | Hs.83656:Rho GDP dissociation inhibitor | 2.88 |
| | 446055 | AI815981 | Hs.12909 | Hs.12909:mucopolin 1 | 2.88 |
| 40 | 423184 | NM_004428 | Hs.1624 | NM_004428:Homo sapiens ephrin-A1 (EF1), | 2.87 |
| | 427700 | AA262294 | Hs.180383 | NM_001946:Homo sapiens dual specificity | 2.87 |
| | 410668 | BE379794 | Hs.159651 | NM_016629:Homo sapiens hypothetical prot | 2.87 |
| | 444143 | AW747996 | Hs.160999 | Hs.160999:ESTs, Weakly similar to I78885 | 2.87 |
| | 407151 | H25836 | Hs.301527 | Hs.301527:ESTs, Moderately similar to un | 2.86 |
| 45 | 449349 | AI825386 | Hs.352579 | Hs.352579:Homo sapiens, chromosome 20 op | 2.86 |
| | 436997 | AA741151 | Hs.137323 | Hs.137323:ESTs | 2.86 |
| | 446143 | BE245342 | Hs.306079 | NM_013336:Homo sapiens protein transport | 2.86 |
| | 417355 | D13168 | Hs.82002 | Hs.82002:endothelin receptor type B | 2.86 |
| 50 | 431685 | AW296135 | Hs.267659 | NM_006113:Homo sapiens vav 3 oncogene (V | 2.86 |
| | 408877 | AA479033 | Hs.130315 | Hs.130315:ESTs | 2.85 |
| | 429615 | AF258627 | Hs.211562 | NM_005502:Homo sapiens ATP-binding casse | 2.85 |
| | 412014 | AI620650 | Hs.43761 | Hs.43761:gap junction protein, alpha 7, | 2.84 |
| | 436749 | AA584890 | Hs.5302 | NM_006149:Homo sapiens lectin, galactosi | 2.84 |
| 55 | 419625 | U91616 | Hs.182885 | NM_004556:Homo sapiens nuclear factor of | 2.84 |
| | 439941 | AI392640 | Hs.18272 | Hs.18272:solute carrier family 38, membe | 2.84 |
| | 436496 | AA281959 | Hs.5210 | NM_004877:Homo sapiens glia maturation f | 2.84 |
| | 422100 | AI096988 | Hs.111554 | NM_005737:Homo sapiens ADP-ribosylation | 2.83 |
| | 439730 | AF035292 | Hs.6654 | Hs.6654:KIAA0657 protein | 2.83 |
| 60 | 447217 | BE465754 | Hs.17778 | NM_003872:Homo sapiens neuropilin 2 (NRP | 2.83 |
| | 428343 | AL043021 | Hs.12705 | Hs.12705:similar to HYPOTHETICAL 43.1 KD | 2.82 |
| | 440524 | R71264 | Hs.16798 | Hs.16798:Homo sapiens mR: cD DKFZp564O24 | 2.82 |
| | 415523 | AL042003 | Hs.296847 | NM_003119:Homo sapiens spastic paraplegi | 2.81 |
| | 439668 | AI091277 | Hs.302634 | Hs.302634:frizzled homolog 8 (Drosophila | 2.81 |
| 65 | 414570 | Y00285 | Hs.76473 | NM_000876:Homo sapiens insulin-like grow | 2.80 |
| | 426535 | AU077012 | Hs.288582 | NM_006287:Homo sapiens tissue factor pat | 2.80 |
| | 409649 | AA159216 | Hs.55505 | Hs.55505:hypothetical protein FLJ20442 | 2.80 |
| | 406655 | M21533 | Hs.277477 | Hs.277477:major histocompatibility compl | 2.79 |
| | 415323 | BE269352 | Hs.949 | NM_000433:Homo sapiens neutrophil cytosol | 2.79 |
| 70 | 443195 | BE148235 | Hs.193063 | Hs.193063:Homo sapiens cD FLJ14201 fis, | 2.78 |
| | 451356 | AA748418 | Hs.164577 | Hs.164577:ESTs | 2.78 |
| | 450708 | AA376654 | Hs.350065 | Hs.350065:Homo sapiens cD FLJ30634 fis, | 2.78 |
| | 433681 | AI004377 | Hs.200360 | Hs.200360:Homo sapiens cD FLJ13027 fis, | 2.77 |
| | 442599 | AF078037 | Hs.324051 | NM_006663:Homo sapiens RelA-associated i | 2.77 |
| 75 | 414509 | AW161311 | Hs.76294 | NM_001780:Homo sapiens CD63 antigen (mel | 2.76 |
| | 431394 | AK000692 | Hs.252351 | Hs.252351:HERV-H LTR-associating 2 | 2.76 |
| | 417331 | AW411297 | Hs.81972 | Hs.81972:SHC (Src homology 2 domain cont | 2.76 |
| | 415995 | NM_004573 | Hs.355888 | NM_004573:Homo sapiens phospholipase C, | 2.75 |
| | 414911 | NM_000107 | Hs.77602 | NM_000107:Homo sapiens damage-specific D | 2.75 |
| 80 | 425976 | C75094 | Hs.334514 | Hs.334514:chromosome 6 open reading fram | 2.75 |
| | 407893 | BE408359 | Hs.43621 | Hs.43621:hypothetical protein MBC3205 | 2.75 |
| | 407903 | AI287341 | Hs.154029 | Hs.154029:bHLH factor Hes4 | 2.75 |
| | 416062 | AA724811 | Hs.334791 | Hs.334791:similar to neurol tetraspanin | 2.75 |
| | 428494 | AA233439 | Hs.184634 | Hs.184634:hypothetical protein FLJ20005 | 2.75 |

| | | | | | |
|----|--------|---------------|-----------|---|------|
| | 421506 | BE302796 | Hs.105097 | NM_003258:Homo sapiens thymidine kise 1, | 2.74 |
| | 427581 | NM_014788 | Hs.179703 | NM_014788:Homo sapiens tripartite motif- | 2.74 |
| | 424527 | AW138558 | Hs.334873 | Hs.334873:carboxypeptidase M | 2.74 |
| 5 | 439578 | AW263124 | Hs.350547 | Hs.350547:nuclear receptor co-repressor/ | 2.74 |
| | 425188 | AK002052 | Hs.155071 | Hs.155071:chromosome 20 open reading fra | 2.74 |
| | 428013 | AF151020 | Hs.181444 | NM_016456:Homo sapiens hypothetical prot | 2.73 |
| | 439333 | AW384710 | Hs.132986 | Hs.132986:Homo sapiens cD FLJ31588 fis, | 2.73 |
| | 450935 | BE514743 | Hs.355753 | NM_005851:Homo sapiens tumor suppressor | 2.73 |
| 10 | 421532 | AW138207 | Hs.146170 | Hs.146170:hypothetical protein FLJ22969 | 2.73 |
| | 440502 | AI824113 | Hs.78281 | Hs.78281:regulator of G-protein sigling | 2.73 |
| | 444981 | AW855398 | Hs.12210 | Hs.12210:tumor endothelial marker 6 | 2.72 |
| | 439219 | N33883 | Hs.41322 | Hs.41322:ESTs | 2.72 |
| | 416847 | L43821 | Hs.80261 | NM_006403:Homo sapiens enhancer of filam | 2.72 |
| 15 | 433179 | AW362945 | Hs.162459 | Hs.162459:ESTs | 2.72 |
| | 424528 | AW073971 | Hs.238954 | Hs.238954:ESTs, Weakly similar to puta | 2.71 |
| | 411213 | AA676939 | Hs.69285 | NM_003873:Homo sapiens neuropilin 1 (NRP | 2.70 |
| | 433012 | NM_004045 | Hs.279910 | NM_004045:Homo sapiens ATX1 antioxidant | 2.70 |
| | 425345 | AU077297 | Hs.155894 | NM_002827:Homo sapiens protein tyrosine | 2.69 |
| 20 | 428923 | BE047698 | Hs.188785 | Hs.188785:ESTs | 2.69 |
| | 427923 | AW274357 | Hs.301406 | Hs.301406:hypothetical protein PP3501 | 2.69 |
| | 446644 | NM_003272 | Hs.15791 | NM_003272:Homo sapiens transmembrane 7 s | 2.68 |
| | 421743 | T35958 | Hs.107614 | Hs.107614:DKFZP564I1171 protein | 2.68 |
| | 416207 | NM_014745 | Hs.79077 | NM_014745:Homo sapiens KIAA0233 gene pro | 2.68 |
| 25 | 420372 | AW960049 | Hs.293660 | Hs.293660:gene overexpressed in astrocyt | 2.68 |
| | 420542 | NM_000505 | Hs.1321 | NM_000505:Homo sapiens coagulation facto | 2.67 |
| | 425069 | AA687465 | Hs.298184 | Hs.298184:potassium voltage-gated channe | 2.67 |
| | 418558 | AW082266 | Hs.86131 | NM_003824:Homo sapiens Fas (TNFRSF6)-ass | 2.67 |
| | 426251 | M24283 | Hs.168383 | NM_000201:Homo sapiens intercellular adh | 2.66 |
| 30 | 406701 | AA780613 | Hs.62954 | Hs.62954:ferritin, heavy polypeptide 1 | 2.66 |
| | 431681 | AK000378 | Hs.267566 | Hs.267566:hypothetical protein FLJ20371 | 2.66 |
| | 412833 | AW960547 | Hs.298262 | Hs.298262:ribosomal protein S19 | 2.66 |
| | 433101 | AW572317 | Hs.12082 | Hs.12082:TIGA1 | 2.66 |
| | 414774 | X02419 | Hs.77274 | NM_002658:Homo sapiens plasminogen activ | 2.66 |
| 35 | 427868 | AI360119.comp | Hs.181013 | NM_002629:Homo sapiens phosphoglycerate | 2.66 |
| | 413929 | BE501689 | Hs.75617 | Hs.75617:collagen, type IV, alpha 2 | 2.66 |
| | 424762 | AL119442 | Hs.183684 | Hs.183684:eukaryotic translation initiat | 2.66 |
| | 422048 | NM_012445 | Hs.288126 | NM_012445:Homo sapiens spondin 2, extrac | 2.65 |
| | 431350 | AI192528 | Hs.164537 | Hs.164537:ESTs | 2.65 |
| 40 | 450184 | W31096 | Hs.237617 | Hs.237617:dipeptidylpeptidase 9 | 2.65 |
| | 419285 | D31887 | Hs.89868 | Hs.89868:KIAA0062 protein | 2.65 |
| | 414217 | AI309298 | Hs.279898 | Hs.279898:Homo sapiens cD: FLJ23165 fis, | 2.64 |
| | 451253 | H48299 | Hs.26126 | NM_006984:Homo sapiens claudin 10 (CLDN1 | 2.64 |
| | 435905 | AW997484 | Hs.5003 | Hs.5003:SLIT-ROBO Rho GTPase-activating | 2.64 |
| 45 | 432581 | AU076465 | Hs.278441 | NM_014634:Homo sapiens KIAA0015 gene pro | 2.63 |
| | 415782 | AA169345 | Hs.123177 | Hs.123177:hypothetical protein BC011406 | 2.63 |
| | 430223 | NM_002514 | Hs.235835 | NM_002514:Homo sapiens nephroblastoma ov | 2.63 |
| | 417526 | AA568906 | Hs.82240 | NM_004177:Homo sapiens syntaxin 3A (STX3 | 2.63 |
| | 409956 | AW103364 | Hs.727 | NM_002192:Homo sapiens inhibin, beta A (| 2.62 |
| 50 | 449843 | R85337 | Hs.24030 | NM_001860:Homo sapiens solute carrier fa | 2.62 |
| | 417389 | BE260964 | Hs.82045 | NM_002391:Homo sapiens midline (neurite | 2.62 |
| | 446312 | BE087853 | Hs.171802 | Hs.171802:Homo sapiens, clone IMAGE:3956 | 2.62 |
| | 435099 | AC004770 | Hs.4756 | Hs.4756:flap structure-specific endonucle | 2.62 |
| | 417920 | S47833 | Hs.82927 | NM_004037:Homo sapiens adenosine monopho | 2.62 |
| 55 | 435702 | AI033647 | Hs.121001 | Hs.121001:Homo sapiens, clone MGC:4552 I | 2.62 |
| | 422959 | AV647015 | Hs.349256 | Hs.349256:paired immunoglobulin-like rec | 2.62 |
| | 419938 | AU076772 | Hs.1279 | NM_001733:Homo sapiens complement compon | 2.62 |
| | 450954 | AI904740 | Hs.25691 | NM_005856:Homo sapiens receptor (calcitri | 2.61 |
| | 421753 | BE314828 | Hs.107911 | Hs.107911:ATP-binding cassette, sub-fam | 2.61 |
| 60 | 443577 | AI078033 | Hs.177170 | Hs.177170:ESTs, Weakly similar to ALU8_M | 2.61 |
| | 453886 | R66282 | Hs.20247 | Hs.20247:ESTs | 2.61 |
| | 421883 | X55079 | Hs.1437 | NM_000152:Homo sapiens glucosidase, alph | 2.60 |
| | 440457 | BE387593 | Hs.21321 | Hs.21321:granule cell differentiation pr | 2.60 |
| | 410295 | AA741357 | Hs.356624 | Hs.356624:ESTs | 2.59 |
| 65 | 420679 | X57152 | Hs.99853 | NM_001436:Homo sapiens fibrillarin (FBL) | 2.59 |
| | 451558 | NM_001089 | Hs.26630 | NM_001089:Homo sapiens ATP-binding casse | 2.59 |
| | 444672 | Z95636 | Hs.11669 | Hs.11669:laminin, alpha 5 | 2.59 |
| | 408669 | AI935591 | Hs.78146 | Hs.78146:platelet/endothelial cell adhes | 2.59 |
| | 426194 | T50872 | Hs.2001 | Hs.2001:thromboxane A synthase 1 (plate | 2.59 |
| 70 | 421814 | L12350 | Hs.108623 | NM_003247:Homo sapiens thrombospondin 2 | 2.59 |
| | 456371 | S76825 | Hs.89695 | Hs.89695:insulin receptor | 2.59 |
| | 429098 | AF030249 | Hs.196176 | NM_001398:Homo sapiens enoyl Coenzyme A | 2.59 |
| | 414443 | AU077268 | Hs.76144 | NM_002609:Homo sapiens platelet-derived | 2.59 |
| | 428484 | AF104032 | Hs.184601 | NM_003486:Homo sapiens solute carrier fa | 2.59 |
| 75 | 453309 | AI791809 | Hs.32949 | NM_005218:Homo sapiens defensin, beta 1 | 2.58 |
| | 412867 | AU076861 | Hs.74637 | NM_003217:Homo sapiens testis enhanced g | 2.58 |
| | 432827 | Z68128 | Hs.3109 | Hs.3109:Rho GTPase activating protein 4 | 2.58 |
| | 412669 | AW880841 | Hs.96908 | NM_006034:Homo sapiens p53-induced prote | 2.58 |
| 80 | 412115 | AK001763 | Hs.73239 | Hs.73239:hypothetical protein FLJ10901 | 2.58 |
| | 452866 | R26969 | Hs.268016 | Hs.268016:Homo sapiens cD: FLJ21243 fis, | 2.57 |
| | 435129 | AI381659 | Hs.267086 | Hs.267086:ESTs | 2.57 |
| | 424482 | BE268621 | Hs.149155 | NM_003374:Homo sapiens voltage-dependent | 2.57 |
| | 410494 | M36564 | Hs.64016 | NM_000313:Homo sapiens protein S (alpha) | 2.56 |
| | 433895 | AI287912 | Hs.3628 | NM_004834:Homo sapiens mitogen-activated | 2.56 |

| | | | | | |
|----|--------|---------------|-----------|--|------|
| | 442566 | R37337 | Hs.12111 | Hs.12111:ESTs | 2.56 |
| | 417640 | D30857 | Hs.82353 | NM_006404:Homo sapiens protein C recepto | 2.56 |
| | 442622 | NM_000435 | Hs.8546 | NM_000435:Homo sapiens Notch homolog 3 (| 2.56 |
| 5 | 430346 | AK000331 | Hs.297641 | Hs.297641:retinoblastoma-associated fact | 2.55 |
| | 419344 | U94905 | Hs.277445 | Hs.277445:diacylglycerol kase, zeta (104 | 2.55 |
| | 426500 | NM_014538 | Hs.170156 | NM_014538:Homo sapiens KIAA0450 gene pro | 2.55 |
| | 408048 | NM_007203 | Hs.42322 | NM_007203:Homo sapiens A kase (PRKA) anc | 2.55 |
| | 450700 | AW732799 | Hs.25348 | NM_005860:Homo sapiens follistatin-like | 2.54 |
| 10 | 417018 | M16038 | Hs.80887 | NM_002350:Homo sapiens v-yes-1 Yamaguchi | 2.54 |
| | 419378 | R24922 | Hs.90078 | Hs.90078:nucleotide-sugar transporter si | 2.54 |
| | 422451 | AA310753 | Hs.42491 | Hs.42491:ESTs, Moderately similar to hyp | 2.53 |
| | 435906 | AI686379 | Hs.110796 | Hs.110796:SAR1 protein | 2.53 |
| | 400231 | | | | 2.53 |
| 15 | 417849 | AW291587 | Hs.82733 | NM_007361:Homo sapiens nidogen 2 (NID2), | 2.53 |
| | 427380 | NM_005534 | Hs.177559 | NM_005534:Homo sapiens interferon gamma | 2.52 |
| | 428385 | AF112213 | Hs.184062 | Hs.184062:chromosome 20 open reading fra | 2.52 |
| | 438000 | AI825880 | Hs.5985 | Hs.5985:non-kise Cdc42 effector protein | 2.52 |
| | 448719 | AA033627 | Hs.21858 | Hs.21858:serine (or cysteine) protease i | 2.52 |
| | 422396 | W21872 | Hs.7907 | Hs.7907:L-fucose kase | 2.52 |
| 20 | 420787 | AA564248 | Hs.351292 | Hs.351292:Homo sapiens cD FLJ32605 fis, | 2.51 |
| | 430590 | AW383947 | Hs.246381 | NM_001251:Homo sapiens CD68 antigen (CD6 | 2.51 |
| | 447026 | BE313144 | Hs.324844 | Hs.324844:hypothetical protein IMAGE3455 | 2.51 |
| | 439223 | AW238299 | Hs.250618 | Hs.250618:UL16 binding protein 2 | 2.50 |
| 25 | 435151 | AA348482 | Hs.4788 | Hs.4788:nicastrin | 2.50 |
| | 448202 | AB002292 | Hs.20695 | NM_014629:Homo sapiens Rho guanine nucle | 2.50 |
| | 449943 | AF104266 | Hs.24212 | Hs.24212:latrophilin | 2.50 |
| | 425743 | BE396495 | Hs.159428 | Hs.159428:BCL2-associated X protein | 2.50 |
| | 444681 | AJ243937 | Hs.288316 | Hs.288316:chromosome 6 open reading fram | 2.50 |
| 30 | 421643 | BE281170 | Hs.106357 | NM_007126:Homo sapiens valosin-containin | 2.50 |
| | 428685 | D63476 | Hs.172813 | NM_003899:Homo sapiens Rho guanine nucle | 2.50 |
| | 432306 | Y18207 | Hs.303090 | NM_005398:Homo sapiens protein phosphata | 2.49 |
| | 421846 | AA017707 | Hs.1432 | NM_002743:Homo sapiens protein kase C su | 2.49 |
| | 421905 | AI660247 | Hs.32699 | Hs.32699:Homo sapiens, Similar to RIKEN | 2.49 |
| 35 | 419493 | AF001212 | Hs.90744 | NM_002815:Homo sapiens proteasome (proso | 2.49 |
| | 422530 | AW972300 | Hs.118110 | NM_004335:Homo sapiens bone marrow strom | 2.48 |
| | 442821 | BE391929 | Hs.8752 | NM_014255:Homo sapiens transmembrane pro | 2.48 |
| | 416919 | T97839 | Hs.80464 | NM_006402:Homo sapiens hepatitis B virus | 2.48 |
| | 443105 | X98753 | Hs.9004 | NM_001897:Homo sapiens chondroitin sulfa | 2.48 |
| 40 | 430040 | AW503115 | Hs.227823 | NM_014287:Homo sapiens pM5 protein (PM5) | 2.48 |
| | 428028 | U52112 | Hs.182018 | NM_001569:Homo sapiens interleukin-1 rec | 2.47 |
| | 424307 | AW293399 | Hs.356377 | Hs.356377:Homo sapiens, clone IMAGE:3633 | 2.46 |
| | 434511 | R28982 | Hs.18106 | Hs.18106:ESTs, Weakly similar to T06291 | 2.46 |
| | 454390 | AB020713 | Hs.56966 | Hs.56966:KIAA0906 protein | 2.46 |
| 45 | 417785 | X59812 | Hs.82568 | NM_000784:Homo sapiens cytochrome P450, | 2.46 |
| | 424673 | AA345051 | Hs.294092 | Hs.294092:Homo sapiens mR full length in | 2.46 |
| | 422003 | AA361760 | Hs.296326 | Hs.296326:ESTs, Weakly similar to A33533 | 2.46 |
| | 432126 | AA865239 | Hs.37196 | Hs.37196:putative G protein coupled rece | 2.46 |
| | 445937 | AI452943 | Hs.321231 | NM_003779:Homo sapiens UDP-Gal:betaGlc | 2.46 |
| 50 | 409354 | N68188 | Hs.159472 | Hs.159472:Homo sapiens cD: FLJ22224 fis, | 2.46 |
| | 401179 | | | | 2.46 |
| | 418151 | AA864238.comp | Hs.83583 | NM_005731:Homo sapiens actin related pro | 2.45 |
| | 422648 | D86983 | Hs.118893 | Hs.118893:Melanoma associated gene | 2.45 |
| | 427759 | BE245578 | Hs.2200 | NM_005041:Homo sapiens perforin 1 (pref | 2.45 |
| 55 | 431222 | X56777 | Hs.273790 | NM_007155:Homo sapiens zo pellucida glyc | 2.45 |
| | 411529 | AA430348 | Hs.317596 | Hs.317596:Homo sapiens cD FLJ12927 fis, | 2.45 |
| | 426825 | AL133415 | Hs.297753 | NM_003380:Homo sapiens vimentin (VIM), m | 2.45 |
| | 422242 | AJ251760 | Hs.273385 | NM_016592:Homo sapiens GS complex locus | 2.45 |
| | 408105 | AW152207 | Hs.270977 | Hs.270977:ESTs | 2.44 |
| 60 | 426410 | BE298446 | Hs.305890 | Hs.305890:BCL2-like 1 | 2.44 |
| | 421064 | AI245432 | Hs.101382 | NM_006291:Homo sapiens tumor necrosis fa | 2.44 |
| | 428157 | AI738719 | Hs.198427 | NM_000189:Homo sapiens hexokise 2 (HK2), | 2.44 |
| | 424398 | BE397787 | Hs.146393 | NM_014685:Homo sapiens homocysteine-indu | 2.44 |
| | 424825 | AF207069 | Hs.153357 | NM_001084:Homo sapiens procollagen-lysin | 2.44 |
| 65 | 426031 | AA295251 | Hs.166066 | Hs.166066:cisplatin resistance associate | 2.43 |
| | 409817 | BE295464 | Hs.56607 | Hs.56607:Williams-Beuren syndrome chromo | 2.43 |
| | 429359 | W00482 | Hs.2399 | NM_004995:Homo sapiens matrix metallopro | 2.43 |
| | 426761 | AI015709 | Hs.172089 | Hs.172089:pro-oncosis receptor inducing | 2.43 |
| | 429332 | AF030403 | Hs.199263 | NM_013233:Homo sapiens serine threonine | 2.43 |
| 70 | 425923 | NM_005026 | Hs.162808 | NM_005026:Homo sapiens phosphoinositide- | 2.43 |
| | 432211 | BE274530 | Hs.273333 | Hs.273333:hypothetical protein FLJ10986 | 2.43 |
| | 433339 | AF019226 | Hs.8036 | Hs.8036:RAB3D, member RAS oncogene famil | 2.42 |
| | 420539 | AA282735 | Hs.44004 | Hs.44004:AD031 protein | 2.42 |
| | 413243 | AA769266 | Hs.193657 | Hs.193657:ESTs | 2.42 |
| 75 | 435029 | AF167706 | Hs.19280 | Hs.19280:cysteine-rich motor neuron 1 | 2.42 |
| | 422374 | AW732869 | Hs.1519 | Hs.1519:protein kase, cAMP-dependent, re | 2.42 |
| | 444501 | AW247624 | Hs.11342 | NM_004148:Homo sapiens ninjurin 1 (NINJ1 | 2.42 |
| | 414919 | AW087337 | Hs.194461 | Hs.194461:ESTs | 2.42 |
| | 419355 | AA428520 | Hs.90061 | NM_006667:Homo sapiens progesterone rece | 2.42 |
| 80 | 436042 | AF284422 | Hs.119178 | Hs.119178:cation-chloride cotransporter- | 2.42 |
| | 418245 | AA088767 | Hs.83883 | Hs.83883:transmembrane, prostate androge | 2.42 |
| | 444215 | AB033075 | Hs.10669 | Hs.10669:development and differentiation | 2.41 |
| | 408683 | R58655 | Hs.46847 | NM_016614:Homo sapiens TRAF and TNF rece | 2.41 |
| | 423701 | AA329856 | Hs.143022 | Hs.143022:ESTs | 2.41 |

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|----|--------|-----------|-----------|---|------|
| 5 | 441783 | BE313412 | Hs.7961 | Hs.7961:Homo sapiens clone 25012 mR sequ | 2.41 |
| | 428072 | BE258602 | Hs.182366 | NM_015292:Homo sapiens heat shock protei | 2.41 |
| | 434599 | AB002313 | Hs.3989 | Hs.3989:plexin B2 | 2.40 |
| | 442351 | W52642 | Hs.8261 | Hs.8261:SPRY domain-containing SOCS box | 2.40 |
| | 407894 | AJ278313 | Hs.41143 | Hs.41143:phospholipase C, beta 1 (phosph | 2.40 |
| | 453449 | W16752 | Hs.32981 | Hs.32981:sema domain, immunoglobulin dom | 2.40 |
| | 408688 | AI634522 | Hs.152925 | Hs.152925:KIAA1268 protein | 2.40 |
| | 422448 | AW372922 | Hs.116774 | Hs.116774:integrin, alpha 1 | 2.40 |
| 10 | 416269 | AA177138 | Hs.161671 | Hs.161671:ESTs | 2.39 |
| | 452679 | Z42387 | Hs.83883 | Hs.83883:transmembrane, prostate androge | 2.39 |
| | 432981 | NM_002733 | Hs.3136 | NM_002733:Homo sapiens protein kise, AMP | 2.38 |
| | 419846 | NM_015977 | Hs.285681 | Hs.285681:Williams Beuren syndrome chrom | 2.38 |
| | 422110 | AJ376736 | Hs.111779 | Hs.111779:secreted protein, acidic, cyst | 2.38 |
| | 413092 | AA126856 | Hs.118665 | Hs.118665:ESTs | 2.38 |
| 15 | 433969 | AW207279 | Hs.271786 | Hs.271786:ESTs, Weakly similar to PC4395 | 2.37 |
| | 451267 | AI033894 | Hs.117865 | Hs.117865:solute carrier family 17 (anio | 2.37 |
| | 447526 | AL048753 | Hs.303649 | NM_002982:Homo sapiens small inducible c | 2.37 |
| | 441623 | AA315805 | Hs.348710 | Hs.348710:Homo sapiens, clone IMAGE:4242 | 2.37 |
| 20 | 420255 | NM_007289 | Hs.1298 | NM_007289:Homo sapiens membrane metallo- | 2.37 |
| | 409274 | NM_003930 | Hs.52644 | NM_003930:Homo sapiens src family associ | 2.36 |
| | 422801 | AF125672 | Hs.287994 | Hs.287994:nuclear receptor co-repressor | 2.36 |
| | 407887 | AA579668 | Hs.41072 | Hs.41072:serine (or cysteine) protease i | 2.36 |
| | 408212 | AA297567 | Hs.43728 | NM_015696:Homo sapiens weakly similar to | 2.36 |
| 25 | 430478 | NM_014349 | Hs.241535 | NM_014349:Homo sapiens apolipoprotein L, | 2.36 |
| | 405102 | | | | 2.35 |
| | 423583 | AL122055 | Hs.129836 | Hs.129836:KIAA1028 protein | 2.35 |
| | 426125 | X87241 | Hs.166994 | NM_005245:Homo sapiens FAT tumor suppres | 2.35 |
| 30 | 425204 | NM_002436 | Hs.1861 | NM_002436:Homo sapiens membrane protein, | 2.35 |
| | 420676 | AI434780 | Hs.4248 | Hs.4248:Homo sapiens PP3781 mR, complete | 2.35 |
| | 421079 | AW404994 | Hs.101695 | Hs.101695:NCK adaptor protein 2 | 2.35 |
| | 410039 | AF207989 | Hs.58014 | Hs.58014:G protein-coupled receptor, fam | 2.34 |
| | 412958 | BE391579 | Hs.75087 | NM_006712:Homo sapiens FAST kise (FASTK) | 2.34 |
| | 430363 | M28713 | Hs.274464 | NM_000398:Homo sapiens diaphorase (DH) (| 2.34 |
| 35 | 425397 | J04088 | Hs.156346 | NM_001067:Homo sapiens topoisomerase (D) | 2.34 |
| | 451035 | AU076785 | Hs.430 | NM_002670:Homo sapiens plastin 1 (I iso) | 2.34 |
| | 449027 | AJ271216 | Hs.22880 | Hs.22880:dipeptidylpeptidase III | 2.34 |
| | 429457 | BE243065 | Hs.202955 | Hs.202955:hypothetical protein FLJ20507 | 2.34 |
| | 417709 | O87434 | Hs.82426 | NM_014734:Homo sapiens KIAA0247 gene pro | 2.34 |
| 40 | 412805 | AW954569 | Hs.278675 | Hs.278675:bromodomain-containing 4 | 2.34 |
| | 427647 | W19744 | Hs.180059 | Hs.180059:Homo sapiens cD FLJ31360 fis, | 2.34 |
| | 430702 | U56979 | Hs.278568 | NM_000186:Homo sapiens H factor 1 (compl | 2.33 |
| | 456804 | AI421645 | Hs.139851 | NM_001233:Homo sapiens caveolin 2 (CAV2) | 2.33 |
| | 453648 | W21493 | Hs.28329 | Hs.28329:protein phosphatase 1, regulato | 2.33 |
| 45 | 450812 | AB002360 | Hs.25515 | Hs.25515:MCF-2 cell line derived transfo | 2.33 |
| | 402575 | | | | 2.33 |
| | 424670 | W61215 | Hs.116651 | NM_005797:Homo sapiens epithelial V-like | 2.32 |
| | 452960 | AK001335 | Hs.31137 | NM_006504:Homo sapiens protein tyrosine | 2.32 |
| 50 | 442968 | AK000606 | Hs.8868 | NM_004871:Homo sapiens golgi SP receptor | 2.32 |
| | 410639 | BE269047 | Hs.65234 | Hs.65234:DEAD/H (Asp-Glu-Ala-Asp) fis) bo | 2.32 |
| | 415169 | W42913 | Hs.78089 | NM_004231:Homo sapiens ATPase, H+ transp | 2.32 |
| | 450160 | BE048099 | Hs.183738 | Hs.183738:FERM, RhoGEF (ARHGEF) and plec | 2.32 |
| | 407223 | H96850 | | H96850:yo03b12.s1 Soares melanocyte 2N6H | 2.32 |
| 55 | 426780 | BE242284 | Hs.172199 | NM_001114:Homo sapiens adenylate cyclase | 2.32 |
| | 434987 | AW975114 | Hs.371677 | Hs.371677:ESTs | 2.32 |
| | 416354 | NM_000633 | Hs.79241 | NM_000633:Homo sapiens B-cell CLL/lympho | 2.31 |
| | 453107 | NM_016113 | Hs.279746 | NM_016113:Homo sapiens transient recepto | 2.31 |
| | 422963 | M79141 | Hs.13234 | Hs.13234:ESTs, Weakly similar to hypothe | 2.31 |
| | 433618 | AA602539 | Hs.345494 | Hs.345494:ESTs, Moderately similar to ZN | 2.31 |
| 60 | 438584 | AA811347 | | AA811347:ob81h06.s1 NCI_CGAP_GC81 Homo s | 2.31 |
| | 446126 | AW085909 | Hs.356618 | Hs.356618:ESTs, Weakly similar to PC4259 | 2.31 |
| | 408716 | AI567839 | Hs.151714 | Hs.151714:peroxisomal proliferator-activ | 2.30 |
| | 433230 | AW136134 | Hs.220277 | Hs.220277:ESTs, Weakly similar to expres | 2.30 |
| | 410168 | AW834050 | Hs.351432 | Hs.351432:tensin | 2.30 |
| 65 | 446342 | BE298665 | Hs.14846 | Hs.14846:Homo sapiens mR; cD DKFZp564D01 | 2.30 |
| | 418452 | BE379749 | Hs.85201 | NM_005127:Homo sapiens C-type (calcium d | 2.30 |
| | 453175 | NM_006834 | Hs.32217 | NM_006834:Homo sapiens RAB32, member RAS | 2.29 |
| | 409012 | AL117435 | Hs.49725 | Hs.49725:DKFZP434I216 protein | 2.29 |
| | 452848 | AI417193 | Hs.288912 | Hs.288912:BBP-like protein 2 | 2.29 |
| 70 | 418838 | AW385224 | Hs.35198 | Hs.35198:ectonucleotide pyrophosphatase/ | 2.29 |
| | 422562 | AI962060 | Hs.118397 | NM_001128:Homo sapiens AE binding protei | 2.28 |
| | 432828 | AB042326 | Hs.287402 | Hs.287402:chondroitin 4-sulfotransferase | 2.28 |
| | 412948 | BE243313 | Hs.334851 | NM_006148:Homo sapiens LIM and SH3 prote | 2.28 |
| | 426068 | AF029778 | Hs.166154 | NM_002226:Homo sapiens jagged 2 (JAG2) | 2.28 |
| 75 | 456919 | NM_003900 | Hs.182248 | NM_003900:Homo sapiens sequestosome 1 (S | 2.28 |
| | 452806 | AW014549 | Hs.58373 | Hs.58373:ESTs | 2.28 |
| | 453983 | H94997 | Hs.16450 | Hs.16450:ESTs | 2.28 |
| | 407736 | N41744 | Hs.349326 | Hs.349326:Homo sapiens cD FLJ30677 fis, | 2.28 |
| 80 | 413211 | AW967107 | Hs.109274 | Hs.109274:hypothetical protein MGCA365 | 2.27 |
| | 422051 | AW327546 | Hs.111024 | Hs.111024:solute carrier family 25 (mito | 2.27 |
| | 438438 | AA257992 | Hs.50651 | Hs.50651:Janus kise 1 (a protein tyrosin | 2.27 |
| | 436278 | BE396290 | Hs.5097 | NM_004710:Homo sapiens syptogyrin 2 (SYN | 2.27 |
| | 454080 | AI199711 | Hs.576 | NM_000147:Homo sapiens fucosidase, alpha | 2.27 |
| | 426542 | AF190746 | Hs.170310 | NM_017424:Homo sapiens cat eye syndrome | 2.27 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 417115 | AW952792 | Hs.334612 | NM_003094:Homo sapiens small nuclear rib | 2.27 |
| | 402901 | | | | 2.26 |
| | 412898 | AI129903 | Hs.74669 | NM_006634:Homo sapiens vesicle-associate | 2.26 |
| | 413020 | R98736 | | R98736:yr31h09.r1 Soares fetal liver spl | 2.26 |
| 5 | 413939 | AL047051 | Hs.199961 | Hs.199961:ESTs, Weakly similar to hypoth | 2.26 |
| | 408681 | AW953853 | Hs.281462 | Hs.281462:hypothetical protein FLJ14251 | 2.25 |
| | 412330 | NM_005100 | Hs.788 | NM_005100:Homo sapiens A kise (PRKA) anc | 2.25 |
| | 442083 | R50192 | Hs.165062 | Hs.165062:ESTs | 2.25 |
| | 418271 | NM_000919 | Hs.83920 | NM_000919:Homo sapiens peptidylglycine a | 2.25 |
| 10 | 433376 | AI249361 | Hs.74122 | NM_001225:Homo sapiens caspase 4, apopto | 2.25 |
| | 438562 | AI566826 | Hs.25890 | Hs.25890:ESTs, Weakly similar to transdu | 2.25 |
| | 443883 | AA114212 | Hs.9930 | NM_001235:Homo sapiens serine (or cystei | 2.25 |
| | 416976 | BE243985 | Hs.80680 | Hs.80680:major vault protein | 2.24 |
| | 416914 | AA344481 | Hs.80426 | Hs.80426:brain and reproductive organ-ex | 2.24 |
| 15 | 400288 | X06256 | Hs.149609 | NM_002205:Homo sapiens integrin, alpha 5 | 2.24 |
| | 407904 | W44735 | Hs.107260 | Hs.107260:putative UDP-Galc:polypeptide | 2.24 |
| | 429690 | AW956329 | Hs.23721 | Hs.23721:ESTs | 2.24 |
| | 443813 | AA876372 | Hs.93961 | Hs.93961:Homo sapiens mR: cD DKFZp667D09 | 2.24 |
| | 427458 | BE208364 | Hs.29283 | Hs.29283:ESTs, Weakly similar to UKHU pr | 2.24 |
| 20 | 454294 | AB000734 | Hs.50640 | NM_003745:Homo sapiens JAK binding prote | 2.24 |
| | 407192 | AA609200 | Hs.366318 | Hs.366318:ESTs | 2.23 |
| | 425751 | T19239 | Hs.1940 | NM_001885:Homo sapiens crystallin, alpha | 2.23 |
| | 456437 | AI924228 | Hs.115185 | Hs.115185:ESTs | 2.23 |
| | 413019 | BE281604 | Hs.75140 | NM_002337:Homo sapiens low density lipop | 2.23 |
| 25 | 418862 | BE550964 | Hs.89399 | Hs.89399:ATP synthase, H+ transporting, | 2.23 |
| | 435284 | AA879470 | Hs.96849 | Hs.96849:Homo sapiens cD FLJ11492 fis, c | 2.23 |
| | 429630 | M85289 | Hs.211573 | NM_005529:Homo sapiens heparan sulfate p | 2.23 |
| | 427609 | AK000436 | Hs.179791 | Hs.179791:RAB20, member RAS oncogene fam | 2.23 |
| | 421917 | AB028943 | Hs.109445 | Hs.109445:hypermethylated in cancer 2 | 2.23 |
| 30 | 446616 | R55964 | Hs.334873 | Hs.334873:carboxypeptidase M | 2.23 |
| | 407232 | X04526 | | X04526:Human liver mR for beta-subunit s | 2.23 |
| | 423798 | AF047033 | Hs.132904 | Hs.132904:solute carrier family 4, sodiu | 2.23 |
| | 446755 | AW451473 | Hs.16134 | NM_005990:Homo sapiens serine/threonine | 2.22 |
| | 452865 | AI924046 | Hs.119567 | Hs.119567:ESTs, Weakly similar to ALU1_H | 2.22 |
| 35 | 431393 | AW971493 | Hs.134269 | Hs.134269:ESTs, Weakly similar to 200439 | 2.22 |
| | 431890 | X17033 | Hs.271986 | NM_002203:Homo sapiens integrin, alpha 2 | 2.22 |
| | 428782 | X12830 | Hs.193400 | NM_000565:Homo sapiens interleukin 6 rec | 2.22 |
| | 446006 | NM_004403 | Hs.13530 | NM_004403:Homo sapiens deafness, autosom | 2.22 |
| | 436418 | AJ245874 | Hs.4245 | Hs.4245:chromosome 11 hypothetical prote | 2.22 |
| 40 | 423869 | BE409301 | Hs.134012 | NM_006688:Homo sapiens C1q-related facto | 2.21 |
| | 437730 | AW071087 | Hs.239176 | Hs.239176:insulin-like growth factor 1 r | 2.21 |
| | 444020 | R92962 | Hs.35052 | Hs.35052:ESTs | 2.21 |
| | 413882 | AA132973 | Hs.184492 | Hs.184492:Homo sapiens mR: cD DKFZp667B0 | 2.21 |
| | 412654 | AI093480 | Hs.374319 | Hs.374319:ESTs | 2.21 |
| 45 | 448988 | Y09763 | Hs.22785 | NM_004961:Homo sapiens gamma-aminobutyri | 2.21 |
| | 426841 | AI052358 | Hs.131741 | Hs.131741:ESTs | 2.21 |
| | 408196 | AL034548 | Hs.43627 | NM_006943:Homo sapiens SRY (sex determin | 2.21 |
| | 451711 | AK000461 | Hs.26890 | Hs.26890:cat eye syndrome chromosome reg | 2.20 |
| | 414325 | AA251929 | Hs.355341 | Hs.355341:Homo sapiens, clone IMAGE:3536 | 2.20 |
| 50 | 424512 | X53002 | Hs.149846 | NM_002213:Homo sapiens integrin, beta 5 | 2.20 |
| | 448883 | BE614989 | Hs.7503 | Hs.7503:hypothetical protein FLJ14153 | 2.20 |
| | 411296 | BE207307 | Hs.10114 | Hs.10114:growth suppressor 1 | 2.20 |
| | 452268 | NM_003512 | Hs.28777 | NM_003512:Homo sapiens H2A histone famil | 2.20 |
| | 416810 | AF035606 | Hs.80019 | NM_013232:Homo sapiens programmed cell d | 2.20 |
| 55 | 441415 | H21497 | Hs.7471 | Hs.7471:BBP-like protein 1 | 2.20 |
| | 444212 | AW503976 | Hs.10649 | NM_004848:Homo sapiens basement membrane | 2.19 |
| | 428044 | AA093322 | Hs.301404 | NM_006743:Homo sapiens R binding motif p | 2.19 |
| | 430017 | AA263172 | Hs.35 | NM_002832:Homo sapiens protein tyrosine | 2.19 |
| | 424490 | AJ278016 | Hs.55565 | Hs.55565:ankyrin repeat domain 3 | 2.19 |
| 60 | 431193 | AW749505 | Hs.296770 | Hs.296770:KIAA1719 protein | 2.19 |
| | 453686 | AL110326 | Hs.304679 | Hs.304679:ESTs, Weakly similar to Z195_H | 2.19 |
| | 448262 | AW880830 | Hs.186273 | Hs.186273:ESTs | 2.19 |
| | 416065 | BE267931 | Hs.78996 | NM_002592:Homo sapiens proliferating cel | 2.19 |
| | 442045 | C05768 | Hs.8078 | Hs.8078:Homo sapiens clone FBD3 Cri-du-c | 2.19 |
| 65 | 423804 | AW403448 | Hs.1706 | NM_006084:Homo sapiens interferon-stimul | 2.19 |
| | 428024 | Z29067 | Hs.2236 | Hs.2236:NIMA (never in mitosis gene a)-r | 2.19 |
| | 424503 | NM_002205 | Hs.149609 | NM_002205:Homo sapiens integrin, alpha 5 | 2.19 |
| | 437696 | Z83844 | Hs.5790 | Hs.5790:hypothetical protein dJ37E16.5 | 2.18 |
| | 405204 | | | | 2.18 |
| 70 | 426158 | NM_001982 | Hs.199067 | NM_001982:Homo sapiens v-erb-b2 erythro | 2.18 |
| | 417418 | NM_002468 | Hs.82116 | NM_002468:Homo sapiens myeloid different | 2.18 |
| | 412773 | H15785 | Hs.74573 | NM_012268:Homo sapiens similar to vacci | 2.18 |
| | 409402 | AF208234 | Hs.695 | NM_000100:Homo sapiens cystatin B (stefi | 2.18 |
| 75 | 443791 | N64458 | Hs.143345 | Hs.143345:ESTs | 2.18 |
| | 435049 | AL122067 | Hs.4746 | Hs.4746:hypothetical protein FLJ21324 | 2.18 |
| | 418389 | AA830613 | Hs.293849 | Hs.293849:ESTs | 2.18 |
| | 450712 | AJ732130 | Hs.270496 | Hs.270496:ESTs, Weakly similar to ALUB_H | 2.18 |
| | 422007 | AJ739435 | Hs.39168 | Hs.39168:ESTs, Weakly similar to T17340 | 2.18 |
| | 453676 | AW853745 | Hs.286035 | Hs.286035:hypothetical protein FLJ22686 | 2.18 |
| 80 | 415718 | F30631 | Hs.200237 | Hs.200237:ESTs | 2.18 |
| | 452688 | AA721140 | Hs.49930 | Hs.49930:ESTs, Weakly similar to B34087 | 2.18 |
| | 415988 | BE407713 | Hs.78943 | NM_000386:Homo sapiens bleomycin hydro | 2.18 |
| | 409453 | AI885516 | Hs.95612 | Hs.95612:ESTs | 2.17 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| 5 | 417512 | X76534 | Hs.82226 | NM_002510:Homo sapiens glycoprotein (tra | 2.17 |
| | 427202 | BE272922 | Hs.173936 | NM_000628:Homo sapiens interleukin 10 re | 2.17 |
| | 440983 | M20581 | Hs.7594 | NM_006931:Homo sapiens solute carrier fa | 2.17 |
| | 416084 | L16991 | Hs.79006 | NM_012145:Homo sapiens deoxythymidylate | 2.17 |
| | 429642 | X68264 | Hs.211579 | NM_006500:Homo sapiens melanoma adhesion | 2.17 |
| | 427213 | AW007211 | Hs.348389 | Hs.348389:hypothetical protein FLJ12876 | 2.17 |
| | 437763 | AA469369 | Hs.5831 | NM_003254:Homo sapiens tissue inhibitor | 2.17 |
| | 454000 | AA040620 | Hs.5672 | Hs.5672:golgi membrane protein S8140 | 2.17 |
| 10 | 424247 | X14008 | Hs.234734 | NM_000239:Homo sapiens lysozyme (rel amy | 2.16 |
| | 403857 | | | | 2.16 |
| | 406648 | AA563730 | Hs.277477 | Hs.277477:major histocompatibility compl | 2.16 |
| | 400265 | | | | 2.16 |
| | 442379 | NM_004613 | Hs.8265 | NM_004613:Homo sapiens transglutaminase 2 | 2.16 |
| 15 | 441892 | AB028981 | Hs.8021 | Hs.8021:KIAA1058 protein | 2.16 |
| | 417446 | AL118671 | Hs.82163 | NM_000898:Homo sapiens monoamine oxidase | 2.16 |
| | 418386 | AA361739 | Hs.84549 | NM_002494:Homo sapiens DH dehydrogenase (u | 2.16 |
| | 414053 | BE391635 | Hs.75725 | NM_003564:Homo sapiens transgelin 2 (TAG | 2.16 |
| | 440906 | AW161556 | Hs.240170 | Hs.240170:hypothetical protein MGC2731 | 2.16 |
| 20 | 447650 | AW160386 | Hs.163667 | Hs.163667:ESTs, Weakly similar to CA1H_H | 2.16 |
| | 408279 | AF216965 | Hs.44095 | Hs.44095:cyclin M3 | 2.16 |
| | 426152 | BE299190 | Hs.167246 | Hs.167246:P450 (cytochrome) oxidoreducta | 2.16 |
| | 437952 | D63209 | Hs.5944 | NM_014585:Homo sapiens solute carrier fa | 2.16 |
| | 415661 | AF057307 | Hs.78575 | Hs.78575:prosaposin (variant Gaucher dis | 2.15 |
| 25 | 425302 | U79115 | Hs.155566 | NM_003805:Homo sapiens CASP2 and RIPK1 d | 2.15 |
| | 425996 | W67330 | Hs.374451 | Hs.374451:ESTs | 2.15 |
| | 413745 | AW247252 | Hs.75514 | NM_000270:Homo sapiens nucleoside phosph | 2.15 |
| | 422070 | AF149785 | Hs.111126 | Hs.111126:pituitary tumor-transforming 1 | 2.15 |
| | 448424 | AW009892 | Hs.31924 | Hs.31924:ESTs | 2.15 |
| 30 | 430035 | NM_003463 | Hs.227777 | NM_003463:Homo sapiens protein tyrosine | 2.15 |
| | 438407 | AJ457122 | Hs.129673 | Hs.129673:eukaryotic translation initiat | 2.15 |
| | 435551 | AF212365 | Hs.5470 | Hs.5470:interleukin 17B receptor | 2.15 |
| | 437741 | BE561610 | Hs.5809 | Hs.5809:putative transmembrane protein; | 2.15 |
| | 441192 | AA526626 | Hs.7736 | NM_016504:Homo sapiens mitochondrial rib | 2.15 |
| 35 | 435750 | AB029012 | Hs.4990 | Hs.4990:KIAA1089 protein | 2.15 |
| | 411165 | NM_000169 | Hs.69089 | NM_000169:Homo sapiens galactosidase, al | 2.14 |
| | 425252 | AW391162 | Hs.349306 | Hs.349306:hypothetical protein FLJ31951 | 2.14 |
| | 427600 | AW630918 | Hs.179774 | NM_002818:Homo sapiens proteasome (proso | 2.14 |
| | 426818 | AA554827 | Hs.292936 | Hs.292936:postmeiotic segregation increa | 2.14 |
| 40 | 442110 | AF113008 | Hs.8102 | NM_001023:Homo sapiens ribosomal protein | 2.14 |
| | 407797 | AK000524 | Hs.39850 | Hs.39850:uridine kisse-like 1 | 2.14 |
| | 443044 | N28522 | Hs.8935 | NM_014298:Homo sapiens quinoline phospho | 2.14 |
| | 437103 | AW139408 | Hs.152940 | Hs.152940:ESTs | 2.14 |
| | 442069 | AW664144 | Hs.297007 | Hs.297007:Homo sapiens cD FLJ32174 fis | 2.14 |
| 45 | 424954 | NM_000546 | Hs.1846 | NM_000546:Homo sapiens tumor protein p53 | 2.14 |
| | 458097 | AW341135 | Hs.58104 | Hs.58104:Homo sapiens, clone IMAGE:47309 | 2.14 |
| | 411925 | AW014588 | Hs.72925 | NM_003475:Homo sapiens chromosome 11 ope | 2.14 |
| | 449644 | AW960707 | Hs.148324 | Hs.148324:ESTs | 2.14 |
| | 422675 | BE018517 | Hs.119140 | NM_001970:Homo sapiens eukaryotic transi | 2.14 |
| 50 | 428586 | M36712 | Hs.2299 | Hs.2299:CD8 antigen, beta polypeptide 1 | 2.14 |
| | 429379 | NM_014840 | Hs.200598 | NM_014840:Homo sapiens KIAA0537 gene pro | 2.13 |
| | 410290 | AA402307 | Hs.322844 | Hs.322844:hypothetical protein DKFZp564A | 2.13 |
| | 443695 | AW979048 | Hs.292566 | Hs.292566:YEA4 protein | 2.13 |
| | 428145 | BE243327 | Hs.182626 | NM_012264:Homo sapiens chromosome 22 ope | 2.13 |
| 55 | 453518 | AW503205 | Hs.27268 | Hs.27268:Homo sapiens cD: FLJ21933 fis | 2.13 |
| | 456534 | X91195 | Hs.100623 | Hs.100623:protein phosphatase 1, regulat | 2.13 |
| | 419972 | AL041465 | Hs.182982 | Hs.182982:golgin-57 | 2.13 |
| | 424950 | AA602917 | Hs.156974 | Hs.156974:ESTs | 2.13 |
| | 427557 | NM_002659 | Hs.179657 | NM_002659:Homo sapiens plasminogen activ | 2.13 |
| 60 | 431449 | M55994 | Hs.256278 | NM_001066:Homo sapiens tumor necrosis fa | 2.13 |
| | 418758 | AW959311 | Hs.172012 | Hs.172012:hypothetical protein DKFZp434J | 2.13 |
| | 434202 | BE382411 | Hs.3764 | NM_000858:Homo sapiens guanylate kisse 1 | 2.13 |
| | 433233 | AB040927 | Hs.301804 | Hs.301804:KIAA1494 protein | 2.12 |
| | 452700 | AJ859390 | Hs.288940 | Hs.288940:transmembrane protein 8 (five | 2.12 |
| 65 | 438033 | T26483 | Hs.6059 | NM_016938:Homo sapiens EGF-containing fi | 2.12 |
| | 400847 | | | | 2.12 |
| | 447547 | NM_007229 | Hs.18842 | NM_007229:Homo sapiens protein kisse C an | 2.12 |
| | 417052 | NM_000712 | Hs.81029 | NM_000712:Homo sapiens biliverdin reduct | 2.12 |
| | 413284 | AU077055 | Hs.289107 | NM_001166:Homo sapiens baculoviral IAP r | 2.11 |
| 70 | 434558 | AW264102 | Hs.39168 | Hs.39168:ESTs, Weakly similar to T17340 | 2.11 |
| | 404030 | | | | 2.11 |
| | 410801 | BE275469 | Hs.66493 | Hs.66493:Down syndrome critical region g | 2.11 |
| | 418613 | AA744529 | Hs.86575 | Hs.86575:mitogen-activated protein kisse | 2.11 |
| | 447087 | AW403870 | Hs.301872 | Hs.301872:hypothetical protein MGC4840 | 2.11 |
| 75 | 433026 | AW160616 | Hs.279921 | NM_016127:Homo sapiens hypothetical prot | 2.11 |
| | 426433 | L38969 | Hs.169875 | NM_007112:Homo sapiens thrombospondin 3 | 2.11 |
| | 442439 | U09759 | Hs.246857 | NM_002752:Homo sapiens mitogen-activated | 2.11 |
| | 437379 | AL359575 | Hs.23765 | Hs.23765:membrane metallo-endopeptidase- | 2.11 |
| | 400208 | | | | 2.11 |
| 80 | 455705 | AW161061 | Hs.356580 | Hs.356580:ESTs, Weakly similar to zinc f | 2.11 |
| | 417599 | AA204688 | Hs.62954 | Hs.62954:feritin, heavy polypeptide 1 | 2.10 |
| | 415728 | AB024597 | Hs.79658 | NM_001894:Homo sapiens casein kisse 1, ep | 2.10 |
| | 439920 | H05430 | Hs.288433 | Hs.288433:neurotrophin | 2.10 |
| | 422309 | U79745 | Hs.114924 | NM_004694:Homo sapiens solute carrier fa | 2.10 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 436114 | AA778232 | Hs.19515 | Hs.19515:ESTs, Highly similar to NRG3_HU | 2.10 |
| | 405517 | | | | 2.10 |
| | 421872 | AA359753 | Hs.22824 | Hs.22824:MYB binding protein (P160) 1a | 2.10 |
| | 437712 | X04588 | Hs.85844 | Hs.85844:neurotrophic tyrosine kise, rec | 2.10 |
| 5 | 431214 | AA294921 | Hs.348024 | NM_002881:Homo sapiens v-ra simian leuk | 2.10 |
| | 412856 | BE386745 | Hs.74631 | NM_001728:Homo sapiens basigin (BSG), mR | 2.10 |
| | 442054 | AI422867 | Hs.88594 | Hs.88594:Homo sapiens, clone IMAGE:43329 | 2.10 |
| | 434845 | BE267057 | Hs.325321 | Hs.325321:WD repeat domain 18 | 2.10 |
| | 426728 | NM_007118 | Hs.367689 | NM_007118:Homo sapiens triple functioi d | 2.10 |
| 10 | 419596 | BE379320 | Hs.91448 | NM_007026:Homo sapiens dual specificity | 2.09 |
| | 448913 | AA194422 | Hs.22564 | NM_004999:Homo sapiens myosin VI (MYO6), | 2.09 |
| | 414721 | X90392 | Hs.77091 | NM_006730:Homo sapiens deoxynucleotidase | 2.09 |
| | 424658 | NM_002406 | Hs.151513 | NM_002406:Homo sapiens mannosyl (alpha-1 | 2.09 |
| 15 | 432805 | X94630 | Hs.3107 | Hs.3107:CD97 antigen | 2.09 |
| | 447032 | AK000310 | Hs.17138 | Hs.17138:hypothetical protein FLJ20303 | 2.09 |
| | 447484 | AA464839 | Hs.292566 | Hs.292566:YEA4 protein | 2.09 |
| | 440188 | AK001812 | Hs.7036 | Hs.7036:N-acetylglucosamine kise | 2.09 |
| | 445584 | AF217518 | Hs.8360 | Hs.8360:PTD012 protein | 2.09 |
| | 402559 | | | | 2.09 |
| 20 | 418043 | AW377752 | Hs.83341 | Hs.83341:AXL receptor tyrosine kise | 2.09 |
| | 448888 | AW196663 | Hs.200242 | Hs.200242:caspase recruitment domain fam | 2.09 |
| | 436910 | AA926944 | Hs.261587 | Hs.261587:GCN2 eIF2alpha kise | 2.09 |
| | 422573 | AW297985 | Hs.295726 | Hs.295726:integrin, alpha V (vitronectin | 2.08 |
| 25 | 416448 | L13210 | Hs.79339 | NM_005567:Homo sapiens lectin, galactosi | 2.08 |
| | 428727 | AF078847 | Hs.191356 | NM_001515:Homo sapiens general transcrip | 2.08 |
| | 410301 | AW502935 | Hs.740 | Hs.740:PTK2 protein tyrosine kise 2 | 2.08 |
| | 449538 | AI559444 | Hs.104679 | Hs.104679:Homo sapiens, clone MGC:18216 | 2.08 |
| | 421205 | AL137540 | Hs.102541 | Hs.102541:netrin 4 | 2.08 |
| | 411779 | AA292811 | Hs.72050 | NM_003551:Homo sapiens non-metastatic ce | 2.08 |
| 30 | 427704 | AW971063 | Hs.292882 | Hs.292882:ESTs | 2.07 |
| | 413518 | BE149455 | Hs.75415 | NM_004048:Homo sapiens beta-2-microglu | 2.07 |
| | 447345 | BE247767 | Hs.18166 | Hs.18166:KIAA0870 protein | 2.07 |
| | 407143 | C14076 | Hs.332329 | Hs.332329:EST | 2.07 |
| 35 | 448431 | BE613061 | Hs.337772 | Hs.337772:hypothetical protein BC009331 | 2.07 |
| | 412760 | AW379030 | Hs.41324 | Hs.41324:ESTs | 2.07 |
| | 446859 | AI494299 | Hs.16297 | NM_005694:Homo sapiens COX17 homolog, cy | 2.07 |
| | 403966 | | | | 2.07 |
| | 409115 | AI223335 | Hs.50651 | NM_002227:Homo sapiens Janus kise 1 (a p | 2.07 |
| 40 | 436823 | AW749865 | Hs.117077 | Hs.117077:zinc finger protein 264 | 2.07 |
| | 414045 | NM_002951 | Hs.75722 | NM_002951:Homo sapiens ribophorin II (RP | 2.06 |
| | 413980 | NM_002437 | Hs.75659 | NM_002437:Homo sapiens MpV17 transgene, | 2.06 |
| | 439414 | NM_001183 | Hs.6551 | NM_001183:Homo sapiens ATPase, H+ transp | 2.06 |
| | 426059 | BE292842 | Hs.166120 | NM_001572:Homo sapiens interferon regula | 2.06 |
| 45 | 429849 | U33053 | Hs.2499 | NM_002741:Homo sapiens protein kise C-li | 2.06 |
| | 402424 | | | | 2.06 |
| | 406626 | X04526 | Hs.215595 | Hs.215595:guanine nucleotide binding pro | 2.06 |
| | 458911 | AA373131 | Hs.24322 | Hs.24322:ATPase, H+ transporting, lysoso | 2.05 |
| | 426086 | T94907 | Hs.188572 | Hs.188572:ESTs | 2.05 |
| 50 | 419726 | U50330 | Hs.1274 | NM_006129:Homo sapiens bone morphogeneti | 2.05 |
| | 452344 | AI264357 | Hs.55405 | Hs.55405:hypothetical protein MGC16212 | 2.05 |
| | 442498 | U54617 | Hs.8364 | NM_002612:Homo sapiens pyruvate dehydrog | 2.05 |
| | 422114 | AW194851 | Hs.111801 | NM_015908:Homo sapiens arsete resistance | 2.05 |
| | 413420 | AW410235 | Hs.75348 | NM_006263:Homo sapiens proteasome (proso | 2.05 |
| 55 | 409430 | R21945 | Hs.346735 | Hs.346735:Homo sapiens, clone IMAGE:3881 | 2.05 |
| | 409932 | AI376750 | Hs.57600 | Hs.57600:adaptor-related protein complex | 2.05 |
| | 434848 | BE256304 | Hs.32148 | Hs.32148:AD-015 protein | 2.04 |
| | 453852 | AW961818 | Hs.374424 | Hs.374424:ESTs | 2.04 |
| | 427637 | AK000816 | Hs.179986 | NM_005803:Homo sapiens flotillin 1 (FLOT | 2.04 |
| | 400264 | | | | 2.04 |
| 60 | 430016 | NM_004736 | Hs.227656 | NM_004736:Homo sapiens xenotropic and po | 2.04 |
| | 410134 | U68140 | Hs.58927 | Hs.58927:nuclear VCP-like | 2.04 |
| | 440975 | AW499914 | Hs.7579 | Hs.7579:importin 9 | 2.04 |
| | 432280 | BE440142 | Hs.2943 | NM_003135:Homo sapiens sigl recognition | 2.04 |
| 65 | 409504 | AA304961 | Hs.699 | NM_000942:Homo sapiens peptidylprolyl is | 2.04 |
| | 412146 | M92444 | Hs.73722 | NM_001641:Homo sapiens APEX nuclease (mu | 2.04 |
| | 434203 | BE262677 | Hs.283558 | Hs.283558:hypothetical protein PRO1855 | 2.04 |
| | 422754 | AA316476 | Hs.171811 | Hs.171811:adenylate kise 2 | 2.04 |
| | 406729 | AA069711 | | AA069711:zm52b11.s1 Stratagene fibroblas | 2.04 |
| 70 | 413086 | AA126841 | Hs.183834 | Hs.183834:ESTs | 2.03 |
| | 424340 | AA339036 | Hs.7033 | Hs.7033:ESTs | 2.03 |
| | 450440 | AB024334 | Hs.25001 | NM_012479:Homo sapiens tyrosine 3-monoox | 2.03 |
| | 424662 | NM_002870 | Hs.151536 | NM_002870:Homo sapiens RAB13, member RAS | 2.03 |
| | 415740 | N80486 | Hs.39911 | Hs.39911:Homo sapiens mR for FLJ00089 pr | 2.03 |
| 75 | 412749 | AA378417 | Hs.74564 | NM_003145:Homo sapiens sigl sequence rec | 2.03 |
| | 408393 | AW015318 | Hs.23165 | Hs.23165:ESTs | 2.03 |
| | 421295 | AW081061 | Hs.103180 | Hs.103180:DC2 protein | 2.03 |
| | 445417 | AK001058 | Hs.12680 | Hs.12680:Homo sapiens cD FLJ10196 fis, c | 2.03 |
| | 414883 | AA926960 | Hs.348669 | NM_001826:Homo sapiens CDC28 protein kis | 2.03 |
| 80 | 447298 | BE617527 | Hs.239818 | Hs.239818:phosphoinositide-3-kise, catal | 2.02 |
| | 459580 | AA022888 | Hs.176065 | Hs.176065:ESTs | 2.02 |
| | 422785 | AI824114 | Hs.289088 | Hs.289088:heat shock 90kD protein 1, atp | 2.02 |
| | 452696 | AI826645 | Hs.211534 | Hs.211534:Homo sapiens cD FLJ31665 fis, | 2.02 |
| | 452056 | AW955065 | Hs.101150 | Hs.101150:KIAA1949 protein | 2.02 |

| | | | | | | |
|------------|---------------------------|--|---|--|--|------|
| 5 | 450690 | AA296696 | Hs.333418 | NM_014164:Homo sapiens FXRD domain-conta | 2.02 | |
| | 423527 | A1206965 | Hs.105861 | Hs.105861:engulfment and cell motility 3 | 2.01 | |
| | 429545 | A1824164 | Hs.356130 | Hs.356130:ESTs | 2.01 | |
| | 439180 | A1393742 | Hs.199067 | Hs.199067:v-erb-b2 erythroblastic leukem | 2.01 | |
| | 437193 | BE259190 | Hs.289721 | Hs.289721:growth arrest-specific 5 | 2.01 | |
| | 436014 | AF281134 | Hs.283741 | Hs.283741:exosome component Rrp46 | 2.01 | |
| | 453329 | T97205 | Hs.193400 | Hs.193400:interleukin 6 receptor | 2.01 | |
| | 407347 | AA829847 | | TZ3514:seq3329 1-NIB Homo sapiens cD clo | 2.01 | |
| | 435370 | AJ964074 | Hs.225838 | Hs.225838:ESTs | 2.01 | |
| | 10 | 430657 | AA482910 | Hs.370602 | Hs.370602:ESTs, Weakly similar to hypoth | 2.01 |
| 15 | 427157 | U51166 | Hs.173824 | NM_003211:Homo sapiens thymine-D glycosy | 2.01 | |
| | 424833 | NM_003894 | Hs.153405 | NM_003894:Homo sapiens period homolog 2 | 2.01 | |
| | 440086 | NM_005402 | Hs.6906 | NM_005402:Homo sapiens v-ral simian leuk | 2.01 | |
| | 438543 | AA810141 | Hs.192182 | Hs.192182:ESTs | 2.01 | |
| | 417426 | NM_002291 | Hs.82124 | NM_002291:Homo sapiens laminin, beta 1 (| 2.01 | |
| | 412790 | NM_014767 | Hs.74583 | NM_014767:Homo sapiens KIAA0275 gene pro | 2.01 | |
| | 445892 | AV655500 | Hs.93961 | Hs.93961:Homo sapiens mR: cD DKFZp667D09 | 2.01 | |
| | 20 | TABLE 39B: | | | | |
| | Pkey: | Unique Eos probeset identifier number | | | | |
| | CAT number: | Gene cluster number | | | | |
| Accession: | Genbank accession numbers | | | | | |
| 25 | Pkey | CAT Number | Accession | | | |
| | 409745 | MH1944_5 | B1030997 AA921874 AW188822 B1027862 A1347618 A1361453 A1088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 B1007625 B1027864 B1009100 B1006275 B1006270 B1031000 B1029864 B1006277 B1007627 B1006266 B1006991 B1006990 B1007763 B1007762 BG997377 AA150780 B1033518 B1027818 BG015789 B1033807 AA341445 AA229762 AA230035 | | | |
| 30 | 418869 | 12789_14 | BG171436 BE079601 BE079534 AA299964 BE392717 BE883402 BE079532 BE018148 BF889427 W00396 | | | |
| | 421902 | 276321_1 | BC013310 AF261085 BC004109 AY007133 BC009081 BC001601 NM_002046 M33197 BC020308 J02642 M36164 BE794233 AV721080 BE255459 BG926429 BG389312 BG477333 A1031799 B1763443 B1260432 AA989106 AV728576 B1091380 AA402499 A1200513 A1284734 A1223995 A1289749 BG283291 BM013814 AW438544 BM450203 F35435 F33262 BE890952 AA401181 BG939668 F35525 B1088182 F34674 F33506 BM471326 F34677 | | | |
| 35 | 400231 | MH494_5 | AW276712 AA187508 F34866 AA114245 AA522581 N23935 A1076923 A1018505 BE879774 BM465637 A1753078 BG222159 AA595947 BF970917 B1094125 AA179841 BE893087 BG775178 BE793983 BE797071 BF339134 BE409272 BE266456 BE796770 BE745957 BG755835 BE266758 BE259342 BM450181 BG748174 BE299322 BM423587 BM467637 BM452667 BM479516 BM452420 BE273297 BM466364 BM450640 BM478743 BM462924 BM455329 BM471815 B1862301 BG331736 H04903 AA374894 BE902964 | | | |
| 40 | 438584 | 1241536_1 | AW977949 AA811347 D79715 | | | |
| | 413020 | 1485885_1 | BE048113 R98736 Z42904 | | | |
| | 400265 | 1145_1 | X58141 NM_001119 A1246786 BE645243 A1685698 A1208590 BE222576 A1191715 A1423108 BF064068 BG057819 A1208589 A1880535 A1262890 A1246261 BF939926 A1282848 A1802409 BE301053 A1884624 A1160385 A1335983 BF440017 BG231884 A1343699 A1280745 A1871338 A1123739 A1871126 AW080375 A1350160 A1300855 A1818598 A1085263 A1306653 AW571658 BF109839 AW273280 A1888380 A1571860 A1357126 AW194105 A1131474 AW316548 AW128942 AW571682 A1583962 AW300674 BF509394 A1891077 BF221538 A1651874 F25731 AW881176 A1685962 D44936 A1753874 BF593905 BE832830 A1637970 BE834103 BE464301 A1908017 A1378261 AA975416 R16732 H47612 H45402 AA668719 AA722441 AA991443 T51951 AW514058 A1277763 AA421907 A1083831 H40630 NM_014190 BM469282 AL524786 AL527067 BF313768 AL042441 AL037806 B1195013 BE219292 BF055534 T95785 BE833037 AV648052 AA382588 W67987 H46049 R92289 H47699 AA380016 AL532433 BG958742 A1292151 H26003 R62487 BG766512 BE815124 AW136122 H96767 R39407 B1044500 H18771 H22071 R09985 R75803 H42172 BE770251 AL529310 F03180 R92185 H18680 R43192 AA401390 AA977941 A1091944 AA993369 AA617840 H14351 A1866242 A1915028 AA780787 AA506995 AA827496 AA634305 AA846358 AA470463 AA618163 AA601963 W74212 AA021520 AA421274 AA903521 AA411402 AA044448 AA983449 AA076114 AA633470 AA581793 AA019060 AA814222 AA693469 N99931 N67840 R26834 BF342340 AA976636 AA360268 AA976223 T95786 AA527774 A1620298 A180888 A149218 AA565201 B1001597 BE676565 AW169797 AW190994 AA299572 A1092819 A1291438 AA459586 AA136373 R50213 BE622752 AA401414 AA180973 AA766800 W96432 B1550308 H52236 AA491029 BG420468 BG827522 | | | |
| 45 | 400208 | 16640_1 | X78817 NM_001666 D50921 AW002308 AW575456 BF507511 AW467767 A1910663 BF905778 BG251264 AL562106 A1890538 AW769258 A1590391 A1913055 AW083235 A1078474 A1925022 AW504628 AW129725 BE466589 AW002786 AW591760 A1968816 AW006268 AW593787 BG236814 AW769893 AW407608 AW075982 A1248207 A1762509 A1812070 A1249937 AW083581 AW080697 BF663046 BG745612 BG979546 AW793245 B1014177 AL519126 BE675314 AW806520 B1870778 BF879549 BE714919 BF847786 BG684161 AV695278 BG491029 BE793244 BE830893 | | | |
| 50 | 400264 | 1145_1 | X58141 NM_001119 A1246786 BE645243 A1685698 A1208590 BE222576 A1191715 A1423108 BF064068 BG057819 A1208589 A1880535 A1262890 A1246261 BF939926 A1282848 A1802409 BE301053 A1884624 A1160385 A1335983 BF440017 BG231884 A1343699 A1280745 A1871338 A1123739 A1871126 AW080375 A1350160 A1300855 A1818598 A1085263 A1306653 AW571658 BF109839 AW273280 A1888380 A1571860 A1357126 AW194105 A1131474 AW316548 AW128942 AW571682 A1583962 AW300674 BF509394 A1891077 BF221538 A1651874 F25731 AW881176 A1685962 D44936 A1753874 BF593905 BE832830 A1637970 BE834103 BE464301 A1908017 A1378261 AA975416 R16732 H47612 H45402 AA668719 AA722441 AA991443 T51951 AW514058 A1277763 AA421907 A1083831 H40630 NM_014190 BM469282 AL524786 AL527067 BF313768 AL042441 AL037806 B1195013 BE219292 BF055534 T95785 BE833037 AV648052 AA382588 W67987 H46049 R92289 H47699 AA380016 AL532433 BG958742 A1292151 H26003 R62487 BG766512 BE815124 AW136122 H96767 R39407 B1044500 H18771 H22071 R09985 R75803 H42172 BE770251 AL529310 F03180 R92185 H18680 R43192 AA401390 AA977941 A1091944 AA993369 AA617840 H14351 A1866242 A1915028 AA780787 AA506995 AA827496 AA634305 AA846358 AA470463 AA618163 AA601963 W74212 AA021520 AA421274 AA903521 AA411402 AA044448 AA983449 AA076114 AA633470 AA581793 AA019060 AA814222 AA693469 N99931 N67840 R26834 BF342340 AA976636 AA360268 AA976223 T95786 AA527774 A1620298 A180888 A149218 AA565201 B1001597 BE676565 AW169797 AW190994 AA299572 A1092819 A1291438 AA459586 AA136373 R50213 BE622752 AA401414 AA180973 AA766800 W96432 B1550308 H52236 AA491029 BG420468 BG827522 | | | |
| 55 | 406729 | 0_0 | AA069711 | | | |
| | 407347 | 810943_1 | TZ3514 A1655785 | | | |
| 60 | TABLE 39C: | | | | | |
| | Pkey: | Unique number corresponding to an Eos probeset | | | | |
| | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. | | | | |
| | Strand: | Indicates DNA strand from which exons were predicted. | | | | |
| 65 | Nt_position: | Indicates nucleotide positions of predicted exons. | | | | |
| 70 | Pkey | Ref | Strand | Nt_position | | |
| | 404240 | 5002624 | Minus | 116132-116407,116653-116922 | | |
| | 404277 | 1834458 | Minus | 91665-91946 | | |
| 75 | TABLE 39C: | | | | | |
| | Pkey: | Unique number corresponding to an Eos probeset | | | | |
| | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. | | | | |
| | Strand: | Indicates DNA strand from which exons were predicted. | | | | |
| 80 | Nt_position: | Indicates nucleotide positions of predicted exons. | | | | |
| | Pkey | Ref | Strand | Nt_position | | |
| | 404240 | 5002624 | Minus | 116132-116407,116653-116922 | | |
| | 404277 | 1834458 | Minus | 91665-91946 | | |

| | | | | |
|----|--------|---------|-------|-----------------------------|
| 5 | 401179 | 9438647 | Plus | 113477-113893 |
| | 405102 | 8076881 | Minus | 120922-121296 |
| | 402575 | 9884830 | Minus | 109742-109883 |
| | 402901 | 8894222 | Minus | 175426-175657 |
| | 405204 | 7230116 | Plus | 126569-126754 |
| 10 | 403857 | 7708910 | Minus | 2524-3408 |
| | 400847 | 9188605 | Plus | 44643-44835 |
| | 404030 | 7671252 | Plus | 149362-151749 |
| | 405517 | 9454624 | Plus | 114757-114877 |
| | 402559 | 9864273 | Plus | 33539-33715 |
| 15 | 403966 | 8568881 | Plus | 158193-158277,160116-160290 |
| | 402424 | 9796344 | Minus | 64925-65073 |

TABLE 40A: ABOUT 977 GENES UP-REGULATED IN STOMACH CANCER

Table 40A lists about 977 genes up-regulated in stomach cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" stomach cancer to "average" normal adult tissues was greater than or equal to 2.0. The "average" stomach cancer level was set to the 90th percentile amongst various stomach cancers. The "average" normal adult tissue level was set to the 90th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal adult tissues

| Pkey | ExAccn | UnigenelD | Unigene Title | R1 |
|--------|-----------|-----------|---|-------|
| 411243 | AB039886 | Hs.69319 | CA11 | 30.66 |
| 418007 | M13509 | Hs.83169 | matrix metalloproteinase 1 (interstitial | 16.94 |
| 444325 | AW152618 | Hs.16757 | ESTs | 13.51 |
| 445891 | AW391342 | Hs.199460 | ESTs | 11.92 |
| 448811 | A1590371 | Hs.174759 | ESTs | 11.08 |
| 431723 | AW058350 | Hs.16762 | Homo sapiens mRNA; cDNA DKFZp564B2062 (f | 10.84 |
| 409757 | NM_001898 | Hs.123114 | cystatin SN | 10.38 |
| 421110 | AJ250717 | Hs.1355 | cathepsin E | 9.11 |
| 428368 | BE440042 | Hs.83326 | matrix metalloproteinase 3 (stromelysin | 8.66 |
| 446998 | N99013 | Hs.16762 | Homo sapiens mRNA; cDNA DKFZp564B2062 (f | 8.50 |
| 406687 | M31126 | Hs.272620 | pregnancy specific beta-1-glycoprotein 9 | 7.11 |
| 428651 | AF196478 | Hs.188401 | annexin A10 | 6.86 |
| 425211 | M18667 | Hs.1867 | progastricsin (pepsinogen C) | 6.51 |
| 423673 | BE003054 | Hs.1695 | matrix metalloproteinase 12 (macrophage | 6.49 |
| 409683 | U33317 | Hs.711 | defensin, alpha 6, Paneth cell-specific | 6.39 |
| 422260 | AA315993 | Hs.105484 | ESTs, Weakly similar to UTB_HUMAN LITHO | 6.31 |
| 428664 | AK001666 | Hs.189095 | similar to SALL1 (sal (Drosophila)-like | 6.25 |
| 409041 | AB033025 | Hs.50081 | KIAA1199 protein | 5.72 |
| 408380 | AF123050 | Hs.44532 | diubiquitin | 5.72 |
| 428953 | AA306610 | Hs.194676 | DKFZP434C013 protein | 5.46 |
| 450685 | L15533 | Hs.423 | pancreatitis-associated protein | 5.40 |
| 409187 | AF154830 | Hs.50966 | carbamoyl-phosphate synthetase 1, mitoch | 5.34 |
| 434206 | AW136973 | Hs.288516 | ESTs, Weakly similar to S69890 mitogen i | 5.16 |
| 421346 | Z34277 | Hs.103707 | apomucin | 5.14 |
| 427585 | D31152 | Hs.179729 | collagen, type X, alpha 1 (Schmid metaph | 5.06 |
| 425679 | X05997 | Hs.159177 | lipase, gastric | 4.94 |
| 421582 | A1910275 | Hs.1406 | trefoil factor 1 (breast cancer, estroge | 4.93 |
| 434414 | A1798376 | Hs.122579 | gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens | 4.92 |
| 422956 | BE545072 | Hs.170675 | hypothetical protein FLJ10461 | 4.89 |
| 448105 | AW591433 | Hs.163443 | ESTs, Weakly similar to TMS2_HUMAN TRANS | 4.84 |
| 423575 | C18863 | Hs.840 | Homo sapiens cDNA FLJ11576 fis, clone HE | 4.72 |
| 413385 | M34455 | Hs.82772 | indoleamine-pyrrole 2,3 dioxygenase | 4.72 |
| 417866 | AW067903 | Hs.228320 | collagen, type XI, alpha 1 | 4.68 |
| 448693 | AW004854 | Hs.202656 | Homo sapiens cDNA: FLJ23537 fis, clone L | 4.53 |
| 441377 | BE218239 | Hs.1247 | ESTs | 4.51 |
| 419278 | AU076799 | Hs.40098 | apolipoprotein A-IV | 4.48 |
| 407811 | AW190902 | | cysteine knot superfamily 1, BMP antagon | 4.47 |
| 403422 | | | | 4.38 |
| 403776 | | | | 4.32 |
| 418478 | U38945 | Hs.1174 | cyclin-dependent kinase inhibitor 2A (me | 4.32 |
| 428242 | H55709 | Hs.2250 | leukemia inhibitory factor (cholinergic | 4.30 |
| 421341 | AJ243212 | Hs.279611 | deleted in malignant brain tumors 1 | 4.30 |
| 451181 | A1796330 | Hs.207461 | ESTs | 4.26 |
| 432168 | AK000563 | Hs.272805 | hypothetical protein FLJ20556 | 4.23 |
| 454464 | AW811606 | Hs.271819 | Homo sapiens cDNA: FLJ22751 fis, clone K | 4.20 |
| 448844 | A1581519 | Hs.177164 | ESTs | 4.14 |
| 428434 | AW363590 | Hs.65551 | ESTs, Weakly similar to AF172993 1 PLUNC | 4.13 |
| 452461 | N78223 | Hs.108106 | transcription factor | 4.08 |
| 409420 | Z15008 | Hs.54451 | laminin, gamma 2 (nicein (100xD), klatini | 4.04 |
| 431611 | U58766 | Hs.264428 | tissue specific transplantation antigen | 4.04 |
| 413719 | BE439580 | Hs.75498 | small inducible cytokine subfamily A (Cy | 4.03 |
| 430044 | AA464510 | Hs.152812 | ESTs | 4.02 |
| 409956 | AW103364 | Hs.1524 | inhibin, beta A (activin A, activin AB a | 4.01 |
| 422420 | U03398 | Hs.99785 | tumor necrosis factor (ligand) superfam | 4.00 |
| 420159 | A1572490 | | Homo sapiens cDNA: FLJ21245 fis, clone C | 3.98 |
| 428227 | AA321649 | Hs.2248 | small inducible cytokine subfamily B (Cy | 3.91 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| 5 | 422168 | AA586894 | Hs.112408 | S100 calcium-binding protein A7 (psorias | 3.87 |
| | 452304 | AA025386 | Hs.61311 | ESTs, Weakly similar to S10590 cysteine | 3.84 |
| | 412140 | AA219691 | Hs.73625 | RAB6 interacting, kinesin-like (rab6ines | 3.82 |
| | 414812 | X72755 | Hs.77367 | monokine induced by gamma interferon | 3.81 |
| | 419833 | AA251131 | Hs.220697 | ESTs | 3.81 |
| | 446232 | AI281848 | Hs.165547 | ESTs | 3.74 |
| | 432398 | AA307808 | Hs.2979 | trefol factor 2 (spasmodic protein 1) | 3.70 |
| | 451105 | AI761324 | | gb:wi60b11.x1 NC1_CGAP_Co16 Homo sapiens | 3.67 |
| 10 | 413281 | AA861271 | Hs.34396 | ESTs | 3.66 |
| | 432867 | AW016936 | Hs.233364 | ESTs | 3.66 |
| | 424046 | AF027866 | Hs.138202 | serine (or cysteine) proteinase inhibitor | 3.65 |
| | 457465 | AW301344 | Hs.195969 | ESTs | 3.65 |
| | 414918 | AI219207 | Hs.72222 | Homo sapiens cDNA FLJ13459 fs, clone PL | 3.61 |
| 15 | 418738 | AW388633 | Hs.6682 | ESTs | 3.60 |
| | 427778 | AA412323 | Hs.105323 | ESTs | 3.60 |
| | 454293 | H49739 | Hs.134013 | ESTs, Moderately similar to NK homeobox | 3.59 |
| | 452194 | AI694413 | Hs.298262 | ESTs, Weakly similar to dJ88J8.1 (H.sapi | 3.57 |
| | 442577 | AA292998 | Hs.163900 | ESTs | 3.57 |
| 20 | 426174 | AA547959 | Hs.115838 | ESTs | 3.53 |
| | 452862 | AW378065 | Hs.8687 | ESTs | 3.51 |
| | 418869 | AW516565 | Hs.258279 | ESTs | 3.48 |
| | 430178 | AW449612 | Hs.152475 | ESTs | 3.48 |
| | 430397 | AI924533 | Hs.105607 | ESTs | 3.46 |
| 25 | 418054 | NM_002318 | Hs.83354 | lysyl oxidase-like 2 | 3.45 |
| | 442295 | AI827248 | Hs.224398 | Homo sapiens cDNA FLJ11469 fs, clone HE | 3.44 |
| | 425921 | NM_007231 | Hs.162211 | solute carrier family 6 (neurotransmitter | 3.44 |
| | 431764 | AA515212 | Hs.271819 | Homo sapiens cDNA: FLJ22751 fs, clone K | 3.43 |
| | 421948 | L42583 | Hs.111758 | keratin 6A | 3.43 |
| 30 | 444381 | BE387335 | Hs.283713 | ESTs, Weakly similar to CA54_HUMAN COLLA | 3.41 |
| | 442896 | R37725 | Hs.261108 | ESTs | 3.41 |
| | 452281 | T93500 | Hs.28792 | Homo sapiens cDNA FLJ11041 fs, clone PL | 3.39 |
| | 444783 | AK001468 | Hs.62180 | anillin (Drosophila Scraps homolog), act | 3.39 |
| | 408832 | AW085690 | Hs.63428 | ESTs | 3.39 |
| 35 | 406585 | M18728 | | gb:Human nonspecific crossreacting antig | 3.37 |
| | 437527 | AI241019 | Hs.145644 | ESTs | 3.37 |
| | 433084 | M18079 | Hs.282265 | fatty acid binding protein 2, intestinal | 3.37 |
| | 452401 | NM_007115 | Hs.29352 | tumor necrosis factor, alpha-induced pro | 3.36 |
| | 441318 | AI078234 | Hs.176130 | ESTs | 3.35 |
| 40 | 458897 | U85642 | Hs.138506 | ESTs | 3.33 |
| | 413808 | J00287 | Hs.182183 | caldesmon 1 | 3.33 |
| | 411274 | NM_002776 | Hs.69423 | kalikrein 10 | 3.32 |
| | 418406 | X73501 | Hs.84905 | cytokeratin 20 | 3.32 |
| | 419559 | Y07828 | Hs.91096 | ring finger protein | 3.32 |
| 45 | 423217 | NM_000094 | Hs.1640 | collagen, type VII, alpha 1 (epidermolys | 3.31 |
| | 423271 | W47225 | Hs.126256 | interleukin 1, beta | 3.31 |
| | 411558 | AA102670 | Hs.70725 | gamma-aminobutyric acid (GABA) A recepto | 3.30 |
| | 427722 | AK000123 | Hs.180479 | hypothetical protein FLJ20116 | 3.30 |
| | 422310 | AA316622 | Hs.98370 | cytochrome P540 family member predicted | 3.29 |
| 50 | 430704 | AW813091 | | gb:RC3-ST0186-240400-111-d07 ST0186 Homo | 3.29 |
| | 411263 | BE297802 | Hs.69360 | kinesin-like 6 (mitotic centromere-assoc | 3.29 |
| | 443211 | AI128388 | Hs.143655 | ESTs | 3.29 |
| | 443426 | AF098158 | Hs.9329 | chromosome 20 open reading frame 1 | 3.28 |
| | 441085 | AW136551 | Hs.181245 | Homo sapiens cDNA FLJ12532 fs, clone NT | 3.28 |
| 55 | 452121 | NM_004081 | Hs.70936 | deleted in azoospermia | 3.27 |
| | 408633 | AW963372 | Hs.46677 | PRO2000 protein | 3.27 |
| | 447342 | AI199268 | Hs.19322 | ESTs | 3.25 |
| | 419229 | AI827237 | Hs.282884 | ESTs | 3.24 |
| | 443957 | AA521049 | Hs.34487 | hypothetical protein FLJ23412 | 3.23 |
| 60 | 452699 | AW295390 | Hs.213062 | ESTs | 3.23 |
| | 425188 | AK002052 | Hs.155071 | hypothetical protein FLJ11190 | 3.23 |
| | 400289 | X07820 | Hs.2258 | matrix metalloproteinase 10 (stromelysin | 3.21 |
| | 408524 | D87942 | Hs.46328 | fucosyltransferase 2 (secretor status in | 3.20 |
| 65 | 437897 | AA770561 | Hs.146170 | hypothetical protein FLJ22969 | 3.20 |
| | 453922 | AF053306 | Hs.36708 | budding uninhibited by benzimidazoles 1 | 3.19 |
| | 453160 | AI263307 | Hs.146228 | ESTs | 3.19 |
| | 406690 | M29540 | Hs.220529 | carcinoembryonic antigen-related cell ad | 3.19 |
| | 430187 | AI799909 | Hs.158989 | ESTs | 3.18 |
| | 416209 | AA236776 | Hs.79078 | MAD2 (mitotic arrest deficient, yeast, h | 3.16 |
| 70 | 447048 | AW393080 | Hs.228320 | Homo sapiens cDNA: FLJ23537 fs, clone L | 3.14 |
| | 408113 | T82427 | Hs.194101 | Homo sapiens cDNA: FLJ20869 fs, clone A | 3.14 |
| | 425465 | L18964 | Hs.1904 | protein kinase C, iota | 3.13 |
| | 425826 | U97698 | Hs.159593 | mucin 6, gastric | 3.13 |
| | 431662 | AA513406 | Hs.152307 | ESTs | 3.13 |
| 75 | 419216 | AU076718 | Hs.164021 | small inducible cytokine subfamily B (Cy | 3.13 |
| | 418203 | X54942 | Hs.83758 | CDC28 protein kinase 2 | 3.12 |
| | 417315 | AI080042 | Hs.180450 | ribosomal protein S24 | 3.11 |
| | 433001 | AF217513 | Hs.279905 | clone HQ0310 PRO0310p1 | 3.11 |
| | 459587 | AA031956 | | gb:zk15e04.s1 Soares_pregnant_uterus_NbH | 3.11 |
| 80 | 450159 | AI702416 | Hs.200771 | ESTs, Weakly similar to CAN2_HUMAN CALPA | 3.11 |
| | 434370 | AF130988 | Hs.58346 | downless (mouse) homolog | 3.10 |
| | 421190 | U95031 | Hs.102482 | mucin 5, subtype B, tracheobronchial | 3.10 |
| | 421379 | Y15221 | Hs.103982 | small inducible cytokine subfamily B (Cy | 3.10 |
| | 420380 | AA640891 | Hs.102406 | ESTs | 3.10 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 414774 | X02419 | Hs.77274 | plasminogen activator, urokinase | 3.10 |
| | 415989 | A1267700 | Hs.111128 | ESTs | 3.09 |
| | 407137 | T97307 | Hs.199067 | v-erb-b2 avian erythroblastic leukemia v | 3.09 |
| | 407289 | AA135159 | Hs.203349 | Homo sapiens cDNA FLJ112149 fis, clone MA | 3.09 |
| 5 | 420297 | A1628272 | Hs.88323 | ESTs | 3.08 |
| | 447519 | U46258 | Hs.23448 | ESTs | 3.08 |
| | 448045 | AJ297436 | Hs.20166 | prostate stem cell antigen | 3.07 |
| | 431956 | AK002032 | Hs.272245 | Homo sapiens cDNA FLJ111170 fis, clone PL | 3.06 |
| 10 | 410286 | A1739159 | Hs.61898 | DKFZP586N2124 protein | 3.05 |
| | 409632 | W74001 | Hs.55279 | serine (or cysteine) proteinase inhibitor | 3.05 |
| | 454034 | NM_000691 | Hs.575 | aldehyde dehydrogenase 3 | 3.05 |
| | 436481 | AA379597 | Hs.5199 | HSPC150 protein similar to ubiquitin-con | 3.05 |
| | 430573 | AA744550 | Hs.136345 | ESTs | 3.05 |
| | 428987 | NM_004751 | Hs.194710 | glucosaminyl (N-acetyl) transferase 3, m | 3.04 |
| 15 | 424252 | AK000520 | Hs.143811 | hypothetical protein FLJ20513 | 3.04 |
| | 436291 | BE568452 | Hs.5101 | protein regulator of cytokinesis 1 | 3.03 |
| | 415992 | C05837 | Hs.145807 | Homo sapiens cDNA FLJ13593 fis, clone PL | 3.03 |
| | 411789 | AF245505 | Hs.72157 | Homo sapiens adican mRNA, complete cds | 3.02 |
| 20 | 417956 | AA210704 | Hs.190465 | ESTs | 3.02 |
| | 408908 | BE296227 | Hs.48915 | serine/threonine kinase 15 | 3.01 |
| | 422330 | D30783 | Hs.115263 | epiregulin | 3.01 |
| | 425071 | NM_013989 | Hs.154424 | deiodinase, iodothyronine, type II | 3.00 |
| | 425761 | AW664214 | Hs.196729 | ESTs | 2.99 |
| 25 | 432978 | AF126743 | Hs.279884 | DNAJ domain-containing | 2.99 |
| | 418546 | AA224827 | | gb:nc32g04.s1 NCI_CGAP_Pr2 Homo sapiens | 2.99 |
| | 425371 | D49441 | Hs.155981 | mesothelin | 2.99 |
| | 422440 | NM_004812 | Hs.116724 | aldo-keto reductase family 1, member B11 | 2.98 |
| | 439453 | BE264974 | Hs.6566 | thyroid hormone receptor interactor 13 | 2.98 |
| 30 | 413278 | BE563085 | Hs.833 | interferon-stimulated protein, 15 kDa | 2.97 |
| | 428450 | NM_014791 | Hs.184339 | KIAA0175 gene product | 2.95 |
| | 424345 | AK001380 | Hs.145479 | Homo sapiens cDNA FLJ10518 fis, clone NT | 2.95 |
| | 433133 | AB027249 | Hs.104741 | PDZ-binding kinase; T-cell originated pr | 2.94 |
| | 432269 | NM_002447 | Hs.2942 | macrophage stimulating 1 receptor (c-met | 2.94 |
| 35 | 432917 | NM_014125 | Hs.279812 | PRO0327 protein | 2.94 |
| | 433384 | AJ021992 | Hs.124244 | ESTs | 2.93 |
| | 432731 | R31178 | Hs.287820 | fibronectin 1 | 2.93 |
| | 420552 | AK000492 | Hs.98806 | hypothetical protein | 2.92 |
| 40 | 428303 | AW974476 | Hs.183601 | regulator of G-protein signalling 16 | 2.92 |
| | 409687 | T51125 | Hs.8493 | ESTs | 2.91 |
| | 434377 | AW137148 | Hs.136348 | osteoblast specific factor 2 (fascin) | 2.89 |
| | 417791 | AW965339 | Hs.111471 | ESTs | 2.89 |
| | 457288 | AA521458 | Hs.192738 | ESTs | 2.89 |
| | 456181 | L36463 | Hs.1030 | ras inhibitor | 2.89 |
| 45 | 450190 | T51387 | | gb:yb20e08.r1 Stratagene fetal spleen (9 | 2.88 |
| | 411573 | AB029000 | Hs.70823 | KIAA1077 protein | 2.88 |
| | 430204 | AA618335 | Hs.146137 | ESTs, Weakly similar to putative [C.eleg | 2.88 |
| | 434808 | AF155108 | Hs.256150 | ESTs, Highly similar to NY-REN-41 antige | 2.87 |
| | 450983 | AA305384 | Hs.25740 | ERO1 (S. cerevisiae)-like | 2.87 |
| 50 | 418670 | AA601036 | Hs.285083 | ESTs | 2.87 |
| | 416661 | AA634543 | Hs.79440 | IGF-II mRNA-binding protein 3 | 2.87 |
| | 409723 | AW885757 | Hs.257862 | ESTs | 2.87 |
| | 435099 | AC004770 | Hs.4756 | flap structure-specific endonuclease 1 | 2.86 |
| | 408660 | AA525775 | Hs.292523 | ESTs | 2.86 |
| 55 | 434032 | AW009951 | Hs.206892 | ESTs | 2.85 |
| | 418216 | AA662240 | Hs.283099 | AF15q14 protein | 2.85 |
| | 453331 | AJ240665 | Hs.8895 | ESTs | 2.85 |
| | 450221 | AA328102 | Hs.24541 | cytoskeleton associated protein 2 | 2.84 |
| | 402075 | | | | 2.84 |
| 60 | 410145 | AW886300 | | gb:RC5-OT0078-100400-023-C11 OT0078 Homo | 2.83 |
| | 410681 | AW246890 | Hs.65425 | calbindin 1, (28kD) | 2.83 |
| | 439867 | AA847510 | Hs.161292 | ESTs | 2.83 |
| | 443715 | AI583187 | Hs.9700 | cyclin E1 | 2.83 |
| | 420005 | AW271106 | Hs.133294 | ESTs | 2.83 |
| 65 | 417366 | BE185289 | Hs.1076 | small proline-rich protein 1B (cornifin) | 2.83 |
| | 422283 | AW411307 | Hs.114311 | CDC45 (cell division cycle 45, S.cerevis | 2.82 |
| | 404567 | | | | 2.82 |
| | 422158 | L10343 | Hs.112341 | protease inhibitor 3, skin-derived (SKAL | 2.82 |
| | 449224 | AW995911 | Hs.299883 | hypothetical protein FLJ23399 | 2.81 |
| 70 | 407584 | W25945 | Hs.18745 | ESTs | 2.81 |
| | 453884 | AA355925 | Hs.36232 | KIAA0186 gene product | 2.81 |
| | 449032 | AA045573 | Hs.22900 | nuclear factor (erythroid-derived 2)-lik | 2.80 |
| | 422809 | AK001379 | Hs.121028 | hypothetical protein FLJ10549 | 2.79 |
| | 449722 | BE280074 | Hs.23960 | cyclin B1 | 2.79 |
| | 445676 | AI247763 | Hs.16928 | ESTs | 2.79 |
| 75 | 424308 | AW975531 | Hs.154443 | minichromosome maintenance deficient (S. | 2.78 |
| | 453028 | AB006532 | Hs.31442 | RecQ protein-like 4 | 2.78 |
| | 421777 | BE562088 | Hs.108196 | HSPC037 protein | 2.78 |
| | 452571 | W31518 | Hs.34665 | ESTs | 2.77 |
| | 420759 | T11832 | Hs.127797 | ESTs | 2.77 |
| 80 | 422675 | BE018517 | Hs.119140 | eukaryotic translation initiation factor | 2.77 |
| | 412723 | AA648459 | Hs.179912 | ESTs | 2.76 |
| | 439670 | AF088076 | Hs.59507 | ESTs, Weakly similar to AC004858 3 U1 sm | 2.76 |
| | 400298 | AA032279 | Hs.61635 | six transmembrane epithelial antigen of | 2.76 |

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|----|--------|-----------|-----------|---|------|
| | 414569 | AF109298 | Hs.118258 | prostate cancer associated protein 1 | 2.76 |
| | 449378 | AW664026 | Hs.59892 | ESTs | 2.75 |
| | 423903 | M57765 | Hs.1721 | interleukin 11 | 2.75 |
| 5 | 412059 | AA317962 | Hs.249721 | ESTs | 2.75 |
| | 431104 | AW970859 | Hs.269109 | ESTs | 2.75 |
| | 439759 | AL359055 | Hs.67709 | Homo sapiens mRNA full length insert cDN | 2.75 |
| | 450701 | H39960 | Hs.288467 | Homo sapiens cDNA FLJ12280 fis, clone MA | 2.75 |
| | 452940 | AA029722 | Hs.20279 | ESTs | 2.74 |
| 10 | 408690 | AW864542 | | gb:PM4-SN0016-120500-003-h02 SN0016 Homo | 2.74 |
| | 407777 | AA161071 | Hs.71465 | squalene epoxidase | 2.73 |
| | 432201 | AJ538613 | Hs.135657 | ESTs | 2.73 |
| | 414416 | AW409985 | Hs.76084 | lamin B2 | 2.73 |
| | 414617 | AJ339520 | Hs.20524 | ESTs, Moderately similar to hexokinase I | 2.73 |
| 15 | 432407 | AA221036 | Hs.285026 | HERV-H LTR-associating 1 | 2.73 |
| | 444301 | AK000136 | Hs.10760 | hypothetical protein FLJ20129 | 2.72 |
| | 450375 | AA009647 | Hs.8850 | a disintegrin and metalloproteinase doma | 2.72 |
| | 441362 | BE614410 | Hs.23044 | RAD51 (S. cerevisiae) homolog (E. coli Re | 2.72 |
| | 408298 | AJ745325 | Hs.271923 | Homo sapiens cDNA: FLJ22785 fis, clone K | 2.72 |
| 20 | 426711 | AA383471 | Hs.180669 | conserved gene amplified in osteosarcoma | 2.71 |
| | 429432 | AJ678059 | Hs.202676 | synaptonemal complex protein 2 | 2.71 |
| | 450506 | NM_004460 | Hs.418 | fibroblast activation protein, alpha | 2.71 |
| | 427528 | AU077143 | Hs.179565 | minichromosome maintenance deficient (S. | 2.71 |
| | 418801 | AA228366 | Hs.115122 | ESTs | 2.71 |
| 25 | 440283 | AJ732892 | Hs.190489 | ESTs | 2.71 |
| | 429486 | AF155827 | Hs.203963 | hypothetical protein FLJ10339 | 2.71 |
| | 408366 | AW511255 | Hs.258082 | ESTs | 2.70 |
| | 406399 | | | | 2.69 |
| | 434217 | AW014795 | Hs.23349 | ESTs | 2.68 |
| 30 | 449785 | AJ25235 | Hs.288300 | Homo sapiens cDNA: FLJ23231 fis, clone C | 2.68 |
| | 446269 | AW263155 | Hs.14559 | hypothetical protein FLJ10540 | 2.68 |
| | 443349 | AJ052572 | Hs.269864 | ESTs | 2.68 |
| | 426514 | BE616633 | Hs.301122 | bone morphogenetic protein 7 (osteogenic | 2.67 |
| | 417079 | U65590 | Hs.81134 | interleukin 1 receptor antagonist | 2.67 |
| 35 | 444754 | T83911 | Hs.11881 | transmembrane 4 superfamily member 4 | 2.67 |
| | 424687 | J05070 | Hs.151738 | matrix metalloproteinase 9 (gelatinase B | 2.66 |
| | 439979 | AW600291 | Hs.6823 | hypothetical protein FLJ10430 | 2.65 |
| | 424408 | AJ754813 | Hs.146428 | collagen, type V, alpha 1 | 2.65 |
| | 430832 | AJ073913 | Hs.100686 | ESTs, Weakly similar to secreted cement | 2.65 |
| 40 | 427217 | AA399272 | Hs.144341 | ESTs | 2.65 |
| | 429170 | NM_001394 | Hs.2359 | dual specificity phosphatase 4 | 2.64 |
| | 450400 | AJ694722 | Hs.279744 | ESTs | 2.64 |
| | 435380 | AA679001 | Hs.192221 | ESTs | 2.64 |
| | 432375 | BE536069 | Hs.2962 | S100 calcium-binding protein P | 2.63 |
| 45 | 453700 | AB009426 | Hs.560 | apolipoprotein B mRNA editing enzyme, ca | 2.63 |
| | 422938 | NM_001809 | Hs.1594 | centromere protein A (17kD) | 2.63 |
| | 453134 | AA032211 | Hs.118493 | ESTs | 2.63 |
| | 420727 | H75701 | Hs.99886 | complement component 4-binding protein, | 2.62 |
| | 408868 | AW292286 | Hs.255058 | ESTs | 2.62 |
| 50 | 414972 | BE263782 | Hs.77695 | KIAA0008 gene product | 2.62 |
| | 440255 | AJ932285 | Hs.160569 | ESTs | 2.62 |
| | 403055 | | | | 2.62 |
| | 443247 | BE614387 | Hs.47378 | ESTs, Moderately similar to hypothetical | 2.62 |
| | 447400 | AK000322 | Hs.18457 | hypothetical protein FLJ20315 | 2.61 |
| 55 | 413753 | U17760 | Hs.301103 | Human DNA sequence from clone 272L16 on | 2.61 |
| | 445114 | AW991959 | Hs.254664 | ESTs | 2.61 |
| | 422397 | AJ223366 | Hs.116051 | myeloma overexpressed gene(in a subset o | 2.60 |
| | 407366 | AF026942 | | gb:Homo sapiens cig33 mRNA, partial sequ | 2.60 |
| | 432009 | AL137424 | | gb:Homo sapiens mRNA; cDNA DKFZp761G2123 | 2.60 |
| 60 | 440249 | AJ246590 | Hs.125325 | ESTs | 2.60 |
| | 433220 | AJ076192 | Hs.131933 | ESTs | 2.60 |
| | 438533 | AJ440266 | Hs.170673 | ESTs, Weakly similar to AF126780 1 retin | 2.60 |
| | 436251 | BE515065 | Hs.5092 | nucleolar protein (KKE/D repeat) | 2.60 |
| | 424717 | H03754 | Hs.152213 | wingless-type MMTV integration site fami | 2.60 |
| 65 | 448988 | Y09763 | Hs.22785 | gamma-aminobutyric acid (GABA) A recepto | 2.60 |
| | 425463 | AK000740 | Hs.157986 | hypothetical protein FLJ20733 | 2.60 |
| | 435370 | AJ964074 | Hs.225838 | ESTs | 2.59 |
| | 432215 | AU076609 | Hs.2934 | ribonucleotide reductase M1 polypeptide | 2.59 |
| | 409142 | AL136877 | Hs.50758 | chromosome-associated polypeptide C | 2.59 |
| 70 | 443919 | AJ091284 | Hs.135224 | ESTs | 2.58 |
| | 413268 | AL039079 | Hs.75256 | regulator of G-protein signaling 1 | 2.58 |
| | 404519 | | | | 2.58 |
| | 414998 | NM_002543 | Hs.77729 | oxidised low density lipoprotein (lectin | 2.57 |
| | 429597 | NM_003816 | Hs.2442 | a disintegrin and metalloproteinase doma | 2.57 |
| 75 | 426841 | AJ052358 | Hs.193726 | ESTs | 2.57 |
| | 416768 | AA363733 | Hs.1032 | regenerating islet-derived 1 alpha (panc | 2.57 |
| | 417933 | X02308 | Hs.82962 | thymidylate synthetase | 2.56 |
| | 433675 | AW977653 | Hs.110771 | Homo sapiens cDNA: FLJ21904 fis, clone H | 2.56 |
| | 441384 | AA447849 | Hs.288660 | protease, serine, 23 | 2.56 |
| 80 | 451939 | U80456 | Hs.27311 | single-minded (Drosophila) homolog 2 | 2.55 |
| | 418867 | D31771 | Hs.89404 | msh (Drosophila) homeo box homolog 2 | 2.55 |
| | 449042 | AW294985 | Hs.301148 | potassium voltage-gated channel, Isk-rel | 2.55 |
| | 416065 | BE267931 | Hs.78996 | proliferating cell nuclear antigen | 2.55 |
| | 414132 | AJ801235 | Hs.48480 | ESTs | 2.55 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| 5 | 431890 | X17033 | Hs.271986 | integrin, alpha 2 (CD49B, alpha 2 subunit) | 2.55 |
| | 407830 | NM_001086 | Hs.587 | arylacetamide deacetylase (esterase) | 2.55 |
| | 434815 | AF155582 | Hs.46744 | core1 UDP-galactose:N-acetylgalactosamin | 2.54 |
| | 415250 | F02614 | Hs.27319 | ESTs | 2.54 |
| | 435647 | AI653240 | Hs.49823 | ESTs | 2.54 |
| 10 | 459306 | AW578452 | Hs.232988 | ESTs, Weakly similar to mucin [H.sapiens | 2.54 |
| | 414361 | AI086138 | Hs.204044 | ESTs | 2.54 |
| | 425782 | U66468 | Hs.159525 | cell growth regulatory with EF-hand doma | 2.53 |
| | 416984 | H38765 | Hs.80706 | diaphorase (NADH/NADPH) (cytochrome b-5 | 2.53 |
| | 431183 | NM_006855 | Hs.250696 | KDEL (Lys-Asp-Glu-Leu) endoplasmic retic | 2.53 |
| 15 | 436043 | AW963838 | Hs.168830 | Homo sapiens cDNA FLJ12136 fis, clone MA | 2.53 |
| | 456743 | AI630124 | Hs.7434 | ESTs | 2.53 |
| | 410268 | AA316181 | Hs.61635 | six transmembrane epithelial antigen of | 2.52 |
| | 424905 | NM_002497 | Hs.153704 | NIMA (never in mitosis gene a)-related k | 2.52 |
| | 411734 | AW374954 | Hs.71779 | Homo sapiens DNA from chromosome 19, cos | 2.52 |
| 20 | 432657 | AA831815 | Hs.270940 | ESTs | 2.51 |
| | 434080 | AI820719 | Hs.154662 | hypothetical protein PRO1472 | 2.51 |
| | 438190 | AA780020 | Hs.136798 | ESTs | 2.51 |
| | 418969 | W33191 | Hs.28907 | hypothetical protein FLJ20258 | 2.51 |
| | 446405 | AW451259 | Hs.57851 | ESTs | 2.51 |
| 25 | 450002 | AI679524 | Hs.201629 | ESTs, Moderately similar to ALU8_HUMAN A | 2.51 |
| | 431808 | M30703 | Hs.270833 | amphiregulin (schwannoma-derived growth | 2.51 |
| | 429093 | NM_000253 | Hs.195799 | microsomal triglyceride transfer protein | 2.50 |
| | 447634 | AW967902 | Hs.5152 | Homo sapiens cDNA: FLJ22618 fis, clone H | 2.50 |
| | 435393 | AW022213 | Hs.143617 | ESTs | 2.50 |
| 30 | 453751 | R36762 | Hs.101282 | Homo sapiens mRNA; cDNA DKFZp434B102 (fr | 2.49 |
| | 445669 | AI570830 | Hs.174870 | ESTs | 2.49 |
| | 445865 | AI262584 | Hs.145575 | ESTs | 2.49 |
| | 448437 | AW470125 | | gb:wx60c04.x1 NCI_CGAP_Pan1 Homo sapiens | 2.49 |
| | 414883 | AA926960 | Hs.77550 | CDC28 protein kinase 1 | 2.49 |
| 35 | 406747 | AI925153 | Hs.217493 | annexin A2 | 2.49 |
| | 446921 | AB012113 | Hs.16530 | small inducible cytokine subfamily A (Cy | 2.49 |
| | 426322 | J05068 | Hs.2012 | transcobalamin I (vitamin B12 binding pr | 2.48 |
| | 412903 | BE007967 | Hs.155795 | ESTs | 2.48 |
| | 422515 | AW500470 | Hs.117950 | multifunctional polypeptide similar to S | 2.48 |
| 40 | 447030 | AW444659 | Hs.232184 | ESTs | 2.48 |
| | 448454 | NM_005879 | Hs.21254 | TRAF interacting protein | 2.48 |
| | 419092 | J05581 | Hs.89603 | mucin 1, transmembrane | 2.48 |
| | 406671 | AA129547 | Hs.285754 | met proto-oncogene (hepatocyte growth fa | 2.48 |
| | 409640 | U78722 | Hs.55481 | zinc finger protein 165 | 2.48 |
| 45 | 424639 | AI917494 | Hs.131329 | ESTs | 2.48 |
| | 404171 | | | | 2.47 |
| | 414747 | U30872 | Hs.77204 | centromere protein F (350/400kD, mitosis | 2.47 |
| | 407839 | AA045144 | Hs.161566 | ESTs | 2.47 |
| | 410406 | AI969703 | Hs.301842 | ESTs | 2.47 |
| 50 | 452220 | BE158006 | Hs.212296 | ESTs | 2.46 |
| | 427691 | AW194426 | Hs.20726 | ESTs | 2.46 |
| | 421493 | BE300341 | Hs.104925 | ectodermal-neural cortex (with BTB-like | 2.46 |
| | 444838 | AV651680 | Hs.208558 | ESTs | 2.46 |
| | 413816 | AW958181 | Hs.189998 | ESTs | 2.46 |
| 55 | 408296 | AL117452 | Hs.44155 | DKFZP586G1517 protein | 2.46 |
| | 436613 | AA972691 | Hs.192974 | Homo sapiens cDNA FLJ12735 fis, clone NT | 2.45 |
| | 445417 | AK001058 | Hs.12680 | Homo sapiens cDNA FLJ10196 fis, clone HE | 2.45 |
| | 432874 | W94322 | Hs.279651 | melanoma inhibitory activity | 2.45 |
| | 425268 | AI807883 | Hs.156932 | ESTs | 2.45 |
| 60 | 425397 | J04088 | Hs.156346 | topoisomerase (DNA) II alpha (170kD) | 2.45 |
| | 408308 | AL033377 | Hs.44197 | hypothetical protein DKFZp564D0462 | 2.45 |
| | 427961 | AW293165 | Hs.143134 | ESTs | 2.45 |
| | 422363 | T55979 | Hs.115474 | replication factor C (activator 1) 3 (38 | 2.45 |
| | 433083 | AL042759 | Hs.191762 | ESTs | 2.45 |
| 65 | 439848 | AW979249 | | gb:EST391359 MAGE resequences, MAGP Homo | 2.44 |
| | 431924 | AK000850 | Hs.272203 | Homo sapiens cDNA FLJ20843 fis, clone AD | 2.44 |
| | 431457 | NM_012211 | Hs.256297 | integrin, alpha 11 | 2.44 |
| | 443949 | AW827419 | Hs.235070 | ESTs | 2.44 |
| | 416498 | U33632 | Hs.79351 | potassium channel, subfamily K, member 1 | 2.44 |
| 70 | 428484 | AF104032 | Hs.184601 | solute carrier family 7 (cationic amino | 2.43 |
| | 431958 | X63629 | Hs.2877 | cadherin 3, type 1, P-cadherin (placenta | 2.43 |
| | 413833 | Z15005 | Hs.75573 | centromere protein E (312kD) | 2.43 |
| | 407243 | AA058357 | Hs.74466 | carcinoembryonic antigen-related cell ad | 2.43 |
| | 410044 | BE566742 | Hs.58169 | highly expressed in cancer, rich in leuc | 2.43 |
| 75 | 424273 | W40460 | Hs.144442 | phospholipase A2, group X | 2.42 |
| | 409533 | AW969543 | Hs.21291 | mitogen-activated protein kinase kinase | 2.42 |
| | 453966 | BE148734 | Hs.252833 | ESTs | 2.42 |
| | 427043 | AA397679 | Hs.298460 | ESTs | 2.42 |
| | 419741 | NM_007019 | Hs.93002 | ubiquitin carrier protein E2-C | 2.42 |
| 80 | 449987 | AW079749 | Hs.184719 | ESTs, Weakly similar to AF116721 112 PRO | 2.42 |
| | 433159 | AB035898 | Hs.150587 | kinesin-like protein 2 | 2.42 |
| | 433396 | BE562958 | Hs.74346 | ESTs, Weakly similar to /prediction | 2.42 |
| | 426427 | M86699 | Hs.169840 | TTK protein kinase | 2.41 |
| | 434725 | AK000796 | Hs.4104 | hypothetical protein | 2.41 |
| | 427719 | AI393122 | Hs.134726 | ESTs | 2.41 |
| | 433312 | AI241331 | Hs.131765 | ESTs | 2.41 |
| | 432615 | AA557191 | Hs.55028 | ESTs | 2.41 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 407047 | X65965 | | gb:H.sapiens SOD-2 gene for manganese su | 2.41 |
| | 419220 | AA811938 | Hs.291759 | ESTs | 2.40 |
| | 416530 | U62801 | Hs.79361 | kalikrein 6 (neurosin, zyme) | 2.40 |
| 5 | 435219 | AA676349 | Hs.190331 | ESTs | 2.40 |
| | 447164 | AF026941 | Hs.17518 | Homo sapiens cig5 mRNA, partial sequence | 2.40 |
| | 416713 | T70174 | | gb:yc18b03.s1 Stratagene tung (937210) H | 2.40 |
| | 418322 | AA284166 | Hs.84113 | cyclin-dependent kinase inhibitor 3 (CDK | 2.40 |
| | 409902 | AI337658 | Hs.156351 | ESTs | 2.40 |
| 10 | 443597 | AI078418 | | gb:oz05e03.x1 Soares_fetal_liver_spleen_ | 2.40 |
| | 404253 | | | | 2.40 |
| | 428970 | BE276891 | Hs.194691 | retinoic acid induced 3 | 2.40 |
| | 443462 | AI064690 | Hs.171176 | ESTs | 2.40 |
| | 418693 | AI750878 | Hs.87409 | thrombospondin 1 | 2.39 |
| 15 | 451237 | AW600293 | | gb:EST00049 pGEM-T library Homo sapiens | 2.39 |
| | 407756 | AA116021 | Hs.38260 | ubiquitin specific protease 18 | 2.39 |
| | 437935 | AW939591 | Hs.5940 | hypothetical protein FLJ20063 | 2.39 |
| | 445625 | BE246743 | Hs.288529 | Homo sapiens cDNA: FLJ22635 fis, clone H | 2.39 |
| | 435937 | AA830893 | Hs.119769 | ESTs | 2.39 |
| 20 | 438993 | AA828995 | | gb:od77b08.s1 NCI_CGAP_Ov2 Homo sapiens | 2.38 |
| | 422082 | AA016188 | Hs.111244 | hypothetical protein | 2.38 |
| | 435849 | BE305242 | Hs.112442 | ESTs, Weakly similar to CLDE_HUMAN CLAUD | 2.38 |
| | 407242 | M18728 | | gb:Human nonspecific crossreacting antig | 2.38 |
| | 450396 | AU077002 | Hs.24950 | regulator of G-protein signalling 5 | 2.38 |
| 25 | 430354 | AA954810 | Hs.239784 | human homolog of Drosophila Scribble | 2.38 |
| | 422578 | AF239666 | Hs.1545 | caudal type homeo box transcription fact | 2.38 |
| | 446342 | BE298665 | Hs.14846 | Homo sapiens mRNA; cDNA DKFZp564D016 (fr | 2.38 |
| | 450737 | AW007152 | Hs.203330 | ESTs | 2.38 |
| | 428070 | T63918 | Hs.182313 | retinol-binding protein 2, cellular | 2.38 |
| 30 | 416111 | AA033813 | Hs.79018 | chromatin assembly factor 1, subunit A (| 2.37 |
| | 433345 | AI681545 | Hs.152982 | Homo sapiens cDNA FLJ13117 fis, clone NT | 2.37 |
| | 427557 | NM_002659 | Hs.179657 | plasminogen activator, urokinase recepto | 2.37 |
| | 423554 | M90516 | Hs.1674 | glutamine-fructose-6-phosphate transamin | 2.37 |
| | 453204 | R10799 | Hs.191990 | ESTs | 2.37 |
| 35 | 453876 | AIW021748 | Hs.110406 | ESTs | 2.36 |
| | 425081 | X74794 | Hs.154443 | minichromosome maintenance deficient (S. | 2.36 |
| | 434682 | AA827165 | Hs.191958 | ESTs | 2.36 |
| | 439737 | AI751438 | Hs.41271 | Homo sapiens mRNA full length insert cDN | 2.36 |
| | 414108 | AI267592 | Hs.75761 | SFRS protein kinase 1 | 2.36 |
| 40 | 417900 | BE250127 | Hs.82906 | CDC20 (cell division cycle 20, S. cerevi | 2.36 |
| | 428046 | AW812795 | Hs.155381 | ESTs, Moderately similar to 138022 hypot | 2.36 |
| | 448826 | AI580252 | Hs.293246 | ESTs, Weakly similar to putative p150 [H | 2.36 |
| | 441020 | W79283 | Hs.35962 | ESTs | 2.36 |
| | 448019 | AW947164 | Hs.195641 | ESTs | 2.36 |
| 45 | 431753 | X76029 | Hs.2841 | neuromedin U | 2.36 |
| | 441703 | AW390054 | Hs.192843 | ESTs | 2.36 |
| | 410361 | BE391804 | Hs.62661 | guanylate binding protein 1, interferon- | 2.36 |
| | 418526 | BE019020 | Hs.85838 | solute carrier family 16 (monocarboxylic | 2.36 |
| | 444478 | W07318 | Hs.240 | M-phase phosphoprotein 1 | 2.36 |
| 50 | 421878 | AA299652 | Hs.111496 | Homo sapiens cDNA FLJ11643 fis, clone HE | 2.35 |
| | 428388 | AA729827 | Hs.101265 | Homo sapiens cDNA: FLJ22593 fis, clone H | 2.35 |
| | 436961 | AW375974 | Hs.156704 | ESTs | 2.35 |
| | 408194 | AA601038 | Hs.191797 | ESTs | 2.35 |
| | 438578 | AA811244 | Hs.164168 | ESTs | 2.35 |
| 55 | 429183 | AB014604 | Hs.197955 | KIAA0704 protein | 2.35 |
| | 435663 | AI023707 | Hs.134273 | ESTs | 2.35 |
| | 430290 | AI734110 | Hs.136355 | ESTs | 2.35 |
| | 423441 | R68649 | Hs.278359 | absent in melanoma 1 like | 2.34 |
| | 453900 | AW003582 | Hs.226414 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 2.33 |
| 60 | 450378 | AW249181 | Hs.19954 | ESTs, Weakly similar to cDNA EST yk386e1 | 2.33 |
| | 432877 | AW974111 | Hs.292477 | ESTs | 2.33 |
| | 451928 | AI823801 | Hs.30315 | ESTs | 2.33 |
| | 426227 | U67058 | Hs.168102 | Human proteinase activated receptor-2 mR | 2.33 |
| 65 | 418245 | AA088767 | Hs.83883 | transmembrane, prostate androgen induced | 2.33 |
| | 415083 | AI632683 | Hs.27179 | Homo sapiens cDNA FLJ12933 fis, clone NT | 2.33 |
| | 435106 | AA100847 | Hs.193380 | ESTs, Highly similar to AF174600 1 F-box | 2.33 |
| | 432193 | AA372264 | Hs.273193 | hypothetical protein FLJ10706 | 2.33 |
| | 458531 | AA367718 | Hs.159083 | ESTs | 2.33 |
| | 449532 | W74653 | Hs.271593 | ESTs | 2.33 |
| 70 | 446354 | AW449650 | Hs.202249 | ESTs | 2.33 |
| | 409703 | NM_006187 | Hs.56009 | 2'-5'-oligoadenylate synthetase 3 | 2.33 |
| | 419373 | NM_003244 | Hs.90077 | TG-interacting factor (TALE family homeo | 2.32 |
| | 435607 | W73428 | Hs.8750 | uncharacterized bone marrow protein BM04 | 2.32 |
| | 405818 | | | | 2.32 |
| 75 | 423132 | AF070647 | Hs.124126 | Homo sapiens clone 24438 mRNA sequence | 2.32 |
| | 444371 | BE540274 | Hs.239 | forkhead box M1 | 2.32 |
| | 432675 | AI791855 | Hs.105884 | ESTs | 2.32 |
| | 411773 | NM_006799 | Hs.72026 | protease, serine, 21 (testisin) | 2.31 |
| | 448569 | BE382657 | Hs.21486 | signal transducer and activator of trans | 2.31 |
| 80 | 434775 | AA648983 | Hs.212911 | ESTs | 2.31 |
| | 407378 | AA299264 | | gb:EST11752 Uterus Homo sapiens cDNA S | 2.31 |
| | 442353 | BE379694 | Hs.49136 | ESTs | 2.31 |
| | 422611 | AA158177 | Hs.118722 | fucosyltransferase B (alpha (1,6) fucosy | 2.31 |
| | 409965 | AA079229 | | gb:zm95f04.r1 Stratagene colon HT29 (937 | 2.31 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 421677 | H64092 | Hs.38282 | ESTs | 2.31 |
| | 419493 | AF001212 | Hs.90744 | proteasome (prosome, macropain) 26S subu | 2.31 |
| | 424435 | AB011167 | Hs.146957 | KIAA0595 protein | 2.30 |
| | 446880 | AJ811807 | Hs.108646 | Homo sapiens cDNA FLJ12534 fis, clone NT | 2.30 |
| 5 | 452795 | AW392555 | Hs.18878 | hypothetical protein FLJ21620 | 2.30 |
| | 452834 | AJ638627 | Hs.105685 | ESTs | 2.30 |
| | 409262 | AK000631 | Hs.52256 | hypothetical protein FLJ20624 | 2.30 |
| | 428125 | AA393071 | Hs.182579 | leucine aminopeptidase | 2.30 |
| 10 | 417655 | AA780791 | Hs.14014 | ESTs, Weakly similar to KIAA0973 protein | 2.29 |
| | 407287 | AJ678812 | Hs.201658 | ESTs, Weakly similar to ALU4_HUMAN ALU S | 2.29 |
| | 428923 | BE047698 | Hs.188785 | ESTs | 2.29 |
| | 452203 | X57522 | Hs.158164 | ATP-binding cassette, sub-family B (MDR/ | 2.29 |
| | 409402 | AF208234 | Hs.695 | cystatin B (stefin B) | 2.29 |
| 15 | 419359 | AL043202 | Hs.90073 | chromosome segregation 1 (yeast homolog) | 2.29 |
| | 451999 | AW176401 | Hs.27424 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypep | 2.29 |
| | 400811 | AF219139 | Hs.87726 | KIAA0154 protein; ADP-ribosylation facto | 2.29 |
| | 436396 | AJ683487 | Hs.299112 | Homo sapiens cDNA FLJ11441 fis, clone HE | 2.28 |
| | 442152 | R39246 | Hs.239666 | Homo sapiens cDNA FLJ13495 fis, clone PL | 2.28 |
| 20 | 420931 | AF044197 | Hs.100431 | small inducible cytokine B subfamily (Cy | 2.28 |
| | 410174 | AA306007 | Hs.59461 | DKFZP434C245 protein | 2.28 |
| | 425247 | NM_005940 | Hs.155324 | matrix metalloproteinase 11 (stromelysin | 2.28 |
| | 438170 | AJ916685 | Hs.194601 | ESTs | 2.28 |
| | 445378 | AV653564 | Hs.226946 | ESTs | 2.28 |
| 25 | 428048 | AA705745 | Hs.185070 | ESTs | 2.28 |
| | 414696 | AF002020 | Hs.76918 | Niemann-Pick disease, type C1 | 2.27 |
| | 446665 | BE613126 | Hs.47783 | ESTs, Weakly similar to T12540 hypotheti | 2.27 |
| | 427660 | AJ741320 | Hs.114121 | Homo sapiens cDNA: FLJ23228 fis, clone C | 2.27 |
| | 422128 | AW881145 | | gb:OVD-OT0033-010400-182-a07 OT0033 Homo | 2.27 |
| 30 | 433535 | AF111106 | Hs.3382 | protein phosphatase 4, regulatory subuni | 2.27 |
| | 415857 | AA866115 | Hs.301646 | Homo sapiens cDNA FLJ11381 fis, clone HE | 2.27 |
| | 421155 | H87879 | Hs.102267 | lysyl oxidase | 2.27 |
| | 405545 | | | ESTs | 2.27 |
| | 449467 | AW205006 | Hs.197042 | ESTs | 2.27 |
| 35 | 445537 | AJ245671 | Hs.12844 | EGF-like-domain, multiple 6 | 2.27 |
| | 450680 | AF131784 | Hs.25318 | Homo sapiens clone 25194 mRNA sequence | 2.26 |
| | 423634 | AW959908 | Hs.16590 | heparin-binding growth factor binding pr | 2.26 |
| | 443868 | W88483 | Hs.293650 | ESTs | 2.26 |
| | 407742 | AF186252 | Hs.38084 | sulfotransferase family, cytosolic, 1C, | 2.26 |
| 40 | 428330 | L22524 | Hs.2256 | matrix metalloproteinase 7 (matrilysin, | 2.26 |
| | 432655 | AA832195 | Hs.292266 | ESTs | 2.26 |
| | 429731 | AK001592 | Hs.212172 | beta,beta-carotene 15,15'-dioxygenase ho | 2.26 |
| | 400514 | | | ESTs | 2.26 |
| | 431846 | BE019924 | Hs.271580 | uroplakin 1B | 2.26 |
| 45 | 439521 | AJ808955 | Hs.58248 | ESTs | 2.26 |
| | 426010 | AA136563 | Hs.1975 | Homo sapiens cDNA: FLJ21007 fis, clone C | 2.26 |
| | 437641 | AA811452 | Hs.291911 | ESTs | 2.26 |
| | 418982 | AJ348838 | Hs.13073 | ESTs | 2.26 |
| | 411393 | AW797437 | Hs.69771 | B-factor, properdin | 2.26 |
| 50 | 414809 | AJ434699 | Hs.77356 | transferrin receptor (p90, CD71) | 2.25 |
| | 419488 | AA316241 | Hs.90691 | nucleophosmin/nucleoplasm 3 | 2.25 |
| | 434540 | NM_016045 | Hs.5184 | TH1 drosophila homolog | 2.25 |
| | 449962 | AA004879 | Hs.187820 | ESTs | 2.25 |
| | 410196 | AJ936442 | Hs.59838 | hypothetical protein FLJ10808 | 2.25 |
| 55 | 456844 | AJ264155 | Hs.152981 | CDP-diacylglycerol synthase (phosphatida | 2.25 |
| | 414368 | W70171 | Hs.75939 | uridine monophosphate kinase | 2.25 |
| | 408353 | BE439838 | Hs.44298 | hypothetical protein | 2.25 |
| | 439223 | AW238299 | Hs.23945 | ESTs | 2.25 |
| | 448753 | AL048858 | Hs.224355 | ESTs, Weakly similar to A39650 protein k | 2.25 |
| 60 | 428479 | Y00272 | Hs.184572 | cell division cycle 2, G1 to S and G2 to | 2.24 |
| | 432403 | AA550815 | Hs.124840 | ESTs | 2.24 |
| | 424971 | AA479005 | Hs.154036 | tumor suppressing subtransferable candid | 2.24 |
| | 432673 | AB028859 | Hs.278605 | ER-associated DNAJ; ER-associated Hsp40 | 2.24 |
| | 446887 | AJ346656 | Hs.156652 | Homo sapiens cDNA: FLJ22800 fis, clone K | 2.24 |
| 65 | 452833 | BE559681 | Hs.30736 | KIAA0124 protein | 2.24 |
| | 409432 | D49372 | Hs.54460 | small inducible cytokine subfamily A (Cy | 2.24 |
| | 422039 | BE567832 | Hs.82148 | hypothetical protein | 2.24 |
| | 429925 | NM_000786 | Hs.226213 | cytochrome P450, 51 (lanosterol 14-alpha | 2.24 |
| | 445413 | AA151342 | Hs.12677 | CGI-147 protein | 2.23 |
| 70 | 423645 | AJ215632 | Hs.147487 | ESTs | 2.23 |
| | 447532 | AK000614 | Hs.18791 | hypothetical protein FLJ20607 | 2.23 |
| | 423515 | AA327017 | Hs.162204 | ESTs | 2.23 |
| | 444743 | AA045648 | Hs.11817 | nudix (nucleoside diphosphate linked moi | 2.23 |
| | 434518 | H56995 | Hs.37372 | Homo sapiens DNA binding peptide mRNA, p | 2.23 |
| 75 | 435602 | AF217515 | Hs.283532 | uncharacterized bone marrow protein BM03 | 2.23 |
| | 449974 | AW970948 | Hs.269403 | ESTs | 2.23 |
| | 424927 | AW973656 | Hs.153850 | hypothetical protein C321D2.4 | 2.23 |
| | 457982 | AW856093 | Hs.183617 | ESTs | 2.23 |
| | 414420 | AA043424 | Hs.76095 | immediate early response 3 | 2.23 |
| 80 | 449019 | AJ949095 | Hs.67776 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 2.23 |
| | 431840 | AA534908 | Hs.2850 | POU domain, class 5, transcription facto | 2.23 |
| | 452930 | AW195285 | Hs.194097 | ESTs | 2.23 |
| | 436391 | AJ227892 | Hs.146274 | ESTs | 2.23 |
| | 439186 | AJ697274 | Hs.6487 | Xq28, 2000bp sequence contig. ORF | 2.23 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 427254 | AL121523 | Hs.97774 | ESTs | 2.22 |
| | 424517 | AI539443 | Hs.137447 | Homo sapiens cDNA FLJ12169 fis, clone MA | 2.22 |
| | 414732 | AW410976 | Hs.77152 | minichromosome maintenance deficient (S. | 2.22 |
| 5 | 411835 | U29343 | Hs.72550 | hyaluronan-mediated motility receptor (R | 2.22 |
| | 427647 | W19744 | Hs.180059 | Homo sapiens cDNA FLJ20653 fis, clone KA | 2.22 |
| | 438223 | AA781171 | | gb:aj24d05.s1 Soares_testis_NHT Homo sap | 2.22 |
| | 434504 | AI887341 | Hs.121590 | Homo sapiens cDNA FLJ12827 fis, clone NT | 2.22 |
| | 450149 | AW969781 | Hs.293440 | ESTs, Moderately similar to ZIC2 protein | 2.22 |
| 10 | 439211 | AI890347 | Hs.271923 | Homo sapiens cDNA: FLJ22785 fis, clone K | 2.22 |
| | 401519 | | | | 2.22 |
| | 441794 | AW197794 | Hs.253338 | ESTs | 2.22 |
| | 412108 | AA100293 | Hs.185043 | ESTs | 2.22 |
| | 431849 | AI670823 | Hs.85573 | Homo sapiens mRNA; cDNA DKFZp566N034 (fr | 2.22 |
| 15 | 444969 | AI203334 | Hs.160628 | ESTs | 2.21 |
| | 408901 | AK001330 | Hs.48855 | hypothetical protein FLJ10468 | 2.21 |
| | 434423 | NM_006769 | Hs.3844 | LIM domain only 4 | 2.21 |
| | 438328 | W07411 | Hs.118212 | ESTs, Moderately similar to ALU3_HUMAN A | 2.21 |
| | 400021 | | | AFFX control: STAT1 | 2.21 |
| 20 | 432140 | AK000404 | Hs.272688 | hypothetical protein FLJ20397 | 2.21 |
| | 434170 | AA626509 | Hs.122329 | ESTs | 2.21 |
| | 423453 | AW450737 | Hs.128791 | CGI-09 protein | 2.21 |
| | 428438 | NM_001955 | Hs.2271 | endothelin 1 | 2.21 |
| | 433102 | AI343966 | Hs.158528 | ESTs | 2.21 |
| 25 | 421470 | R27496 | Hs.1378 | annexin A3 | 2.21 |
| | 425499 | T62489 | | gb:yc03f09.r1 Stratagene lung (S37210) H | 2.21 |
| | 438280 | AW015534 | Hs.217493 | annexin A2 | 2.21 |
| | 440381 | AA917808 | Hs.190495 | ESTs | 2.20 |
| | 453779 | N35187 | Hs.43388 | ESTs | 2.20 |
| 30 | 433627 | AF078866 | Hs.284296 | Homo sapiens cDNA: FLJ22993 fis, clone K | 2.20 |
| | 417944 | AI077196 | Hs.82985 | collagen, type V, alpha 2 | 2.20 |
| | 452299 | AW206330 | Hs.73239 | hypothetical protein FLJ10901 | 2.20 |
| | 422689 | AW856665 | | gb:RC3-CT0297-290100-013-d03 CT0297 Homo | 2.20 |
| | 448457 | H65629 | Hs.245997 | ESTs | 2.20 |
| 35 | 416221 | BE513171 | Hs.79086 | mitochondrial ribosomal protein L3 | 2.20 |
| | 426125 | X87241 | Hs.166994 | FAT tumor suppressor (Drosophila) homolo | 2.20 |
| | 430603 | AA148164 | Hs.247280 | HBV associated factor | 2.20 |
| | 425274 | BE281191 | Hs.155462 | minichromosome maintenance deficient (mi | 2.20 |
| | 452679 | Z42387 | Hs.4299 | Homo sapiens cDNA: FLJ20965 fis, clone A | 2.20 |
| 40 | 410619 | BE512730 | Hs.65114 | keratin 18 | 2.20 |
| | 424332 | AA338919 | Hs.101615 | ESTs | 2.20 |
| | 442490 | AW965078 | Hs.30212 | thyroid receptor interacting protein 15 | 2.20 |
| | 418661 | NM_001949 | Hs.1189 | Human mRNA for KIAA0075 gene, partial cd | 2.20 |
| | 419341 | N71463 | Hs.118888 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.20 |
| 45 | 427920 | Z11502 | Hs.181107 | annexin A13 | 2.19 |
| | 413879 | AA132961 | Hs.212533 | Homo sapiens cDNA: FLJ22572 fis, clone H | 2.19 |
| | 419752 | AA249573 | Hs.152618 | ESTs | 2.19 |
| | 441436 | AW137772 | Hs.185980 | ESTs | 2.19 |
| | 413095 | AA494359 | Hs.30715 | ESTs | 2.19 |
| 50 | 403208 | | | | 2.19 |
| | 422596 | AF063611 | Hs.118633 | 2'-5'-oligoadenylate synthetase-like | 2.19 |
| | 444261 | AA298958 | Hs.10724 | MDS023 protein | 2.19 |
| | 419474 | AW968619 | Hs.155849 | ESTs | 2.19 |
| | 453883 | AI638516 | Hs.77448 | aldehyde dehydrogenase 4 (glutamate gamma | 2.18 |
| 55 | 423401 | NM_001992 | Hs.128087 | coagulation factor II (thrombin) recepto | 2.18 |
| | 453450 | AW797627 | Hs.89474 | ADP-ribosylation factor 6 | 2.18 |
| | 440250 | AA876179 | Hs.134650 | ESTs | 2.18 |
| | 444334 | BE296785 | Hs.10848 | KIAA0187 gene product | 2.18 |
| | 437616 | AI797163 | Hs.207954 | ESTs | 2.18 |
| 60 | 451807 | W52854 | Hs.27099 | DKFZP564J0863 protein | 2.18 |
| | 430441 | BE398091 | Hs.6880 | DKFZP434D156 protein | 2.18 |
| | 414602 | AW630088 | Hs.76550 | Homo sapiens mRNA; cDNA DKFZp564B1264 (f | 2.18 |
| | 411678 | AI907114 | Hs.71465 | squalene epoxidase | 2.18 |
| | 453735 | AI066629 | Hs.125073 | ESTs | 2.18 |
| 65 | 450499 | AA235207 | Hs.250456 | hypothetical protein DKFZp762F2011 | 2.18 |
| | 452291 | AF015592 | Hs.28853 | CDC7 (cell division cycle 7, S. cerevisi | 2.18 |
| | 421532 | AW138207 | Hs.146170 | hypothetical protein FLJ22969 | 2.18 |
| | 444342 | NM_014398 | Hs.10887 | similar to lysosome-associated membrane | 2.18 |
| | 451099 | R52795 | Hs.25954 | interleukin 13 receptor, alpha 2 | 2.18 |
| 70 | 444207 | AI565004 | Hs.79572 | cathepsin D (lysosomal aspartyl) protease | 2.18 |
| | 425873 | NM_013390 | Hs.160417 | transmembrane protein 2 | 2.17 |
| | 417404 | NM_007350 | Hs.82101 | pleckstrin homology-like domain, family | 2.17 |
| | 449437 | AI702038 | Hs.100057 | Homo sapiens cDNA: FLJ22902 fis, clone K | 2.17 |
| | 446995 | AI355012 | | gb:qu16d10.x1 NCI_CGAP_Ov23 Homo sapiens | 2.17 |
| 75 | 431548 | AI834273 | Hs.9711 | Homo sapiens cDNA FLJ13018 fis, clone NT | 2.17 |
| | 411127 | AA668995 | Hs.218329 | hypothetical protein | 2.17 |
| | 439961 | AA857451 | Hs.269696 | ESTs | 2.17 |
| | 429125 | AA446854 | Hs.271004 | ESTs | 2.17 |
| | 407103 | AA424881 | Hs.256301 | ESTs | 2.17 |
| 80 | 435990 | AI015862 | Hs.131793 | ESTs | 2.17 |
| | 415116 | AA160363 | Hs.269956 | ESTs | 2.17 |
| | 440052 | AI633744 | Hs.195648 | ESTs | 2.17 |
| | 423961 | D13666 | Hs.136348 | osteoblast specific factor 2 (fascidin | 2.17 |
| | 431070 | AW408164 | Hs.249184 | transcription factor 19 (SC1) | 2.16 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 443599 | AI079559 | Hs.134125 | ESTs | 2.16 |
| | 423623 | AB011117 | Hs.129943 | KIAA0545 protein | 2.16 |
| | 427258 | AA400091 | Hs.39421 | ESTs | 2.16 |
| 5 | 418113 | AI272141 | Hs.83484 | SRY (sex determining region Y)-box 4 | 2.16 |
| | 450835 | BE262773 | Hs.25584 | hypothetical protein FLJ10767 | 2.16 |
| | 428698 | AA852773 | Hs.297939 | ESTs, Weakly similar to T17344 hypotheti | 2.16 |
| | 421408 | AI688223 | Hs.104114 | H.sapiens HCG 1 mRNA | 2.16 |
| | 449057 | AB037784 | Hs.22941 | KIAA1363 protein | 2.16 |
| 10 | 408947 | AL080093 | Hs.49117 | Homo sapiens mRNA; cDNA DKFZp564N1662 (f | 2.16 |
| | 443552 | NG5982 | Hs.109434 | ESTs | 2.16 |
| | 448153 | Y10805 | Hs.20521 | HMT1 (hnRNP methyltransferase, S. cerevi | 2.16 |
| | 424653 | AW977534 | Hs.151469 | calcium/calmodulin-dependent serine prot | 2.16 |
| | 431341 | AA307211 | Hs.251531 | proteasome (prosome, macropain) subunit, | 2.16 |
| 15 | 452865 | AI924046 | Hs.119567 | ESTs | 2.16 |
| | 432789 | D26361 | Hs.3104 | KIAA0042 gene product | 2.16 |
| | 438580 | AA811262 | Hs.299202 | ESTs | 2.16 |
| | 422192 | AA305159 | Hs.113019 | fts485 | 2.15 |
| | 425607 | U09860 | Hs.158333 | protease, serine, 7 (enterokinase) | 2.15 |
| 20 | 447289 | AW247017 | Hs.36978 | melanoma antigen, family A, 3 | 2.15 |
| | 447674 | BE270640 | Hs.19192 | cyclin-dependent kinase 2 | 2.15 |
| | 441021 | AW578716 | Hs.7644 | H1 histone family, member 2 | 2.15 |
| | 442432 | BE093589 | Hs.38178 | Homo sapiens cDNA: FLJ23458 fis, clone H | 2.15 |
| | 426471 | M22440 | Hs.170009 | transforming growth factor, alpha | 2.15 |
| 25 | 431941 | AK000106 | Hs.272227 | Homo sapiens cDNA FLJ20099 fis, clone CO | 2.15 |
| | 414761 | AU077228 | Hs.77256 | enhancer of zeste (Drosophila) homolog 2 | 2.15 |
| | 447033 | AI357412 | Hs.157601 | ESTs | 2.15 |
| | 410407 | X66839 | Hs.63287 | carbonic anhydrase IX | 2.15 |
| | 446077 | BE251048 | Hs.22579 | Homo sapiens clone CDABP0036 mRNA sequen | 2.15 |
| 30 | 420900 | AL045633 | Hs.44269 | ESTs | 2.15 |
| | 411975 | AI916058 | Hs.144583 | ESTs, Weakly similar to gag [H.sapiens] | 2.15 |
| | 419239 | AA468183 | Hs.184598 | Homo sapiens cDNA: FLJ23241 fis, clone C | 2.15 |
| | 449571 | AW016812 | Hs.200266 | ESTs | 2.15 |
| | 452721 | AJ269529 | Hs.30377 | Homo sapiens EST from clone 470080, full | 2.15 |
| 35 | 410491 | AA465131 | Hs.64001 | Homo sapiens clone 25218 mRNA sequence | 2.14 |
| | 410664 | NM_006033 | Hs.65370 | lipase, endothelial | 2.14 |
| | 435730 | AB020635 | Hs.4984 | KIAA0828 protein | 2.14 |
| | 452835 | AK001269 | Hs.30738 | hypothetical protein FLJ10407 | 2.14 |
| | 452092 | BE245374 | Hs.27842 | hypothetical protein FLJ11210 | 2.14 |
| 40 | 401708 | | | | 2.14 |
| | 411400 | AA311919 | Hs.69851 | GAR1 protein | 2.14 |
| | 448526 | AB028946 | Hs.21361 | KIAA1023 protein | 2.14 |
| | 421175 | AI879099 | Hs.102397 | GIOT-3 for gonadotropin inducible transc | 2.14 |
| | 412338 | AA151527 | Hs.69485 | Homo sapiens cDNA FLJ12436 fis, clone NT | 2.14 |
| 45 | 420894 | AA744597 | Hs.88854 | ESTs | 2.14 |
| | 409235 | AA188827 | Hs.7988 | ESTs, Weakly similar to endo-alpha-D-man | 2.14 |
| | 412870 | N22788 | Hs.82407 | Homo sapiens HSPC296 mRNA, partial cds | 2.14 |
| | 447760 | AI431328 | Hs.291179 | ESTs, Weakly similar to topoisomerase I | 2.14 |
| | 413511 | AI627178 | Hs.75412 | Arginine-rich protein | 2.13 |
| 50 | 432945 | AL043683 | Hs.271357 | ESTs, Weakly similar to unnamed protein | 2.13 |
| | 418592 | X99226 | Hs.284153 | Fanconi anemia, complementation group A | 2.13 |
| | 441790 | AW294909 | Hs.132208 | ESTs | 2.13 |
| | 425298 | AK000209 | Hs.155556 | hypothetical protein FLJ20202 | 2.13 |
| | 450956 | AW193531 | Hs.205647 | ESTs, Moderately similar to ALU1_HUMAN A | 2.13 |
| 55 | 419569 | AI971651 | Hs.91143 | jagged 1 (Alagille syndrome) | 2.13 |
| | 421508 | NM_004833 | Hs.105115 | absent in melanoma 2 | 2.13 |
| | 453975 | AW009808 | Hs.270829 | ESTs | 2.13 |
| | 413670 | AB000115 | Hs.75470 | hypothetical protein, expressed in osteo | 2.13 |
| 60 | 422783 | AA598956 | Hs.120439 | ethanolamine kinase | 2.13 |
| | 444542 | AI161293 | Hs.146862 | ESTs, Weakly similar to KIAA0525 protein | 2.13 |
| | 410418 | D31382 | Hs.63325 | transmembrane protease, serine 4 | 2.13 |
| | 419791 | AI579909 | Hs.105104 | ESTs | 2.13 |
| | 414860 | BE255593 | Hs.77502 | methionine adenosyltransferase II, alpha | 2.13 |
| | 425860 | L29339 | Hs.1964 | solute carrier family 5 (sodium/glucose | 2.13 |
| 65 | 414839 | X63692 | Hs.77462 | DNA (cytosine-5)-methyltransferase 1 | 2.13 |
| | 437050 | AA766420 | Hs.291606 | ESTs | 2.13 |
| | 430217 | N47863 | Hs.180450 | ribosomal protein S24 | 2.13 |
| | 420923 | AF097021 | Hs.273321 | differentially expressed in hematopoieti | 2.12 |
| | 409012 | AL117435 | Hs.49725 | DKFZP434I216 protein | 2.12 |
| 70 | 450645 | AL117441 | Hs.25264 | DKFZP434N126 protein | 2.12 |
| | 431322 | AW970622 | | gb:EST382704 MAGE resequences, MAGK Homo | 2.12 |
| | 451356 | AA748418 | Hs.164577 | ESTs | 2.12 |
| | 429534 | AW976987 | Hs.163327 | ESTs | 2.12 |
| | 428365 | AA295331 | Hs.183861 | Homo sapiens cDNA FLJ20042 fis, clone CO | 2.12 |
| 75 | 441495 | AW294603 | Hs.127039 | ESTs | 2.12 |
| | 443564 | AI921685 | Hs.199713 | ESTs | 2.12 |
| | 410839 | NM_006849 | Hs.66581 | protein disulfide isomerase | 2.12 |
| | 433640 | AW390125 | Hs.240443 | Homo sapiens cDNA: FLJ23538 fis, clone L | 2.12 |
| | 442947 | R40800 | Hs.21303 | ESTs | 2.12 |
| 80 | 414987 | AA524394 | Hs.165544 | ESTs | 2.12 |
| | 450510 | AA010056 | Hs.242998 | ESTs | 2.12 |
| | 427475 | AA403151 | Hs.191605 | ESTs | 2.12 |
| | 444670 | H58373 | Hs.37494 | ESTs | 2.12 |
| | 452099 | BE612992 | Hs.27931 | hypothetical protein FLJ10607 similar to | 2.12 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 433748 | R12244 | | gb:yf33c12.r1 Soares fetal liver spleen | 2.12 |
| | 415138 | C18356 | Hs.78045 | tissue factor pathway inhibitor 2 | 2.11 |
| | 438138 | R98299 | Hs.177502 | ESTs | 2.11 |
| 5 | 414788 | X78342 | Hs.77313 | cyclin-dependent kinase (CDC2-like) 10 | 2.11 |
| | 415474 | NM_014252 | Hs.78457 | solute carrier family 25 (mitochondrial) | 2.11 |
| | 416472 | AA180756 | Hs.193094 | ESTs, Moderately similar to ALU4_HUMAN A | 2.11 |
| | 412490 | AW803564 | Hs.288850 | Homo sapiens cDNA: FLJ22528 fis, clone H | 2.11 |
| | 410718 | AI920783 | Hs.191435 | ESTs | 2.11 |
| 10 | 425811 | AL039104 | Hs.159557 | karyopherin alpha 2 (RAG cohort 1, impor | 2.11 |
| | 433344 | AI741506 | Hs.186753 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.11 |
| | 447197 | R36075 | | gb:yh88b01.s1 Soares placenta Nb2HP Homo | 2.11 |
| | 431621 | AW292329 | Hs.163481 | ESTs | 2.11 |
| | 418522 | AA605038 | Hs.7149 | Homo sapiens cDNA: FLJ21950 fis, clone H | 2.11 |
| 15 | 433849 | BE465884 | Hs.280728 | ESTs | 2.11 |
| | 438038 | AI732629 | Hs.194161 | ESTs, Weakly similar to TA2R HUMAN, BETA | 2.11 |
| | 422032 | AA476966 | Hs.110857 | polymerase (RNA) III (DNA directed) poly | 2.11 |
| | 409717 | AW452871 | Hs.56043 | CGI-115 protein | 2.11 |
| | 410566 | AA373210 | Hs.43047 | Homo sapiens cDNA FLJ13585 fis, clone PL | 2.11 |
| 20 | 445837 | AI261700 | Hs.145544 | ESTs | 2.11 |
| | 414334 | AA824298 | Hs.21331 | hypothetical protein FLJ10036 | 2.11 |
| | 436326 | BE085236 | Hs.181244 | major histocompatibility complex, class | 2.10 |
| | 423880 | BE278111 | Hs.134200 | DKFZP564C186 protein | 2.10 |
| | 421574 | AJ000152 | Hs.105924 | defensin, beta 2 | 2.10 |
| 25 | 437103 | AW139408 | Hs.152940 | ESTs | 2.10 |
| | 435550 | AI224456 | Hs.4934 | H.sapiens polyA site DNA | 2.10 |
| | 450747 | AI064821 | Hs.48306 | ESTs, Highly similar to EWS_HUMAN RNA-BI | 2.10 |
| | 437033 | AW248364 | Hs.5409 | RNA polymerase I subunit | 2.10 |
| | 417640 | D30857 | Hs.82353 | protein C receptor, endothelial (EPCR) | 2.10 |
| 30 | 431120 | AA492588 | | gb:ng99c08.s1 NCL_CGAP_Thy1 Homo sapiens | 2.10 |
| | 430510 | AW162916 | Hs.241576 | hypothetical protein PRO2577 | 2.10 |
| | 429669 | BE185499 | Hs.2471 | KIAA0020 gene product | 2.10 |
| | 407881 | AW072003 | Hs.40968 | heparan sulfate (glucosamine) 3-O-sulfot | 2.10 |
| | 436124 | AA705012 | Hs.269584 | ESTs | 2.10 |
| 35 | 436415 | BE265254 | Hs.5181 | proliferation-associated 2C4, 38kD | 2.10 |
| | 451121 | AW973795 | Hs.128927 | Homo sapiens cDNA FLJ13903 fis, clone TH | 2.10 |
| | 453968 | AA847843 | Hs.62711 | ESTs | 2.10 |
| | 437549 | AA759149 | | gb:ah70e03.s1 Soares testis_NHT Homo sap | 2.10 |
| | 407887 | AA579668 | Hs.41072 | serine (or cysteine) proteinase inhibito | 2.10 |
| 40 | 447720 | AL038765 | Hs.161304 | ESTs | 2.09 |
| | 434769 | AA648884 | Hs.134278 | Homo sapiens cDNA FLJ12676 fis, clone NT | 2.09 |
| | 429743 | AA804398 | Hs.288995 | hypothetical protein FLJ20813 | 2.09 |
| | 447815 | AI432199 | Hs.247084 | ESTs | 2.09 |
| | 441675 | AI914329 | Hs.5461 | ESTs | 2.09 |
| 45 | 434274 | AA628539 | Hs.116252 | ESTs, Moderately similar to ALU1_HUMAN A | 2.09 |
| | 411571 | AA122393 | Hs.70811 | hypothetical protein FLJ20516 | 2.09 |
| | 442525 | AF150282 | Hs.145945 | ESTs | 2.09 |
| | 423750 | AF165883 | Hs.132415 | prefoldin 2 | 2.09 |
| | 449199 | AI990122 | Hs.196988 | ESTs | 2.09 |
| 50 | 415363 | AI670947 | Hs.78406 | phosphatidylinositol-4-phosphate 5-kinas | 2.09 |
| | 432543 | AA552690 | Hs.152423 | Homo sapiens cDNA: FLJ21274 fis, clone C | 2.09 |
| | 418462 | BE001596 | Hs.85266 | integrin, beta 4 | 2.09 |
| | 432093 | H28383 | | gb:yf52c03.r1 Soares breast 3NbHBst Homo | 2.09 |
| | 407862 | BE548267 | Hs.50724 | Homo sapiens cDNA FLJ10934 fis, clone OV | 2.09 |
| 55 | 434442 | AA737415 | Hs.152826 | ESTs | 2.09 |
| | 442671 | AI005668 | Hs.134779 | EST | 2.09 |
| | 428771 | AB028992 | Hs.193143 | KIAA1069 protein | 2.09 |
| | 430335 | D80007 | Hs.239499 | KIAA0185 protein | 2.08 |
| | 425087 | R62424 | Hs.126059 | ESTs | 2.08 |
| 60 | 412530 | AA766268 | Hs.266273 | Homo sapiens cDNA FLJ13346 fis, clone OV | 2.08 |
| | 443450 | N66045 | Hs.133529 | ESTs | 2.08 |
| | 418753 | BE217818 | Hs.87016 | Homo sapiens cDNA: FLJ22938 fis, clone K | 2.08 |
| | 432204 | AI916132 | Hs.121593 | Homo sapiens cDNA FLJ13123 fis, clone NT | 2.08 |
| | 439018 | AW300887 | Hs.26638 | ESTs, Weakly similar to unnamed protein | 2.08 |
| 65 | 418300 | AI433074 | Hs.86682 | Homo sapiens cDNA: FLJ21578 fis, clone C | 2.08 |
| | 431628 | AF146277 | Hs.265561 | CD2-associated protein | 2.08 |
| | 446528 | AU076640 | Hs.15243 | nucleolar protein 1 (120kD) | 2.08 |
| | 432284 | AA532807 | Hs.105822 | ESTs | 2.08 |
| | 411372 | AI147861 | Hs.213289 | low density lipoprotein receptor (famili | 2.08 |
| 70 | 459319 | NM_000059 | | gb:Homo sapiens breast cancer 2, early o | 2.08 |
| | 408730 | AV660717 | Hs.47144 | DKFZP585N0819 protein | 2.08 |
| | 443607 | AI452512 | Hs.134069 | ESTs | 2.08 |
| | 422058 | AA862231 | | gb:oe13g03.s1 NCL_CGAP_Ov2 Homo sapiens | 2.08 |
| | 409220 | BE243323 | Hs.51233 | tumor necrosis factor receptor superfam | 2.08 |
| 75 | 429504 | X99133 | Hs.204238 | lipocalin 2 (oncogene 24p3) | 2.08 |
| | 409686 | AK000002 | Hs.55879 | Homo sapiens mRNA for FLJ00036 protein, | 2.08 |
| | 438394 | BE379623 | Hs.27693 | CGI-124 protein | 2.08 |
| | 413092 | AA126856 | Hs.118665 | ESTs | 2.08 |
| | 413715 | AW851121 | Hs.75497 | Homo sapiens cDNA: FLJ22139 fis, clone H | 2.08 |
| 80 | 423020 | AA383092 | Hs.1608 | replication protein A3 (14kD) | 2.07 |
| | 438378 | AW970529 | Hs.86434 | Homo sapiens cDNA: FLJ21816 fis, clone H | 2.07 |
| | 453379 | AA035261 | Hs.61753 | ESTs | 2.07 |
| | 432125 | AW972667 | Hs.287510 | Homo sapiens cDNA FLJ12300 fis, clone MA | 2.07 |
| | 449370 | AK002114 | Hs.23495 | hypothetical protein FLJ11252 | 2.07 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 449318 | AW236021 | Hs.108788 | ESTs, Weakly similar to zeste [D.melanog | 2.07 |
| | 450096 | AI682088 | Hs.223368 | ESTs | 2.07 |
| | 454011 | M31008 | Hs.37009 | alkaline phosphatase, intestinal | 2.07 |
| 5 | 427876 | AI494291 | Hs.111977 | ESTs | 2.07 |
| | 422901 | R81936 | Hs.121576 | aspartate beta-hydroxylase | 2.07 |
| | 419235 | AW470411 | Hs.288433 | neurotrophin | 2.07 |
| | 449207 | AL044222 | Hs.23255 | nucleoporin 15SkD | 2.07 |
| | 408243 | Y00787 | Hs.624 | interleukin 8 | 2.07 |
| 10 | 415652 | T79213 | Hs.272073 | ESTs | 2.07 |
| | 446546 | BE167687 | Hs.156628 | ESTs | 2.07 |
| | 411765 | H43346 | | gb:yp09a04.r1 Soares breast 3NbHBst Homo | 2.07 |
| | 423472 | AF041260 | Hs.129057 | breast carcinoma amplified sequence 1 | 2.07 |
| | 436211 | AK001581 | Hs.80961 | polymerase (DNA directed), gamma | 2.07 |
| 15 | 456157 | AW979153 | | gb:EST391263 MAGE resequences, MAGP Homo | 2.06 |
| | 407143 | C14076 | Hs.248968 | EST | 2.06 |
| | 454269 | AV61060 | Hs.296411 | ESTs, Moderately similar to KF1A_HUMAN K | 2.06 |
| | 432440 | X63597 | Hs.2996 | sucrase-isomaltase | 2.06 |
| | 410668 | BE379794 | Hs.65403 | hypothetical protein | 2.06 |
| 20 | 422765 | AW409701 | Hs.1578 | baculoviral IAP repeat-containing 5 (sur | 2.06 |
| | 450434 | AA166950 | Hs.18645 | ESTs, Weakly similar to partial CDS [C.e | 2.06 |
| | 439832 | T81829 | Hs.14870 | ESTs | 2.06 |
| | 456264 | AW974175 | Hs.105251 | ESTs | 2.06 |
| | 431201 | AA678405 | Hs.8854 | Human transcription unit PVT gene, exons | 2.06 |
| 25 | 445021 | AK002025 | Hs.12251 | Homo sapiens cDNA FLJ11163 fis, clone PL | 2.06 |
| | 438714 | AA814859 | Hs.294112 | ESTs | 2.06 |
| | 445318 | AW500652 | Hs.200885 | ESTs | 2.06 |
| | 439951 | AI347067 | Hs.124636 | ESTs | 2.06 |
| | 433681 | AI004377 | Hs.200360 | Homo sapiens cDNA FLJ13027 fis, clone NT | 2.06 |
| 30 | 428307 | W27393 | Hs.183648 | protein tyrosine phosphatase, receptor t | 2.06 |
| | 426874 | N67325 | Hs.247132 | ESTs | 2.06 |
| | 451295 | AI557212 | Hs.17132 | ESTs | 2.06 |
| | 432584 | AA928829 | Hs.47099 | Homo sapiens cDNA: FLJ21212 fis, clone C | 2.06 |
| | 433027 | AF191018 | Hs.279923 | putative nucleotide binding protein, est | 2.06 |
| 35 | 433716 | AA608808 | Hs.225118 | ESTs | 2.06 |
| | 429412 | NM_006235 | Hs.2407 | POU domain, class 2, associating factor | 2.06 |
| | 426235 | AI631964 | Hs.34447 | ESTs | 2.06 |
| | 449026 | BE500946 | Hs.209105 | ESTs | 2.06 |
| | 437016 | AU076916 | Hs.5398 | guanine monophosphate synthetase | 2.06 |
| 40 | 400019 | | | AFFX control: STAT1 | 2.06 |
| | 408873 | AL046017 | Hs.23247 | ESTs | 2.06 |
| | 442547 | AA306997 | Hs.268362 | ESTs, Weakly similar to hypothetical pro | 2.06 |
| | 455778 | BE088746 | | gb:CM2-BT0693-210300-123-d09 BT0693 Homo | 2.06 |
| | 439975 | AW328081 | Hs.6817 | Homo sapiens putative oncogene protein m | 2.06 |
| 45 | 433037 | NM_014158 | Hs.279938 | HSPC067 protein | 2.06 |
| | 440086 | NM_005402 | Hs.288757 | v-rat simian leukemia viral oncogene hom | 2.06 |
| | 436414 | BE264633 | Hs.143638 | WD repeat domain 4 | 2.05 |
| | 411770 | NM_014278 | Hs.71992 | heat shock protein (hsp110 family) | 2.05 |
| | 407293 | AA602234 | Hs.270551 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.05 |
| 50 | 409459 | D86407 | Hs.54481 | low density lipoprotein receptor-related | 2.05 |
| | 436238 | AK002163 | Hs.301724 | ESTs, Highly similar to unnamed protein | 2.05 |
| | 400517 | AF242388 | Hs.149585 | lensin | 2.05 |
| | 439943 | AW083789 | Hs.124620 | ESTs | 2.05 |
| | 421904 | BE143533 | Hs.109309 | hypothetical protein FLJ20035 | 2.05 |
| 55 | 417850 | AA215724 | Hs.82741 | primase, polypeptide 1 (49kD) | 2.05 |
| | 417491 | AW376842 | Hs.1085 | guanylate cyclase 2C (heat stable entero | 2.05 |
| | 453775 | NM_002916 | Hs.35120 | replication factor C (activator 1) 4 (37 | 2.05 |
| | 435525 | AI831297 | Hs.123310 | ESTs | 2.05 |
| | 412627 | BE391959 | Hs.74276 | chloride intracellular channel 1 | 2.05 |
| 60 | 439702 | AW085525 | Hs.134182 | ESTs | 2.05 |
| | 440006 | AK000517 | Hs.6844 | hypothetical protein FLJ20510 | 2.05 |
| | 432979 | AA573263 | Hs.120860 | ESTs | 2.05 |
| | 417308 | H50720 | Hs.81892 | KIAA0101 gene product | 2.05 |
| | 432925 | AA878324 | Hs.192734 | ESTs | 2.05 |
| 65 | 446311 | AW007294 | Hs.149795 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.05 |
| | 427871 | AW992405 | Hs.59622 | ESTs, Weakly similar to unknown [H.sapie | 2.05 |
| | 453804 | AA300204 | Hs.35276 | KIAA0852 protein | 2.05 |
| | 449939 | T86420 | Hs.272139 | ESTs | 2.05 |
| | 455666 | BE065813 | | gb:RC2-BT0318-110100-012-a08 BT0318 Homo | 2.05 |
| 70 | 417819 | AI253112 | Hs.133540 | ESTs | 2.04 |
| | 427747 | AW411425 | Hs.180655 | serine/threonine kinase 12 | 2.04 |
| | 415009 | C75253 | Hs.220950 | ESTs | 2.04 |
| | 437829 | AI358522 | Hs.270188 | ESTs | 2.04 |
| | 435381 | AW136397 | Hs.247572 | ESTs | 2.04 |
| 75 | 439778 | AL109729 | Hs.18948 | ESTs, Highly similar to HPS1_HUMAN PROTE | 2.04 |
| | 428753 | AW939252 | Hs.192927 | hypothetical protein FLJ20251 | 2.04 |
| | 446475 | AI908188 | Hs.209245 | ESTs | 2.04 |
| | 431394 | AK000692 | Hs.252351 | HERV-H LTR-associating 2 | 2.04 |
| | 423701 | AA329856 | Hs.143022 | ESTs | 2.04 |
| 80 | 430680 | AW138724 | Hs.168974 | ESTs, Highly similar to ALU7_HUMAN ALU S | 2.04 |
| | 422369 | AF005216 | Hs.115541 | Janus kinase 2 (a protein tyrosine kinas | 2.04 |
| | 432481 | AW451645 | Hs.151504 | Homo sapiens cDNA FLJ11973 fis, clone HE | 2.04 |
| | 443746 | AW861379 | Hs.160602 | ESTs | 2.04 |
| | 400792 | AA635062 | Hs.50094 | Homo sapiens mRNA; cDNA DKFp434O0515 (f | 2.04 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| 5 | 432393 | AW205863 | Hs.133988 | ESTs, Weakly similar to I52825 gene MAC2 | 2.04 |
| | 430785 | Z30201 | | gb:HHEA22G Atrium cDNA library Human hea | 2.04 |
| | 428343 | AL043021 | Hs.12705 | ESTs, Weakly similar to plakophilin 2b | 2.04 |
| | 419329 | AY007220 | Hs.288998 | S100-type calcium binding protein A14 | 2.04 |
| | 452488 | N74921 | Hs.184389 | ESTs | 2.04 |
| 10 | 403485 | | | | 2.04 |
| | 413313 | NM_002047 | Hs.75280 | glycyl-tRNA synthetase | 2.04 |
| | 407634 | AW016569 | Hs.301280 | ESTs, Highly similar to AF241831 1 intra | 2.04 |
| | 433326 | AJ379486 | Hs.159430 | ESTs | 2.04 |
| | 451129 | BE072881 | | gb:RC2-BT0548-200300-012-e09 BT0548 Homo | 2.03 |
| 15 | 429165 | AW009886 | Hs.118258 | prostate cancer associated protein 1 | 2.03 |
| | 422963 | M79141 | Hs.13234 | ESTs | 2.03 |
| | 418684 | U82987 | Hs.87246 | Bcl-2 binding component 3 | 2.03 |
| | 407824 | AA147884 | Hs.9812 | ESTs | 2.03 |
| | 434551 | BE387162 | Hs.280858 | ESTs, Highly similar to XPB_HUMAN DNA-RE | 2.03 |
| 20 | 440246 | W52010 | Hs.191379 | ESTs | 2.03 |
| | 444006 | BE395085 | Hs.10086 | type I transmembrane protein Fn14 | 2.03 |
| | 431301 | AA502384 | Hs.151529 | ESTs | 2.03 |
| | 452705 | H49805 | Hs.246005 | ESTs | 2.03 |
| | 421724 | AB037832 | Hs.107287 | KIAA1411 protein | 2.03 |
| 25 | 420637 | AW976153 | | gb:EST388262 MAGE resequences, MAGN Homo | 2.03 |
| | 450200 | AW975625 | Hs.173088 | ESTs | 2.03 |
| | 447474 | AW614220 | Hs.189402 | ESTs | 2.03 |
| | 418852 | BE537037 | Hs.273294 | hypothetical protein FLJ20069 | 2.03 |
| | 445019 | AI205540 | Hs.281295 | ESTs | 2.03 |
| 30 | 435202 | AJ971313 | Hs.170204 | KIAA0551 protein | 2.03 |
| | 431842 | NM_005764 | Hs.271473 | epithelial protein up-regulated in carci | 2.03 |
| | 436198 | AK001125 | Hs.300922 | Homo sapiens cDNA FLJ10263 fis, clone HE | 2.03 |
| | 440773 | AA352702 | Hs.37747 | hypothetical protein FLJ12484 | 2.03 |
| | 443425 | AI056776 | Hs.133397 | ESTs | 2.03 |
| 35 | 454166 | AW993356 | Hs.2055 | ubiquitin-activating enzyme E1 (A1S9T an | 2.03 |
| | 407975 | X89426 | Hs.41716 | endothelial cell-specific molecule 1 (NO | 2.03 |
| | 428299 | AL038004 | Hs.29419 | ESTs | 2.03 |
| | 418735 | N48769 | Hs.44609 | ESTs | 2.03 |
| | 442053 | R35343 | Hs.24968 | Human DNA sequence from clone RP1-233G16 | 2.03 |
| 40 | 415757 | AA830854 | Hs.187810 | ESTs | 2.03 |
| | 432559 | AW452948 | Hs.257631 | ESTs | 2.03 |
| | 425912 | AL137629 | Hs.162189 | serine/threonine kinase with Dbl- and pl | 2.02 |
| | 419395 | BE268326 | Hs.90280 | 5-aminoimidazole-4-carboxamide ribonucle | 2.02 |
| | 417576 | AA339449 | Hs.82285 | phosphoribosylglycylamide formyltransfer | 2.02 |
| 45 | 418559 | AA225048 | Hs.104207 | ESTs | 2.02 |
| | 410855 | X97795 | Hs.66718 | RAD54 (S.cerevisiae)-like | 2.02 |
| | 433906 | AI167816 | Hs.43355 | ESTs | 2.02 |
| | 422072 | AB018255 | Hs.111138 | KIAA0712 gene product | 2.02 |
| | 419546 | AA244199 | | gb:nc06c05.s1 NCI_CGAP_Pr1 Homo sapiens | 2.02 |
| 50 | 446229 | AJ744964 | Hs.14449 | KIAA1609 protein | 2.02 |
| | 450516 | AA902656 | Hs.21943 | NIF3 (Ngg1 interacting factor 3, S.pombe | 2.02 |
| | 431721 | AB032996 | Hs.268044 | KIAA1170 protein | 2.02 |
| | 419807 | R77402 | | gb:y75f11.s1 Soares placenta Nb2HP Homo | 2.02 |
| | 438192 | AI859065 | Hs.16808 | ESTs, Weakly similar to paraplegin-like | 2.02 |
| 55 | 401866 | | | | 2.02 |
| | 443129 | R16075 | Hs.21668 | ESTs | 2.02 |
| | 426991 | AK001536 | Hs.285803 | Homo sapiens cDNA FLJ12852 fis, clone NT | 2.01 |
| | 414731 | AI890434 | Hs.77135 | Homo sapiens mRNA; cDNA DKFZp586A191 (fr | 2.01 |
| | 424783 | AA913909 | Hs.153088 | TATA box binding protein (TBP)-associate | 2.01 |
| 60 | 413293 | AL047483 | Hs.75270 | GTP-binding protein homologous to Saccha | 2.01 |
| | 435787 | AW162767 | Hs.100914 | hypothetical protein FLJ10352 | 2.01 |
| | 422599 | BE387202 | Hs.118638 | non-metastatic cells 1, protein (NM23A) | 2.01 |
| | 442660 | AW138174 | Hs.130651 | ESTs | 2.01 |
| | 456553 | AA721325 | Hs.189058 | ESTs, Weakly similar to cAMP-regulated g | 2.01 |
| 65 | 431630 | NM_002204 | Hs.265829 | integrin, alpha 3 (antigen CD49C, alpha | 2.01 |
| | 431300 | AA502346 | | gb:ne26b03.s1 NCI_CGAP_Co3 Homo sapiens | 2.01 |
| | 443180 | R15875 | Hs.70945 | ESTs | 2.01 |
| | 450914 | AI743761 | Hs.142528 | ESTs | 2.01 |
| | 448275 | BE514434 | Hs.20830 | synaptic Ras GTPase activating protein 1 | 2.01 |
| 70 | 405484 | | | | 2.01 |
| | 436469 | AK001455 | Hs.5198 | Down syndrome critical region gene 2 | 2.01 |
| | 451273 | NM_014811 | Hs.26163 | KIAA0649 gene product | 2.01 |
| | 439696 | W95298 | Hs.171882 | ESTs | 2.01 |
| | 432378 | AI493046 | Hs.146133 | ESTs | 2.01 |
| 75 | 417975 | AA641836 | Hs.30085 | Homo sapiens cDNA: FLJ23186 fis, clone L | 2.01 |
| | 453665 | AA626250 | Hs.181165 | eukaryotic translation elongation factor | 2.01 |
| | 419981 | AA897581 | Hs.128773 | ESTs | 2.01 |
| | 445808 | AV655234 | Hs.298083 | ESTs | 2.01 |
| | 435767 | H73505 | Hs.117874 | ESTs | 2.01 |
| 80 | 430466 | AF052573 | Hs.241517 | polymerase (DNA directed), theta | 2.01 |
| | 452747 | BE153855 | Hs.61460 | ESTs | 2.01 |
| | 422790 | AA809875 | Hs.25933 | ESTs | 2.01 |
| | 443303 | U67319 | Hs.9216 | caspase 7, apoptosis-related cysteine pr | 2.01 |
| | 433929 | AI375499 | Hs.27379 | ESTs | 2.01 |
| | 410008 | AA079552 | | gb:zm20h12.s1 Stratagene pancreas (93720 | 2.01 |
| | 448954 | AB014564 | Hs.22616 | KIAA0664 protein | 2.00 |
| | 440774 | AI420611 | Hs.127832 | ESTs | 2.00 |

| | | | | | |
|----|--------|----------|-----------|--|------|
| 5 | 451351 | AW058261 | Hs.168213 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.00 |
| | 442961 | BE614474 | Hs.289074 | Homo sapiens cDNA FLJ13986 fis, clone Y7 | 2.00 |
| | 424420 | BE614743 | Hs.146688 | prostaglandin E synthase | 2.00 |
| | 407154 | H79677 | | gb:yu76g10.s1 Soares fetal liver spleen | 2.00 |
| | 410240 | AL157424 | Hs.61289 | synaptotagmin 2 | 2.00 |
| | 426830 | AA385751 | Hs.160392 | ESTs | 2.00 |
| | 435014 | BE560898 | Hs.10026 | ribosomal protein L17 isolog | 2.00 |
| | 408620 | AI918693 | Hs.81848 | RAD21 (S. pombe) homolog | 2.00 |
| | 432829 | W60377 | Hs.57772 | ESTs | 2.00 |
| 10 | 406752 | AI285598 | Hs.217493 | annexin A2 | 2.00 |

TABLE 40A:

| | | |
|----|-------------|---------------------------------------|
| 15 | Pkey: | Unique Eos probeset identifier number |
| | CAT number: | Gene cluster number |
| | Accession: | Genbank accession numbers |

| | | | |
|----|--------|------------|---|
| 20 | Pkey | CAT number | Accession |
| | 408690 | 107490_1 | AW864542 AA056567 AW882724 |
| | 409965 | 116301_1 | AA079229 AA079201 AA078874 |
| | 410008 | 116812_1 | AA079552 BE142525 BE142527 |
| | 410145 | 1178960_1 | AW886300 AW887902 AW887893 AW886291 AW592641 |
| | 411765 | 125700_1 | H43346 AA248302 AA095182 |
| 25 | 416713 | 1610889_1 | T70174 H79244 T69850 H79151 |
| | 418546 | 176677_1 | AA224827 T59708 T59843 BE156903 |
| | 419546 | 185766_1 | AA244199 AA244272 H57440 |
| | 419807 | 188252_1 | R77402 AA262462 AA250988 R06794 |
| | 420637 | 195241_1 | AW976153 AA278945 AA747691 |
| 30 | 422058 | 210815_1 | AA862231 AA659033 AA302799 AA302798 |
| | 422128 | 211994_1 | AW881145 AA490718 M85637 AA304575 T06067 AA331991 |
| | 422689 | 219896_1 | AW856665 AA315006 AW954733 |
| | 425499 | 252539_1 | T62489 T62634 AA828581 AA358569 |
| 35 | 430704 | 322217_1 | AW813091 AW206655 AA484440 |
| | 430785 | 323486_1 | Z30201 AA486132 T72025 |
| | 431120 | 328264_1 | AA492588 AA492498 AA492571 |
| | 431300 | 331217_1 | AA502346 BE159863 |
| | 431322 | 331543_1 | AW970622 AA503009 AA502998 AA502989 AA502805 T92188 |
| 40 | 432009 | 34025_1 | AL137424 BE007148 T52277 |
| | 432093 | 341283_1 | H28383 AW972670 H28359 AA525808 |
| | 433748 | 37385_1 | R12244 H71290 AI110858 AF090916 AF075357 AA011531 |
| 45 | 434414 | 38585_1 | AI798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231 |
| | | | AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139 |
| | | | AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730 |
| | | | AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957 |
| | | | N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659 |
| | | | BE081531 H59570 |
| | 437549 | 438403_1 | AA759149 AW751066 AW844938 |
| 50 | 438223 | 452646_1 | AA781171 AI202139 AI202098 |
| | 438993 | 467651_1 | AA828995 AA834879 AI926361 |
| | 439848 | 477806_1 | AW979249 D63277 AA846968 |
| | 443597 | 574739_1 | AI078418 W80626 AW387769 |
| | 446995 | 702707_1 | AI355012 AW812856 |
| | 447197 | 711623_1 | R36075 AI366546 R36167 |
| 55 | 448437 | 763310_1 | AW470125 AI734872 AI749559 AW856504 AI583942 AW779036 AW843429 AW844876 AI520713 AW847236 |
| | 450190 | 827655_1 | T51387 AW191595 T51271 AI686285 |
| | 451105 | 859083_1 | AI761324 AW880941 AW880937 |
| | 451129 | 859870_1 | BE072881 BE072946 AI762181 |
| | 451237 | 863269_1 | AW600293 AI767468 |
| 60 | 455666 | 1349545_1 | BE065813 BE065788 BE065889 BE065832 |
| | 455778 | 1364506_1 | BE088746 BE088802 BE088755 BE088876 BE088947 BE088881 BE088952 |
| | 456157 | 158261_1 | AW979153 AA176967 AA826015 |

TABLE 40C:

| | | |
|----|--------------|--|
| 65 | Pkey: | Unique number corresponding to an Eos probeset |
| | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. |
| | Strand: | Indicates DNA strand from which exons were predicted. |
| 70 | NI_position: | Indicates nucleotide positions of predicted exons. |

| | | | | |
|----|--------|---------|--------|---|
| 75 | Pkey | Ref | Strand | NI_position |
| | 400514 | 9796594 | Minus | 78844-79025,80850-80991,89754-89941,93750-93891 |
| | 401519 | 6649315 | Plus | 157315-157950 |
| | 401708 | 2951946 | Plus | 154511-155298 |
| | 401866 | 8018106 | Plus | 73126-73623 |
| | 402075 | 8117407 | Plus | 121907-122035,122804-122921,124019-124161,124455-124610,125672-126076 |
| | 403055 | 8748904 | Minus | 109532-110225 |
| | 403208 | 7630829 | Minus | 147706-147903,148667-148804 |
| | 403422 | 9665041 | Minus | 151169-151561 |
| 80 | 403485 | 9966528 | Plus | 2888-3001,3198-3532,3655-4117 |
| | 403776 | 7770611 | Minus | 1414-1513,1624-1756 |
| | 404171 | 9930793 | Plus | 173667-173783,176876-177055 |
| | 404253 | 9367202 | Minus | 55675-56055 |

| | | | | |
|---|--------|---------|-------|---|
| 5 | 404519 | 8152000 | Plus | 12817-13000 |
| | 404567 | 7249169 | Minus | 101320-101501 |
| | 405484 | 5922025 | Plus | 199214-199579,199672-199920,200262-200495 |
| | 405545 | 1054740 | Plus | 118677-118807,119091-119296,121626-121823 |
| | 405818 | 4071056 | Plus | 29055-29196 |
| | 406399 | 9256288 | Minus | 63448-63554 |

TABLE 41A: ABOUT 634 SEQUENCES UP-REGULATED IN STOMACH CANCER

Table 41A lists about 634 genes up-regulated in stomach cancer compared to normal adult tissues that are likely to be extracellular or cell-surface proteins. These were selected as for Table 40A and the predicted protein contained a structural domain that is indicative of extracellular localization (e.g. ig, fn3, egf, 7tm domains). Predicted protein domains are noted.

| | | | | | |
|----|----------------|---|-----------|-----------------|---|
| 15 | Pkey: | Unique Eos probe/identifier number | | | |
| | ExAccn: | Exemplar Accession number, Genbank accession number | | | |
| | UnigeneID: | Unigene number | | | |
| | Unigene Title: | Unigene gene title | | | |
| | PSDomain: | Protein Structural Domain | | | |
| 20 | R1: | Ratio of tumor to normal adult tissues | | | |
| | Pkey | ExAccn | UnigeneID | Unigene Title | PSDomain |
| | 411243 | AB039886 | Hs.69319 | CA11 | SS |
| | 418007 | M13509 | Hs.83169 | matrix metallo | hemopexin,Peptidase_M10,SS |
| | 448811 | AI590371 | Hs.174759 | ESTs | TM |
| 25 | 409757 | NM_001898 | Hs.123114 | cystatin SN | cystatin,SS |
| | 421110 | AJ250717 | Hs.1355 | cathepsin E | asp,SS |
| | 428368 | BE440042 | Hs.83326 | matrix metallo | hemopexin,Peptidase_M10,SS |
| | 406687 | M31126 | Hs.272620 | pregnancy speci | hemopexin, TM, |
| | 428651 | AF196478 | Hs.188401 | annexin A10 | annexin, TM, |
| 30 | 425211 | M18667 | Hs.1867 | progastricin (| asp, TM,SS |
| | 423673 | BE003054 | Hs.1695 | matrix metallo | hemopexin,Peptidase_M10,SS |
| | 409683 | U33317 | Hs.711 | defensin, alpha | defensins,Defensin_propep,SS |
| | 428664 | AK001666 | Hs.189095 | similar to SALL | zf-C2H2,TM,SS |
| | 408380 | AF123050 | Hs.44532 | diubiquitin | ubiquitin,7tm_3,ANF_receptor,sushi,7tm_1,TM, |
| 35 | 428953 | AA306610 | Hs.194676 | DKFZP434C013 pr | art,TNFR_c6,DEAD,Slathmin,TM,SS |
| | 450685 | L15533 | Hs.423 | pancreatitis-as | lectin_c,TM,SS |
| | 409187 | AF154830 | Hs.50966 | carbamoyl-phosp | GATase,CPSase_L_chain,CPSase_sm_chain,MGS,TM, |
| | 434206 | AW136973 | Hs.288516 | ESTs, Weakly si | PH,TM, |
| | 421346 | Z34277 | Hs.103707 | apomucin | Cys_knot,vwd, |
| 40 | 427585 | D31152 | Hs.179729 | collagen, type | C1q,Collagen,TM,SS |
| | 425679 | X05997 | Hs.159177 | lipase, gastric | abhydrolase,SS |
| | 421582 | AI910275 | Hs.1406 | trefoil factor | trefoil,trypsin,TM,SS |
| | 422956 | BE545072 | Hs.122579 | hypothetical pr | TM |
| | 448105 | AW591433 | Hs.170675 | ESTs, Weakly si | trypsin,TM, |
| 45 | 413385 | M34455 | Hs.840 | indoleamine-pyr | IDO,TM, |
| | 417866 | AW067903 | Hs.82772 | collagen, type | TSPN,Collagen,COLFI,SS |
| | 419278 | AU076799 | Hs.1247 | apolipoprotein | Apolipoprotein,SS |
| | 407811 | AW190902 | Hs.40098 | cysteine knot s | SS |
| | 403422 | | | | SS |
| 50 | 403776 | | | | IL8,TM,SS |
| | 418478 | U38945 | Hs.1174 | cyclin-dependen | ank,TM,SS |
| | 428242 | H55709 | Hs.2250 | leukemia inhibi | LJF_OSM,SS |
| | 421341 | AJ243212 | Hs.279611 | deleted in mali | SS |
| | 428434 | AW363590 | Hs.65551 | ESTs, Weakly si | SS |
| 55 | 409420 | Z15008 | Hs.54451 | laminin, gamma | laminin_EGF,laminin_B,SS |
| | 431611 | U58766 | Hs.264428 | tissue specific | Epimerase,TM,SS |
| | 413719 | BE439580 | Hs.75498 | small inducible | IL8,SS |
| | 409956 | AW103364 | Hs.727 | inhibin, beta A | TGF-beta,TGFb_propeptide,SS |
| | 422420 | U03398 | Hs.1524 | tumor necrosis | TNF,TM, |
| 60 | 428227 | AA321649 | Hs.2248 | small inducible | IL8,TM,SS |
| | 422168 | AA586894 | Hs.112408 | S100 calcium-bi | efhand,TM, |
| | 412140 | AA219691 | Hs.73625 | RAB5 interactin | kinesin,TM,SS |
| | 414812 | X72755 | Hs.77367 | monokine induce | IL8,SS |
| | 419833 | AA251131 | Hs.220697 | ESTs | WHEP-TRS,TM, |
| 65 | 446232 | AI281848 | Hs.165547 | ESTs | 7tm_3,TM, |
| | 432398 | AA307808 | Hs.2979 | trefoil factor | trefoil,TM,SS |
| | 432867 | AW016936 | Hs.233364 | ESTs | GSHPx,TM,SS |
| | 424046 | AF027866 | Hs.138202 | serine (or cyst | serpin,TM, |
| | 414918 | AI219207 | Hs.72222 | Homo sapiens cD | TM |
| 70 | 454293 | H49739 | Hs.134013 | ESTs, Moderate | TM |
| | 442577 | AA292998 | Hs.163900 | ESTs | TM |
| | 426174 | AA547959 | Hs.115838 | ESTs | SS |
| | 418869 | AW516565 | Hs.258279 | ESTs | Sema,TM, |
| | 418054 | NM_002318 | Hs.83354 | lysyl oxidase-I | Lysyl_oxidase,SRCR,SS |
| 75 | 442295 | AI827248 | Hs.224398 | Homo sapiens cD | Collagen,COLFI,vwc,TM,SS |
| | 425921 | NM_007231 | Hs.162211 | solute carrier | SNF,TM, |
| | 421948 | L42583 | Hs.111758 | keratin 5A | filamen,TM, |
| | 444783 | AK001468 | Hs.62180 | anillin (Drosop | PH,TM, |
| | 437527 | AI241019 | Hs.145644 | ESTs | PIP5K,TM,SS |
| 80 | 433084 | M18079 | Hs.282265 | fatty acid bind | lipocafin,SS |
| | 452401 | NM_007115 | Hs.29352 | tumor necrosis | Xlink,CUB,TM,SS |
| | 458897 | U85642 | Hs.138506 | ESTs | TM |
| | 413808 | J00287 | Hs.182183 | caldesmon 1 | asp,TM,SS |
| | 411274 | NM_002776 | Hs.69423 | kallikrein 10 | trypsin,TM, |

| | | | | | | |
|----|--------|-----------|-----------|-----------------|---|------|
| 5 | 418406 | X73501 | Hs.84905 | cytokeratin 20 | filament, TM, | 3.32 |
| | 419559 | Y07828 | Hs.91096 | ring finger pro | zf-C3HC4,zf-B_box, TM, | 3.32 |
| | 423217 | NM_000094 | Hs.1640 | collagen, type | fn3, Collagen, Kunitz_BPT1, vwa, SS | 3.31 |
| | 411558 | AA102670 | Hs.70725 | gamma-aminobuty | neur_chan, TM, SS | 3.30 |
| | 427722 | AK000123 | Hs.180479 | hypothetical pr | PH, SS | 3.30 |
| | 422310 | AA316622 | Hs.98370 | cytochrome P540 | p450, SS | 3.30 |
| | 411263 | BE297802 | Hs.69360 | kinesin-like 6 | kinesin, TM, | 3.29 |
| | 443426 | AF098158 | Hs.9329 | chromosome 20 o | TM | 3.28 |
| 10 | 452121 | NM_004081 | Hs.70936 | deleted in azoo | TM | 3.27 |
| | 447342 | AI199268 | Hs.19322 | ESTs | TM, SS | 3.25 |
| | 452699 | AW295390 | Hs.213062 | ESTs | TM | 3.23 |
| | 425188 | AK002052 | Hs.155071 | hypothetical pr | TM | 3.23 |
| | 400289 | X07820 | Hs.2258 | matrix metallo | hemopexin, SS | 3.21 |
| 15 | 408524 | D87942 | Hs.46328 | fucoyltransfer | Glyco_transf_11, TM, SS | 3.20 |
| | 437897 | AA770561 | Hs.145170 | hypothetical pr | TM | 3.20 |
| | 453922 | AF053306 | Hs.36708 | budding uninhib | TM | 3.19 |
| | 406690 | M29540 | Hs.220529 | carcinoembryoni | ig, TM, SS | 3.19 |
| | 416209 | AA236776 | Hs.79078 | MAD2 (mitotic a | HORMA, SS | 3.16 |
| 20 | 408113 | T82427 | Hs.194101 | Homo sapiens cD | 7tm_3, TM, | 3.14 |
| | 425455 | L18964 | Hs.1904 | protein kinase | Slk_Sno, DAG_PE-bind, OPR, pkise, pkise_C, TM, SS | 3.13 |
| | 419216 | AU076718 | Hs.164021 | small inducible | IL8, TM, SS | 3.13 |
| | 418203 | XS4942 | Hs.83758 | CDC28 protein k | CKS, TM, | 3.12 |
| | 417315 | AI080042 | Hs.180450 | ribosomal prote | TM, SS | 3.11 |
| 25 | 433001 | AF217513 | Hs.279905 | clone HQ0310 PR | TM, SS | 3.11 |
| | 459587 | AA031956 | | gb:zkl5e04.s1 S | UM, TM, | 3.11 |
| | 421379 | Y15221 | Hs.103982 | small inducible | IL8, TM, SS | 3.10 |
| | 414774 | X02419 | Hs.77274 | plasminogen act | kringle, trypsin, SS | 3.10 |
| | 407289 | AA135159 | Hs.203349 | Homo sapiens cD | TM | 3.09 |
| 30 | 447519 | U46258 | Hs.23448 | ESTs | histone, Ribosomal_L22e, TM, | 3.08 |
| | 448045 | AJ297436 | Hs.20166 | prostate stem c | TM, SS | 3.07 |
| | 431956 | AK002032 | Hs.272245 | Homo sapiens cD | RA, SS | 3.06 |
| | 409632 | W74001 | Hs.55279 | serine (or cyst | serpin, TM, | 3.05 |
| | 454034 | NM_000691 | Hs.575 | aldehyde dehydr | aldedh, TM, | 3.05 |
| 35 | 436481 | AA379597 | Hs.5199 | HSPC150 protein | UQ_con, TM, | 3.05 |
| | 428987 | NM_004751 | Hs.194710 | glucosaminyl (N | Branch, TM, SS | 3.04 |
| | 424252 | AK000520 | Hs.143811 | hypothetical pr | casein_kappa, SS | 3.04 |
| | 436291 | BE568452 | Hs.5101 | protein regulat | TM | 3.03 |
| | 411789 | AF245505 | Hs.72157 | Homo sapiens ad | ig, LRRCT, SS | 3.02 |
| 40 | 417956 | AA210704 | Hs.190465 | ESTs | sushi, SS | 3.02 |
| | 408908 | BE296227 | Hs.48915 | serine/threonin | pkise, TM, SS | 3.01 |
| | 422330 | D30783 | Hs.115263 | epiregulin | EGF, TM, SS | 3.01 |
| | 425071 | NM_013989 | Hs.154424 | deiodinase, iod | T4_deiodise, TM, SS | 3.00 |
| | 425761 | AW664214 | Hs.196729 | ESTs | SH3, TM, | 2.99 |
| 45 | 432978 | AF126743 | Hs.279884 | DNAJ domain-con | DJ, TM, | 2.99 |
| | 418546 | AA224827 | | gb:nc32g04.s1 N | vwa, integrin_A, FG-GAP, TM, SS | 2.99 |
| | 425371 | D49441 | Hs.155981 | mesothelin | TM, SS | 2.99 |
| | 422440 | NM_004812 | Hs.116724 | aldo-keto reduc | aldo_ket_red, TM, | 2.98 |
| | 439453 | BE264974 | Hs.6566 | thyroid hormone | AAA, TM, | 2.98 |
| 50 | 413278 | BE563085 | Hs.833 | interferon-stim | ubiquitin, TM, | 2.97 |
| | 428450 | NM_014791 | Hs.184339 | KIAA0175 gene p | pkise, KA1, TM, | 2.95 |
| | 424345 | AK001380 | Hs.145479 | Homo sapiens cD | TM, SS | 2.95 |
| | 433133 | AB027249 | Hs.104741 | PDZ-binding kin | pkise, TM, | 2.94 |
| | 432269 | NM_002447 | Hs.2942 | macrophage stim | pkise, Sema, Plexin_repeat, TIG, TM, SS | 2.94 |
| 55 | 432917 | NM_014125 | Hs.279812 | PRO0327 protein | TM | 2.94 |
| | 432731 | R31178 | Hs.287820 | fibronectin 1 | SS | 2.93 |
| | 420552 | AK000492 | Hs.98806 | hypothetical pr | SS | 2.92 |
| | 428303 | AW974476 | Hs.183601 | regulator of G- | RGS, TM, | 2.92 |
| | 409687 | T51125 | Hs.8493 | ESTs | Ets, SAM_PNT, TM, | 2.91 |
| 60 | 457288 | AA521458 | Hs.192738 | ESTs | TM | 2.89 |
| | 456181 | L36463 | Hs.1030 | ras inhibitor | RA, VPS9, TM, SS | 2.89 |
| | 450190 | T51387 | | gb:yb20e08.r1 S | SH3, TM, | 2.88 |
| | 430204 | AA618335 | Hs.146137 | ESTs, Weakly si | TM | 2.88 |
| | 434808 | AF155108 | Hs.256150 | ESTs, Highly si | TM | 2.87 |
| 65 | 450983 | AA305384 | Hs.25740 | ERO1 (S. cerevi | SS | 2.87 |
| | 418670 | AA601036 | Hs.285083 | ESTs | TM | 2.87 |
| | 416661 | AA634543 | Hs.79440 | IGF-II mRNA-bin | KH-domain, TM, | 2.87 |
| | 435099 | AC004770 | Hs.4756 | flap structure- | XPG_I, XPG_N, TM, | 2.86 |
| | 402075 | | | | serpin, TM, | 2.84 |
| 70 | 410681 | AW246890 | Hs.65425 | calbindin 1, (2 | efhand, FHA, BRCT, adh_short, adh_short_C2, TM, | 2.83 |
| | 439867 | AA847510 | Hs.161292 | ESTs | TM | 2.83 |
| | 443715 | AI583187 | Hs.9700 | cyclin E1 | cyclin, TM, SS | 2.83 |
| | 417366 | BE185289 | Hs.1076 | small protine-r | Corinfin, TM, | 2.83 |
| | 422283 | AW411307 | Hs.114311 | CDC45 (cell div | CDC45, TM, SS | 2.82 |
| 75 | 404567 | | | | HECT, zf-UBR1, TM, | 2.82 |
| | 422158 | L10343 | Hs.112341 | protease inhibi | wap, SS | 2.82 |
| | 449224 | AW995911 | Hs.299883 | hypothetical pr | fn3, TM, | 2.81 |
| | 407584 | W25945 | Hs.18745 | ESTs | PK, SS | 2.81 |
| | 453884 | AA355925 | Hs.36232 | KIAA0186 gene p | TM | 2.81 |
| 80 | 449032 | AA045573 | Hs.22900 | nuclear factor | bZIP, Chromo_shadow, TM, SS | 2.80 |
| | 422809 | AK001379 | Hs.121028 | hypothetical pr | IQ, TM, | 2.79 |
| | 449722 | BE280074 | Hs.23960 | cyclin B1 | cyclin, TM, | 2.79 |
| | 453028 | AB006532 | Hs.31442 | RecQ protein-li | DEAD, helicase_C, TM, | 2.78 |
| | 421777 | BE562088 | Hs.108196 | HSPC037 protein | TM | 2.78 |

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|----|--------|-----------|-----------|-------------------|--|------|
| | 452571 | W31518 | Hs.34665 | ESTs | TM | |
| | 422675 | BE018517 | Hs.119140 | eukaryotic tran | eIF-5a, TM, | 2.77 |
| | 400298 | AA032279 | Hs.61635 | six transmembra | TM | 2.77 |
| 5 | 414569 | AF109298 | Hs.118258 | prostate cancer | TM | 2.76 |
| | 449378 | AW664026 | Hs.59892 | ESTs | TM | 2.76 |
| | 423903 | M57765 | Hs.1721 | interleukin 11 | TM, SS | 2.75 |
| | 431104 | AW970859 | Hs.269109 | ESTs | Sema, TM, SS | 2.75 |
| | 452940 | AA029722 | Hs.20279 | ESTs | 7tm_1, TM, SS | 2.75 |
| 10 | 432201 | AI538613 | Hs.135657 | ESTs | trypsin, TM, | 2.74 |
| | 414617 | AI339520 | Hs.20524 | ESTs, Moderatel | hexokise, TM, | 2.73 |
| | 444301 | AK000136 | Hs.10760 | hypothetical pr | LRR, TM, | 2.73 |
| | 426711 | AA383471 | Hs.180689 | conserved gene | TM | 2.72 |
| | 429432 | AI678059 | Hs.202676 | synaptonemal co | TM | 2.71 |
| 15 | 450506 | NM_004460 | Hs.418 | fibroblast aci | Peptidase_S9, DPPIV_N_term, SS | 2.71 |
| | 427528 | AU077143 | Hs.179565 | minichromosome | MCM, TM, SS | 2.71 |
| | 418801 | AA228366 | Hs.115122 | ESTs | integrin_A, FGF-GAP, TM, SS | 2.71 |
| | 429486 | AF155827 | Hs.203963 | hypothetical pr | SNF2_N, helicase_C, TM, | 2.71 |
| | 408366 | AW511255 | Hs.258082 | ESTs | SS | 2.71 |
| 20 | 406399 | | | | kazal, TM, SS | 2.70 |
| | 446269 | AW263155 | Hs.14559 | hypothetical pr | TM | 2.69 |
| | 426514 | BE616633 | Hs.301122 | bone morphogene | TGF-beta, TGFb_propeptide, TM, SS | 2.68 |
| | 417079 | U65590 | Hs.81134 | interleukin 1 r | IL1, SS | 2.67 |
| | 444754 | T83911 | Hs.11881 | transmembrane 4 | TM, SS | 2.67 |
| 25 | 424687 | J05070 | Hs.151738 | matrix metallopro | fn2, hemopexin, Peptidase_M10, SS | 2.67 |
| | 439979 | AW600291 | Hs.6823 | hypothetical pr | TM | 2.66 |
| | 430832 | AI073913 | Hs.100686 | ESTs, Weakly si | TM, SS | 2.65 |
| | 429170 | NM_001394 | Hs.2359 | dual specificit | DSPC, Rhodanese, TM, | 2.65 |
| | 450400 | AI694722 | Hs.279744 | ESTs | TM | 2.64 |
| 30 | 435380 | AA679001 | Hs.192221 | ESTs | Occludin, TM, SS | 2.64 |
| | 432375 | BE536069 | Hs.2962 | S100 calcium-bi | S_100, efnand, TM, SS | 2.64 |
| | 453700 | AB009426 | Hs.560 | apolipoprotein | dCMP_cyt_deam, sugar_tr, TM, SS | 2.63 |
| | 422938 | NM_001809 | Hs.1594 | centromere prot | histone, TM, | 2.63 |
| | 453134 | AA032211 | Hs.118493 | ESTs | adh_short, TM, SS | 2.63 |
| 35 | 420727 | H75701 | Hs.99886 | complement comp | sushi, | 2.63 |
| | 408868 | AW292286 | Hs.255058 | ESTs | TM | 2.62 |
| | 414972 | BE263782 | Hs.77695 | KIAA0008 gene p | TM | 2.62 |
| | 403055 | | | | filament, TM, SS | 2.62 |
| 40 | 447400 | AK000322 | Hs.18457 | hypothetical pr | zf-C3HC4, TM, | 2.62 |
| | 413753 | U17760 | Hs.301103 | Human DNA seque | laminin_EGF, laminin_Nterm, SS | 2.61 |
| | 433220 | AI076192 | Hs.131933 | ESTs | TM | 2.61 |
| | 436251 | BE515065 | Hs.5092 | nucleolar prote | Nop, TM, SS | 2.60 |
| | 448988 | Y09763 | Hs.22785 | gamma-aminobuty | neur_chan, TM, SS | 2.60 |
| | 425463 | AK000740 | Hs.157986 | hypothetical pr | TM | 2.60 |
| 45 | 435370 | AI964074 | Hs.225838 | ESTs | EGF, fn3, fibrinogen_C, TM, SS | 2.59 |
| | 432215 | AU076609 | Hs.2934 | ribonucleotide | ribonucleo_red, ribonuc_red_ig, TM, | 2.59 |
| | 409142 | AL136877 | Hs.50758 | chromosome-asso | SMC_N, TM, SS | 2.59 |
| | 443919 | AI091284 | Hs.135224 | ESTs | adh_short, TM, SS | 2.58 |
| | 413268 | AL039079 | Hs.75256 | regulator of G- | RGS, TM, | 2.58 |
| 50 | 404519 | | | | defensins, SS | 2.58 |
| | 414998 | NM_002543 | Hs.77729 | oxidised low de | TM | 2.57 |
| | 429597 | NM_003816 | Hs.2442 | a disintegrin a | TM, SS | 2.57 |
| | 426841 | AI052358 | Hs.193726 | ESTs | asp, TM, SS | 2.57 |
| 55 | 416768 | AA363733 | Hs.1032 | regenerating is | lectin_c, SS | 2.57 |
| | 417933 | X02308 | Hs.82962 | thymidylate syn | thymidylat_synt, SS | 2.56 |
| | 441384 | AA447849 | Hs.288660 | protease, serin | TM | 2.56 |
| | 451939 | U80456 | Hs.27311 | single-minded (| PAC, PAS, BPL, BPL_C, TM, | 2.56 |
| | 418867 | D31771 | Hs.89404 | msh (Drosophila | homeobox, TM, | 2.55 |
| | 416065 | BE267931 | Hs.78996 | proliferating c | TM | 2.55 |
| 60 | 431890 | X17033 | Hs.271986 | integrin, alpha | vwa, integrin_A, FGF-GAP, TM, SS | 2.55 |
| | 407830 | NM_001086 | Hs.587 | arylacetamide d | COesterase, 7tm_1, TM, SS | 2.55 |
| | 434815 | AF155582 | Hs.46744 | core 1 UDP-galac | SS | 2.54 |
| | 435647 | AI653240 | Hs.49823 | ESTs | TM | 2.54 |
| | 459306 | AW578452 | Hs.232988 | ESTs, Weakly si | TM, SS | 2.54 |
| 65 | 414361 | AI086138 | Hs.204044 | ESTs | TM | 2.54 |
| | 425782 | U66468 | Hs.159525 | cell growth reg | SS | 2.54 |
| | 416984 | H38765 | Hs.80706 | diaphorase (NAD | TM | 2.53 |
| | 431183 | NM_006855 | Hs.250696 | KDEL (Lys-Asp-G | ER_lumen_recept, IRK, DEAD, helicase_C, TM, SS | 2.53 |
| | 456743 | AI630124 | Hs.7434 | ESTs | TM | 2.53 |
| 70 | 410268 | AA316181 | Hs.61635 | six transmembra | TM | 2.52 |
| | 424905 | NM_002497 | Hs.153704 | NIMA (never in | pkise, TM, | 2.52 |
| | 432657 | AA831815 | Hs.270940 | ESTs | TM | 2.51 |
| | 434080 | AI820719 | Hs.154662 | hypothetical pr | DJ_CXXCXGXG, TM, SS | 2.51 |
| | 418969 | W33191 | Hs.28907 | hypothetical pr | SH3, TM, | 2.51 |
| 75 | 431808 | M30703 | Hs.270833 | amphiregulin (s | EGF, TM, SS | 2.51 |
| | 429093 | NM_000253 | Hs.195799 | microsomal trig | Vitellogenin_N, TM, SS | 2.50 |
| | 447634 | AW967902 | Hs.5152 | Homo sapiens cD | TM | 2.50 |
| | 436393 | AW022213 | Hs.143617 | ESTs | Galactosyl_T_2, TM, SS | 2.50 |
| | 453751 | R36762 | Hs.101282 | Homo sapiens mR | TM | 2.49 |
| 80 | 445865 | AI262584 | Hs.145575 | ESTs | SS | 2.49 |
| | 414883 | AA926960 | Hs.77550 | CDC28 protein k | CKS, TM, | 2.49 |
| | 406747 | AI925153 | Hs.217493 | annexin A2 | TM | 2.49 |
| | 446921 | AB012113 | Hs.16530 | small inducible | IL8, SS | 2.49 |
| | 426322 | J05068 | Hs.2012 | transcobalamin | Cobalamin_bind, TM, SS | 2.48 |

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|----|--------|-----------|-----------|-------------------|---------------------------------|------|
| 5 | 422515 | AW500470 | Hs.117950 | multifunctional | AIRC,SAICAR_synth,TM, | 2.48 |
| | 447030 | AW444659 | Hs.232184 | ESTs | TM | 2.48 |
| | 448454 | NM_005879 | Hs.21254 | TRAF interactin | zf-C3HC4,TM, | 2.48 |
| | 419092 | J05581 | Hs.89603 | mucin 1, transmem | SEA,TM,SS | 2.48 |
| | 409640 | U78722 | Hs.55481 | zinc finger pro | zf-C2H2,SCAN,TM, | 2.48 |
| 10 | 404171 | | | | sodfe,TM, | 2.47 |
| | 414747 | U30872 | Hs.77204 | centromere prot | SS | 2.47 |
| | 410406 | AI969703 | Hs.301842 | ESTs | FGGY,TM, | 2.47 |
| | 452220 | BE158006 | Hs.212296 | ESTs | FG-GAP,TM,SS | 2.46 |
| | 421493 | BE300341 | Hs.104925 | ectodermal-neur | BTB,Kelch,TM, | 2.46 |
| 15 | 444838 | AV651680 | Hs.208558 | ESTs | integrin_A,FG-GAP,TM,SS | 2.46 |
| | 413816 | AW958181 | Hs.189998 | ESTs | AMP-binding,G_glu_transpept,TM, | 2.46 |
| | 436613 | AA972691 | Hs.192974 | Homo sapiens cD | TM,SS | 2.45 |
| | 432874 | W94322 | Hs.279651 | melanoma inhibi | SH3,SS | 2.45 |
| | 425397 | J04088 | Hs.156346 | topoisomerase (| HATPase_c,SS | 2.45 |
| 20 | 422363 | T55979 | Hs.115474 | replication fac | TM | 2.45 |
| | 431924 | AK000850 | Hs.272203 | Homo sapiens cD | SH3,TM, | 2.44 |
| | 431457 | NM_012211 | Hs.256297 | integrin, alpha | FG-GAP,vwa,TM,SS | 2.44 |
| | 416498 | U33632 | Hs.79351 | potassium chann | TM | 2.44 |
| | 428484 | AF104032 | Hs.184601 | solute carrier | aa_permeases,TM, | 2.43 |
| 25 | 431958 | X63629 | Hs.2877 | cadherin 3, typ | cadherin,Cadherin_C_term,TM,SS | 2.43 |
| | 413833 | Z15005 | Hs.75573 | centromere prot | kinesin,TM, | 2.43 |
| | 407243 | AA058357 | Hs.74466 | carcinoembryoni | TM,SS | 2.43 |
| | 410044 | BE566742 | Hs.58169 | highly expresse | TM,SS | 2.43 |
| | 424273 | W40460 | Hs.144442 | phospholipase A | phoslip,TM,SS | 2.42 |
| 30 | 409533 | AW969543 | Hs.21291 | mitogen-activat | TM,SS | 2.42 |
| | 419741 | NM_007019 | Hs.93002 | ubiquitin carri | UQ_con,efhand,TM,SS | 2.42 |
| | 449987 | AW079749 | Hs.184719 | ESTs, Weakly si | ABC_tran,ABC_membrane,TM, | 2.42 |
| | 433159 | AB035898 | Hs.150587 | kinesin-like pr | kinesin,Myosin_tail,TM,SS | 2.42 |
| | 439396 | BE562958 | Hs.74346 | ESTs, Weakly si | SS | 2.42 |
| 35 | 426427 | M86699 | Hs.169840 | TTK protein kin | pkise,TM, | 2.41 |
| | 434725 | AK000796 | Hs.4104 | hypothetical pr | TM | 2.41 |
| | 433312 | AJ241331 | Hs.131765 | ESTs | zf-C2H2,SS | 2.41 |
| | 407047 | X65965 | | gb:H.sapiens SO | sodfe,TM, | 2.41 |
| | 419220 | AA811938 | Hs.291759 | ESTs | TM,SS | 2.40 |
| 40 | 416530 | U62801 | Hs.79361 | kallikrein 6 (n | trypsin_pro_isomerase,TM,SS | 2.40 |
| | 435219 | AA676349 | Hs.190331 | ESTs | TM | 2.40 |
| | 418322 | AA284166 | Hs.84113 | cyclin-dependen | SS | 2.40 |
| | 404253 | | | | histone,TM,SS | 2.40 |
| | 428970 | BE276891 | Hs.194691 | retinoic acid i | 7tm_3,TM, | 2.40 |
| 45 | 418693 | AJ750878 | Hs.87409 | thrombospondin | EGF,TSPN,tsp_1,tsp_3,vwc,SS | 2.39 |
| | 451237 | AW600293 | | gb:EST00049 pGE | TM | 2.39 |
| | 407756 | AA116021 | Hs.38260 | ubiquitin speci | UCH-1,UCH-2,SS | 2.39 |
| | 437935 | AW939591 | Hs.5940 | hypothetical pr | TM,SS | 2.39 |
| | 445625 | BE246743 | Hs.288529 | Homo sapiens cD | TM | 2.39 |
| 50 | 435937 | AA830893 | Hs.119769 | ESTs | TM | 2.39 |
| | 438993 | AA828995 | | gb:od77b08.s1 N | integrin_B,TM,SS | 2.38 |
| | 422082 | AA016188 | Hs.111244 | hypothetical pr | TM | 2.38 |
| | 450396 | AU077002 | Hs.24950 | regulator of G- | RGS,TM, | 2.38 |
| | 422578 | AF239666 | Hs.1545 | caudal type hom | homeobox,SS | 2.38 |
| 55 | 428070 | T63918 | Hs.182313 | retinol-binding | lipocalin,TM, | 2.38 |
| | 416111 | AA033813 | Hs.79018 | chromatin assem | TM,SS | 2.37 |
| | 433345 | AJ681545 | Hs.152982 | Homo sapiens cD | TM | 2.37 |
| | 427557 | NM_002659 | Hs.179657 | plasminogen act | UPAR_LY6,SS | 2.37 |
| | 423554 | M90516 | Hs.1674 | glutamine-fruct | GATase_2,Sis,TM,SS | 2.37 |
| 60 | 453204 | R10799 | Hs.191990 | ESTs | TM | 2.37 |
| | 425081 | X74794 | Hs.154443 | minichromosome | MCM,TM, | 2.36 |
| | 434682 | AA827165 | Hs.191958 | ESTs | TM | 2.36 |
| | 414108 | AJ267592 | Hs.75761 | SFRS protein ki | pkise,TM, | 2.36 |
| | 417900 | BE250127 | Hs.82906 | CDC20 (cell div | WD40,TM, | 2.36 |
| 65 | 428046 | AW812795 | Hs.155381 | ESTs, Moderatel | ank,SS | 2.36 |
| | 448019 | AW947164 | Hs.195641 | ESTs | TM | 2.36 |
| | 431753 | X76029 | Hs.2841 | neuromedin U | NMU,TM,SS | 2.36 |
| | 410361 | BE391804 | Hs.62661 | guanylate bindi | GBP,TM,SS | 2.36 |
| | 418526 | BE019020 | Hs.85838 | solute carrier | MCT,TM,SS | 2.36 |
| 70 | 444478 | W07318 | Hs.240 | M-phase phospho | kinesin,SS | 2.36 |
| | 436961 | AW375974 | Hs.156704 | ESTs | TM | 2.35 |
| | 408194 | AA601038 | Hs.191797 | ESTs | TM | 2.35 |
| | 438578 | AA811244 | Hs.164168 | ESTs | formyl_transf,AIRS,GARS,TM, | 2.35 |
| | 429183 | AB014604 | Hs.197955 | KIAA0704 protei | TM | 2.35 |
| 75 | 453900 | AW003582 | Hs.226414 | ESTs, Weakly si | TM | 2.33 |
| | 432877 | AW974111 | Hs.292477 | ESTs | Ets,SAM_PNT,TM, | 2.33 |
| | 451928 | AJ823801 | Hs.30315 | ESTs | TM | 2.33 |
| | 418245 | AA088767 | Hs.83883 | transmembrane, | kd1_recept_a,TM,SS | 2.33 |
| | 435106 | AA100847 | Hs.193380 | ESTs, Highly si | TM | 2.33 |
| 80 | 432193 | AA372264 | Hs.273193 | hypothetical pr | TM,SS | 2.33 |
| | 449532 | W74653 | Hs.271593 | ESTs | TM | 2.33 |
| | 409703 | NM_006187 | Hs.56009 | Z'-5'oligoadeny | NTP_transf_2,TM,SS | 2.33 |
| | 419373 | NM_003244 | Hs.90077 | TG-interacting | homeobox,SS | 2.32 |
| | 435607 | W73428 | Hs.8750 | uncharacterized | SS | 2.32 |
| | 405818 | | | | TM,SS | 2.32 |
| | 444371 | BE540274 | Hs.239 | forkhead box M1 | Fork_head,SS | 2.32 |
| | 432675 | AJ791855 | Hs.105884 | ESTs | PDEase,TM, | 2.32 |

| | | | | | | |
|----|--------|-----------|-----------|-------------------|---|------|
| | 411773 | NM_006799 | Hs.72026 | protease, serin | trypsin,SS | 2.31 |
| | 434775 | AA648983 | Hs.212911 | ESTs | TM,SS | 2.31 |
| | 422611 | AA158177 | Hs.118722 | lucosyltransfer | SS | 2.31 |
| 5 | 419493 | AF001212 | Hs.90744 | proteasome (pro | SS | 2.31 |
| | 424435 | AB011167 | Hs.146957 | KIAA0595 protei | TM | 2.30 |
| | 409262 | AK000631 | Hs.52256 | hypothetical pr | WD40,TM,SS | 2.30 |
| | 428125 | AA393071 | Hs.182579 | leucine aminope | Peptidase_M17,TM,SS | 2.30 |
| | 417655 | AA780791 | Hs.14014 | ESTs, Weakly si | TM | 2.29 |
| 10 | 407287 | AI678812 | Hs.201658 | ESTs, Weakly si | ras,TM,SS | 2.29 |
| | 428923 | BE047698 | Hs.188785 | ESTs | TM,SS | 2.29 |
| | 452203 | X57522 | Hs.158164 | ATP-binding cas | ABC_tran,ABC_membrane,TM, | 2.29 |
| | 409402 | AF208234 | Hs.695 | cystatin B (ste | cystatin,SS | 2.29 |
| | 419359 | AL043202 | Hs.90073 | chromosome segr | TM,SS | 2.29 |
| 15 | 451999 | AW176401 | Hs.27424 | DEAD/H (Asp-Glu | TM,SS | 2.29 |
| | 400811 | AF219139 | Hs.87726 | KIAA0154 protei | Cobalamin_bind,SS | 2.29 |
| | 420931 | AF044197 | Hs.100431 | small inducible | IL8,TM,SS | 2.28 |
| | 425247 | NM_005940 | Hs.155324 | matrix metallopro | hemopexin,Peptidase_M10,TM,SS | 2.28 |
| 20 | 438170 | AI916685 | Hs.194601 | ESTs | 2-Hacid_DH,TM, | 2.28 |
| | 445378 | AV653564 | Hs.226946 | ESTs | TM | 2.28 |
| | 428048 | AA705745 | Hs.185070 | ESTs | AMP-binding,TM, | 2.28 |
| | 414696 | AF002020 | Hs.76918 | Niemann-Pick di | Patched,TM,SS | 2.27 |
| | 433535 | AF111106 | Hs.3382 | protein phosphat | TM | 2.27 |
| | 421155 | H87879 | Hs.102267 | lysyl oxidase | Lysyl_oxidase,SS | 2.27 |
| 25 | 405545 | | | | ABC_tran,ABC_membrane,TM,SS | 2.27 |
| | 445537 | AJ245671 | Hs.12844 | ECF-like-domain | ECF,SS | 2.27 |
| | 423634 | AW959908 | Hs.1690 | heparin-binding | TM,SS | 2.26 |
| | 407742 | AF186252 | Hs.38084 | sulfotransferase | Sulfotransfer,SS | 2.26 |
| | 428330 | L22524 | Hs.2256 | matrix metallopro | Peptidase_M10,SS | 2.26 |
| 30 | 429731 | AK001592 | Hs.212172 | beta,beta-carot | TM | 2.26 |
| | 400514 | | | | p450,TM,SS | 2.26 |
| | 431846 | BE019924 | Hs.271580 | uroplakin 1B | transmembrane4,TM,SS | 2.26 |
| | 426010 | AA136563 | Hs.1975 | Homo sapiens cD | TM | 2.26 |
| | 437641 | AA811452 | Hs.291911 | ESTs | TM | 2.26 |
| 35 | 411393 | AW797437 | Hs.69771 | B-factor, prope | sushi,trypsin,ywa,DEAD,rm,EGF,fn3,fibrinogen_C,SS | 2.26 |
| | 414809 | AI434699 | Hs.77356 | transferrin rec | PA,Ribosomal_S2,TM, | 2.25 |
| | 419488 | AA316241 | Hs.90691 | nucleophosmin/n | SS | 2.25 |
| | 434540 | NM_016045 | Hs.5184 | TH1 drosophila | TM | 2.25 |
| | 410196 | AJ936442 | Hs.59838 | hypothetical pr | UBACT_repeat,TM, | 2.25 |
| 40 | 456844 | AI264155 | Hs.152981 | CDP-diacylglyce | Cydidyllyltrans,TM, | 2.25 |
| | 408353 | BE439838 | Hs.44298 | hypothetical pr | Ribosomal_S17,TM, | 2.25 |
| | 448753 | AL048858 | Hs.224355 | ESTs, Weakly si | TM | 2.25 |
| | 428479 | Y00272 | Hs.184572 | cell division c | pkase,TM,SS | 2.24 |
| | 424971 | AA479005 | Hs.154036 | tumor suppressi | ion_trans,PH,TM, | 2.24 |
| 45 | 432673 | AB028859 | Hs.278605 | ER-associated D | DJ,DJ_C,TM,SS | 2.24 |
| | 409432 | D49372 | Hs.54460 | small inducible | IL8,TM,SS | 2.24 |
| | 429925 | NM_000786 | Hs.226213 | cytochrome P450 | p450,TM,SS | 2.24 |
| | 445413 | AA151342 | Hs.12677 | CGI-147 protein | UPF0099,TM,SS | 2.23 |
| | 447532 | AK000614 | Hs.18791 | hypothetical pr | TM | 2.23 |
| 50 | 423515 | AA327017 | Hs.162204 | ESTs | SS | 2.23 |
| | 444743 | AA045648 | Hs.11817 | nudix (nucleosi | mutT,TM, | 2.23 |
| | 434518 | H56995 | Hs.37372 | Homo sapiens DN | TM | 2.23 |
| | 435602 | AF217515 | Hs.283532 | uncharacterized | TM,SS | 2.23 |
| | 449974 | AW970948 | Hs.269403 | ESTs | TM,SS | 2.23 |
| 55 | 424927 | AW973666 | Hs.153850 | hypothetical pr | TM | 2.23 |
| | 414420 | AA043424 | Hs.76095 | immediate early | TM | 2.23 |
| | 431840 | AA534908 | Hs.2860 | POU domain, cla | homeobox,pou,TM,SS | 2.23 |
| | 452930 | AW195285 | Hs.194097 | ESTs | SS | 2.23 |
| | 436391 | AJ227892 | Hs.146274 | ESTs | SS | 2.23 |
| 60 | 439186 | AK697274 | Hs.6487 | Xq28, 2000bp se | Epimerase,SS | 2.23 |
| | 414732 | AW410976 | Hs.77152 | minichromosome | MCM,TM, | 2.22 |
| | 411835 | U29343 | Hs.72550 | hyaluronan-medi | TM | 2.22 |
| | 438223 | AA781171 | | gb:aj24d05.s1 S | myosin_head,TM, | 2.22 |
| | 450149 | AW969781 | Hs.293440 | ESTs, Moderatel | TM | 2.22 |
| 65 | 401519 | | | | filament,TM, | 2.22 |
| | 441794 | AW197794 | Hs.253338 | ESTs | ank,TM, | 2.22 |
| | 408901 | AK001330 | Hs.48855 | hypothetical pr | TM | 2.21 |
| | 434423 | NM_006769 | Hs.3844 | LIM domain only | LIM,TM, | 2.21 |
| 70 | 432140 | AK000404 | Hs.272688 | hypothetical pr | SS | 2.21 |
| | 423453 | AW450737 | Hs.128791 | CGI-09 protein | Granin,CDP-OH_P_transf,TM, | 2.21 |
| | 428438 | NM_001955 | Hs.2271 | endothelin 1 | endothelin,TM,SS | 2.21 |
| | 421470 | R27496 | Hs.1378 | annexin A3 | annexin,TM,SS | 2.21 |
| | 440381 | AA917808 | Hs.190495 | ESTs | TM,SS | 2.20 |
| | 453779 | N35187 | Hs.43388 | ESTs | TM,SS | 2.20 |
| 75 | 433627 | AF078866 | Hs.284296 | Homo sapiens cD | SURF4,TM, | 2.20 |
| | 417944 | AU077195 | Hs.82985 | collagen, type | COLF1,Collagen,vwc,TM,SS | 2.20 |
| | 422689 | AW856655 | | gb:RC3-CT0297.2 | SNF2_N,TM, | 2.20 |
| | 448457 | H65629 | Hs.245997 | ESTs | TM,SS | 2.20 |
| | 426125 | X87241 | Hs.166994 | FAT tumor suppr | EGF,cadherin,laminin_G,TM,SS | 2.20 |
| 80 | 430603 | AA148164 | Hs.247280 | HBV associated | zf-C3HC4,TM, | 2.20 |
| | 425274 | BE281191 | Hs.155462 | minichromosome | MCM,TM, | 2.20 |
| | 452679 | Z42387 | Hs.4299 | Homo sapiens cD | TM | 2.20 |
| | 410619 | BE512730 | Hs.65114 | keratin 18 | filament,TM, | 2.20 |
| | 424332 | AA338919 | Hs.101615 | ESTs | SS | 2.20 |

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|----|--------|-----------|-----------|------------------|---|------|
| | 418661 | NM_001949 | Hs.1189 | Human mRNA for | E2F_TDP,TM,SS | 2.20 |
| | 419341 | N71463 | Hs.118888 | ESTs, Weakly si | UPF0016,TM,SS | 2.20 |
| | 427920 | Z11502 | Hs.181107 | annexin A13 | annexin,TM, | 2.19 |
| | 403208 | | | | lectin_c,TM,SS | 2.19 |
| 5 | 422596 | AF063611 | Hs.118633 | Z-5oligoadeny | ubiquitin,SS | 2.19 |
| | 444261 | AA298958 | Hs.10724 | MDS023 protein | TM | 2.19 |
| | 423401 | NM_001992 | Hs.128087 | coagulation fac | 7tm_1,TM,SS | 2.18 |
| | 453450 | AW797627 | Hs.89474 | ADP-ribosylatio | SS | 2.18 |
| | 444334 | BE296785 | Hs.10848 | .KIAA0187 gene p | SS | 2.18 |
| 10 | 437616 | AI797163 | Hs.207954 | ESTs | SMC_N,TM,SS | 2.18 |
| | 451807 | W52854 | Hs.27099 | DKFZP564J0863 p | TM | 2.18 |
| | 430441 | BE398091 | Hs.6880 | DKFZP434D156 pr | TM | 2.18 |
| | 411678 | AI907114 | Hs.71465 | squalene epoxid | Monooxygese,TM, | 2.18 |
| | 452291 | AF015592 | Hs.28853 | CDC7 (cell divi | pkise,TM, | 2.18 |
| 15 | 444342 | NM_014398 | Hs.10887 | similar to lyso | Lamp,TM,SS | 2.18 |
| | 451099 | RS2795 | Hs.25954 | interleukin 13 | ln3,TM,SS | 2.18 |
| | 425873 | NM_013390 | Hs.160417 | transmembrane p | TM | 2.17 |
| | 417404 | NM_007350 | Hs.82101 | pleckstrin homo | TM | 2.17 |
| | 446995 | AI355012 | | gb:qu16d10.x1 N | TM | 2.17 |
| 20 | 439961 | AA857451 | Hs.269696 | ESTs | TM | 2.17 |
| | 429125 | AA446854 | Hs.271004 | ESTs | TM | 2.17 |
| | 407103 | AA424881 | Hs.256301 | ESTs | TM | 2.17 |
| | 415116 | AA160363 | Hs.269956 | ESTs | ER_human_recept,TM,SS | 2.17 |
| | 440052 | AI633744 | Hs.195648 | ESTs | PAC,TM,SS | 2.17 |
| 25 | 423961 | D13666 | Hs.136348 | osteoblast spec | Fascidin,TM,SS | 2.17 |
| | 431070 | AW408164 | Hs.249184 | transcription f | FHA,SS | 2.16 |
| | 443599 | AI079559 | Hs.134125 | ESTs | TM | 2.16 |
| | 427258 | AA400091 | Hs.39421 | ESTs | TM | 2.16 |
| | 418113 | AI272141 | Hs.83484 | SRY (sex determ | HMG_box,TM, | 2.16 |
| 30 | 450835 | BE262773 | Hs.25584 | hypothetical pr | ArlGap,SS | 2.16 |
| | 449057 | AB037784 | Hs.22941 | KIAA1363 protei | TM | 2.16 |
| | 448153 | Y10805 | Hs.20521 | HMT1 (hnRNP met | TM,SS | 2.16 |
| | 424653 | AW977534 | Hs.151469 | calcium/calmodu | Guanylate_kin,PDZ,pkise,SH3,TM, | 2.16 |
| 35 | 431341 | AA307211 | Hs.251531 | proteasome (pro | proteasome,TM, | 2.16 |
| | 452865 | AI924046 | Hs.119567 | ESTs | PMP22_Claudin,TM,SS | 2.16 |
| | 432789 | D26361 | Hs.3104 | KIAA0042 gene p | TM | 2.16 |
| | 438580 | AA811262 | Hs.299202 | ESTs | pkise,TM, | 2.16 |
| | 422192 | AA305159 | Hs.113019 | fts485 | SS | 2.15 |
| 40 | 425607 | U09860 | Hs.158333 | protease, serin | ldl_recept_a,trypsin,CUB,SrcR,MAM,SEA,TM,SS | 2.15 |
| | 447289 | AW247017 | Hs.36978 | melanoma antige | 3Beta_HSD,Epimerase,MAGE,TM, | 2.15 |
| | 447674 | BE270640 | Hs.19192 | cyclin-dependen | pkise,TM, | 2.15 |
| | 441021 | AW578716 | Hs.7644 | H1 histone fami | linker_histone,TM, | 2.15 |
| | 426471 | M22440 | Hs.170009 | transforming gr | EGF,TM,SS | 2.15 |
| 45 | 431941 | AK000106 | Hs.272227 | Homo sapiens cD | pkise,Furin-like,TM,SS | 2.15 |
| | 414761 | AU077228 | Hs.77256 | enhancer of zes | SET,TM, | 2.15 |
| | 410407 | X66839 | Hs.63287 | carbonic anhydr | carb_anhydrase,TM,SS | 2.15 |
| | 420900 | AL045633 | Hs.44269 | ESTs | Ald_Xan_dh_C,FAD_binding_5,TM, | 2.15 |
| | 419239 | AA468183 | Hs.184598 | Homo sapiens cD | TM | 2.15 |
| 50 | 452721 | AJ269529 | Hs.30377 | Homo sapiens ES | TM | 2.15 |
| | 410664 | NM_006033 | Hs.65370 | lipase, endothe | Ribosomal_L22,lipase,PLAT,TM,SS | 2.14 |
| | 452835 | AK001269 | Hs.30738 | hypothetical pr | TM | 2.14 |
| | 452092 | BE245374 | Hs.27842 | hypothetical pr | Acyltransferase,TM,SS | 2.14 |
| | 401708 | | | | SS | 2.14 |
| 55 | 411400 | AA311919 | Hs.69851 | GAR1 protein | TM | 2.14 |
| | 448526 | AB028946 | Hs.21361 | KIAA1023 protei | TM | 2.14 |
| | 421175 | AI879099 | Hs.102397 | GIOT-3 for gona | zf-C2H2,KRAB,TM,SS | 2.14 |
| | 413511 | AJ627178 | Hs.75412 | Arginine-rich p | TM | 2.13 |
| 60 | 432945 | AL043683 | Hs.271357 | ESTs, Weakly si | PK,SS | 2.13 |
| | 418592 | X99226 | Hs.284153 | Fanconi anemia, | TM | 2.13 |
| | 425298 | AK000209 | Hs.155556 | hypothetical pr | TM | 2.13 |
| | 450956 | AW193531 | Hs.205647 | ESTs, Moderatel | pkise,TM,SS | 2.13 |
| | 419569 | AJ971651 | Hs.91143 | jagged 1 (Alagi | EGF_DSL,TM,SS | 2.13 |
| | 421508 | NM_004833 | Hs.105115 | absent in melan | TM | 2.13 |
| 65 | 413670 | AB000115 | Hs.75470 | hypothetical pr | TM | 2.13 |
| | 422783 | AA598956 | Hs.120439 | ethanolamine ki | Choline_kise,TM, | 2.13 |
| | 410418 | D31382 | Hs.63325 | transmembrane p | trypsin,ldl_recept_a,TM,SS | 2.13 |
| | 414860 | BE255593 | Hs.77502 | methionine aden | S-AdoMet_synt,SS | 2.13 |
| | 425860 | L29339 | Hs.1964 | solute carrier | SSF,Ribosomal_S17e,TM, | 2.13 |
| 70 | 414839 | X63692 | Hs.77462 | DNA (cytosine-5 | zf-CXXC,BAH,TM,SS | 2.13 |
| | 437050 | AA766420 | Hs.291606 | ESTs | TM | 2.13 |
| | 430217 | N47863 | Hs.180450 | ribosomal prote | TM,SS | 2.13 |
| | 409012 | AL117435 | Hs.49725 | DKFZP434I216 pr | RhoGEF,TM, | 2.12 |
| | 428365 | AA295331 | Hs.183861 | Homo sapiens cD | TM | 2.12 |
| | 410839 | NM_006849 | Hs.66581 | protein disulf | thioered,TM, | 2.12 |
| 75 | 450510 | AA010056 | Hs.242998 | ESTs | TM,SS | 2.12 |
| | 427475 | AA403151 | Hs.191605 | ESTs | SS | 2.12 |
| | 433748 | R12244 | | gb:yrf33c12.r1 S | AMP-binding,TM, | 2.12 |
| | 415138 | C18356 | Hs.78045 | tissue factor p | Kunitz_BPT1,G-gamma,TM,SS | 2.11 |
| 80 | 414788 | X78342 | Hs.77313 | cyclin-dependen | pkise,TM,SS | 2.11 |
| | 415474 | NM_014252 | Hs.78457 | solute carrier | mito_carr,TM, | 2.11 |
| | 416472 | AA180756 | Hs.193094 | ESTs, Moderatel | TM | 2.11 |
| | 410718 | AI920783 | Hs.191435 | ESTs | SQS_PSY,TM,SS | 2.11 |
| | 425811 | AL039104 | Hs.159557 | karyopherin alp | Armadillo_seg,IBB,TM,SS | 2.11 |

| | | | | | | |
|----|--------|-----------|-----------|-------------------|--|------|
| | 447197 | R36075 | | gb:yh88b01.s1 S | SDF,TM, | |
| | 431621 | AW292329 | Hs.163481 | ESTs | PH_Band_41,TM,SS | 2.11 |
| | 433849 | BE465884 | Hs.280728 | ESTs | SS | 2.11 |
| 5 | 438038 | AI732629 | Hs.194161 | ESTs, Weakly si | Cytidyllyltrans,TM, | 2.11 |
| | 422032 | AA476966 | Hs.110857 | polymerase (RNA | TFIIS,TM,SS | 2.11 |
| | 409717 | AW452871 | Hs.56043 | CGI-115 protein | TM | 2.11 |
| | 445837 | AI261700 | Hs.145544 | ESTs | TM | 2.11 |
| | 423880 | BE278111 | Hs.134200 | DKFZP564C186 pr | TM | 2.11 |
| 10 | 421574 | AJ000152 | Hs.105924 | defensin, beta | Defensin_beta,TM,SS | 2.10 |
| | 437103 | AW139408 | Hs.152940 | ESTs | Choline_kise,TM, | 2.10 |
| | 450747 | AI064821 | Hs.48306 | ESTs, Highly si | rm,TM, | 2.10 |
| | 437033 | AW248364 | Hs.5409 | RNA polymerase | TM | 2.10 |
| | 417640 | D30857 | Hs.82353 | protein C recep | TM,SS | 2.10 |
| 15 | 431120 | AA492588 | | gb:ng99c08.s1 N | TM,SS | 2.10 |
| | 430510 | AW162916 | Hs.241576 | hypothetical pr | TM | 2.10 |
| | 429669 | BE185499 | Hs.2471 | KIAA0020 gene p | TM | 2.10 |
| | 407881 | AW072003 | Hs.40968 | heparan sulfate | SS | 2.10 |
| | 436415 | BE265254 | Hs.5181 | proliferation-a | Peptidase_M24,TM,SS | 2.10 |
| 20 | 407887 | AA579668 | Hs.41072 | serine (or cyst | serpin,TM, | 2.10 |
| | 447815 | AI432199 | Hs.247084 | ESTs | LIM,TM, | 2.10 |
| | 434274 | AA628539 | Hs.116252 | ESTs, Moderatel | rm,TM,SS | 2.09 |
| | 411571 | AA122393 | Hs.70811 | hypothetical pr | SS | 2.09 |
| | 442525 | AF150282 | Hs.145945 | ESTs | pkise,TM, | 2.09 |
| 25 | 423750 | AF165883 | Hs.132415 | prefoldin 2 | TM | 2.09 |
| | 449199 | AI990122 | Hs.196988 | ESTs | ras,TM, | 2.09 |
| | 415363 | AI570947 | Hs.78406 | phosphatidyino | PIP5K,pkise,TM,SS | 2.09 |
| | 418462 | BE001596 | Hs.85266 | integrin, beta | integrin_B,fn3,TM,SS | 2.09 |
| | 430335 | D80007 | Hs.239499 | KIAA0185 protei | S1,TM, | 2.09 |
| 30 | 443450 | N66045 | Hs.133529 | ESTs | TM | 2.08 |
| | 418753 | BE217818 | Hs.87016 | Homo sapiens cD | TM | 2.08 |
| | 439018 | AW300887 | Hs.26638 | ESTs, Weakly si | TM,SS | 2.08 |
| | 431628 | AF146277 | Hs.265561 | CD2-associated | SH3,SS | 2.08 |
| | 446528 | AU076640 | Hs.15243 | nucleolar prote | Nol1_Nop2_Sun,TM, | 2.08 |
| 35 | 411372 | AI147861 | Hs.213289 | low density lip | EGF_kd1_recept_a,kd1_recept_b,TM,SS | 2.08 |
| | 459319 | NM_000059 | | gb:Homo sapiens | BRCA2_repeat,TM, | 2.08 |
| | 408730 | AV660717 | Hs.47144 | DKFZP586N0819 p | TM,SS | 2.08 |
| | 409220 | BE243323 | Hs.51233 | tumor necrosis | TNFR_c6,death,TM, | 2.08 |
| 40 | 429504 | X99133 | Hs.204238 | lipocalin 2 (on | lipocalin,SS | 2.08 |
| | 409686 | AK000002 | Hs.55879 | Homo sapiens mR | ABC_tran,ABC_membrane,TM, | 2.08 |
| | 413092 | AA126856 | Hs.118665 | ESTs | EGF,TM,SS | 2.08 |
| | 413715 | AW851121 | Hs.75497 | Homo sapiens cD | cyclin,TM, | 2.08 |
| | 423020 | AA383092 | Hs.1608 | replication pro | TM | 2.07 |
| 45 | 438378 | AW970529 | Hs.86434 | Homo sapiens cD | TM,SS | 2.07 |
| | 432125 | AW972667 | Hs.287510 | Homo sapiens cD | Band_41,TM,SS | 2.07 |
| | 449370 | AK002114 | Hs.23495 | hypothetical pr | TM,SS | 2.07 |
| | 454011 | M31008 | Hs.37009 | alkaline phosph | alk_phosphatase,TM,SS | 2.07 |
| | 427876 | AI494291 | Hs.111977 | ESTs | TM | 2.07 |
| | 422901 | R81936 | Hs.121576 | aspartate beta- | SS | 2.07 |
| 50 | 449207 | AL044222 | Hs.23255 | nucleoporin 155 | TM,SS | 2.07 |
| | 408243 | Y00787 | Hs.624 | interleukin 8 | IL8,TM,SS | 2.07 |
| | 446546 | BE167687 | Hs.156628 | ESTs | Sulfotransfer,TM,SS | 2.07 |
| | 423472 | AF041260 | Hs.129057 | breast carcinom | TM | 2.07 |
| | 436211 | AK001581 | Hs.80961 | polymerase (DNA | TM | 2.07 |
| 55 | 456157 | AW979153 | | gb:EST391263 MA | transmembrane4,TM, | 2.07 |
| | 407143 | C14076 | Hs.248968 | EST | TM | 2.06 |
| | 432440 | X63597 | Hs.2996 | sucrase-isomalt | Glyco_hydro_31,trefolil,TM,SS | 2.06 |
| | 410668 | BE379794 | Hs.65403 | hypothetical pr | TM | 2.06 |
| 60 | 422765 | AW409701 | Hs.1578 | baculoviral IAP | BIR,TM, | 2.06 |
| | 439832 | T81829 | Hs.14870 | ESTs | SS | 2.06 |
| | 445318 | AW500652 | Hs.200885 | ESTs | TM | 2.06 |
| | 439951 | AI347067 | Hs.124636 | ESTs | TM,SS | 2.06 |
| | 428307 | W27393 | Hs.183648 | protein tyrosin | TM | 2.06 |
| | 432584 | AA928829 | Hs.47099 | Homo sapiens cD | SS | 2.06 |
| 65 | 433027 | AF191018 | Hs.279923 | putative nucleo | MMR_HSR1,TM, | 2.06 |
| | 433716 | AA608808 | Hs.225118 | ESTs | TM | 2.06 |
| | 429412 | NM_006235 | Hs.2407 | POU domain, cla | TM | 2.06 |
| | 449026 | BE500946 | Hs.209105 | ESTs | TM | 2.06 |
| | 437016 | AU076916 | Hs.5398 | guanine monophos | GATase,GMP_synl_C,TM, | 2.06 |
| 70 | 442547 | AA306997 | Hs.268362 | ESTs, Weakly si | SS | 2.06 |
| | 455778 | BE088746 | | gb:CM2-BT0693-2 | TM | 2.06 |
| | 439975 | AW328081 | Hs.5817 | Homo sapiens pu | TM,SS | 2.06 |
| | 433037 | NM_014158 | Hs.279938 | HSPC067 protein | TM | 2.06 |
| | 440086 | NM_005402 | Hs.288757 | v-rat simian le | ras,TM, | 2.06 |
| 75 | 436414 | BE264633 | Hs.143638 | WD repeat domai | WD40,TM, | 2.05 |
| | 411770 | NM_014278 | Hs.71992 | heat shock prot | HSP70,TM, | 2.05 |
| | 409459 | D86407 | Hs.54481 | low density lip | EGF_kd1_recept_a,kd1_recept_b,TM,SS | 2.05 |
| | 436238 | AK002163 | Hs.301724 | ESTs, Highly si | MMR_HSR1,TM, | 2.05 |
| | 400517 | AF242388 | Hs.149585 | tensin | TM | 2.05 |
| 80 | 421904 | BE143533 | Hs.109309 | hypothetical pr | SS | 2.05 |
| | 417850 | AA215724 | Hs.82741 | primase, polype | SS | 2.05 |
| | 417491 | AW376842 | Hs.1085 | guanylate cyclase | pkise,guanylate_cyc,ANF_receptor,TM,SS | 2.05 |
| | 453775 | NM_002916 | Hs.35120 | replication fac | AAA,TM,SS | 2.05 |
| | 435525 | AI831297 | Hs.123310 | ESTs | TM | 2.05 |

| | | | | | | |
|----|-------------|---------------------------------------|---------------------------------|-----------------|---------------------------------|------|
| 5 | 412627 | BE391959 | Hs.74276 | chloride intrac | G-patch,jg,MuTS_C,TM, | 2.05 |
| | 439702 | AW085525 | Hs.134182 | ESTs | A2M,SS | 2.05 |
| | 440006 | AK000517 | Hs.6844 | hypothetical pr | TM | 2.05 |
| | 417308 | H60720 | Hs.81892 | KJAA0101 gene p | TM | 2.05 |
| | 446311 | AW007294 | Hs.149795 | ESTs, Weakly si | pkise,TM, | 2.05 |
| | 427871 | AW992405 | Hs.59622 | ESTs, Weakly si | SS | 2.05 |
| | 453804 | AA300204 | Hs.35276 | KJAA0852 protei | TM,SS | 2.05 |
| | 449939 | T86420 | Hs.272139 | ESTs | DIL,myosin_head,TM,SS | 2.05 |
| 10 | 417819 | AI253112 | Hs.133540 | ESTs | TM | 2.04 |
| | 427747 | AW411425 | Hs.180655 | serine/threonin | pkise,TM, | 2.04 |
| | 415009 | C75253 | Hs.220950 | ESTs | TM | 2.04 |
| | 437829 | AI358522 | Hs.270188 | ESTs | TM | 2.04 |
| | 428753 | AW939252 | Hs.192927 | hypothetical pr | TM | 2.04 |
| 15 | 446475 | AI908188 | Hs.209245 | ESTs | OPR,TM, | 2.04 |
| | 431394 | AK000692 | Hs.252351 | HERV-H LTR-asso | ig,TM,SS | 2.04 |
| | 423701 | AA329856 | Hs.143022 | ESTs | TM | 2.04 |
| | 422369 | AF005216 | Hs.115541 | Janus kinase 2 | SH2,pkise,TM, | 2.04 |
| | 432481 | AW451645 | Hs.151504 | Homo sapiens cD | TSPN,Collagen,TM,SS | 2.04 |
| 20 | 443746 | AW861379 | Hs.160602 | ESTs | TM | 2.04 |
| | 400792 | AA635062 | Hs.50094 | Homo sapiens mR | zf-C3HC4,CARD,BIR,TM, | 2.04 |
| | 428343 | AL043021 | Hs.12705 | ESTs, Weakly si | TM | 2.04 |
| | 419329 | AY007220 | Hs.288998 | S100-type calci | TM | 2.04 |
| | 403485 | | | | filament,TM, | 2.04 |
| 25 | 413313 | NM_002047 | Hs.75280 | glycyl-tRNA syn | WHEP-TRS,7tm_2,TM,SS | 2.04 |
| | 433326 | AI379486 | Hs.159430 | ESTs | TM | 2.03 |
| | 440246 | WS2010 | Hs.191379 | ESTs | serpin,TM, | 2.03 |
| | 444006 | BE395085 | Hs.10086 | type I transmem | TM,SS | 2.03 |
| | 452705 | H49805 | Hs.246005 | ESTs | TM | 2.03 |
| 30 | 421724 | AB037832 | Hs.107287 | KJAA1411 protei | TM | 2.03 |
| | 447474 | AW614220 | Hs.189402 | ESTs | SS | 2.03 |
| | 418852 | BE537037 | Hs.273294 | hypothetical pr | TM | 2.03 |
| | 431842 | NM_005764 | Hs.271473 | epithelial prot | TM,SS | 2.03 |
| | 440773 | AA352702 | Hs.37747 | hypothetical pr | TM | 2.03 |
| 35 | 443425 | AI056776 | Hs.133397 | ESTs | TM,SS | 2.03 |
| | 407975 | X89426 | Hs.41716 | endothelial cel | IGFBP,SS | 2.03 |
| | 428299 | AL038004 | Hs.29419 | ESTs | TM,SS | 2.03 |
| | 415757 | AA830854 | Hs.187810 | ESTs | TM | 2.03 |
| | 432559 | AW452948 | Hs.257631 | ESTs | PAC,TM,SS | 2.03 |
| 40 | 425912 | AL137629 | Hs.162189 | serine/threonin | fn3,ig,PH,RhoGEF,TM,SS | 2.02 |
| | 419395 | BE268326 | Hs.90280 | 5-aminoimidazol | AICARFT_IMPCHas,MGS,TM, | 2.02 |
| | 417576 | AA339449 | Hs.82285 | phosphoribosylg | AIRS,formyl_transf,GARS,TM, | 2.02 |
| | 418559 | AA225048 | Hs.104207 | ESTs | TM | 2.02 |
| | 410855 | X97795 | Hs.66718 | RAD54 (S.cerevi | SNF2_N,helicase_C,TM, | 2.02 |
| 45 | 422072 | AB018255 | Hs.111138 | KJAA0712 gene p | TM | 2.02 |
| | 419546 | AA244199 | | gb:nc06c05.s1 N | Y_phosphatase,TM, | 2.02 |
| | 450516 | AA902656 | Hs.21943 | NIF3 (Ngg1 inte | DUF34,TM, | 2.02 |
| | 419807 | R77402 | | gb:yi75f11.s1 S | TM | 2.02 |
| | 438192 | AI859065 | Hs.16808 | ESTs, Weakly si | TM,SS | 2.02 |
| 50 | 401866 | | | | filament,TM,SS | 2.02 |
| | 443129 | R16075 | Hs.21668 | ESTs | TM,SS | 2.02 |
| | 424783 | AA913909 | Hs.153088 | TATA box bindin | TM | 2.01 |
| | 413293 | AL047483 | Hs.75270 | GTP-binding pro | ras,TM,SS | 2.01 |
| | 435787 | AW162767 | Hs.100914 | hypothetical pr | SS | 2.01 |
| 55 | 422599 | BE387202 | Hs.118638 | non-metastatic | NDK,SS | 2.01 |
| | 431630 | NM_002204 | Hs.265829 | integrin, alpha | FG-GAP,integrin_A,TM,SS | 2.01 |
| | 448275 | BE514434 | Hs.20830 | synaptic Ras GT | kinesin,PHD,abhydrolase_2,TM,SS | 2.01 |
| | 405484 | | | | filament,SS | 2.01 |
| 60 | 436469 | AK001455 | Hs.5198 | Down syndrome c | TM | 2.01 |
| | 451273 | NM_014811 | Hs.26163 | KJAA0649 gene p | TM | 2.01 |
| | 432378 | AI493046 | Hs.146133 | ESTs | TM | 2.01 |
| | 419981 | AA897581 | Hs.128773 | ESTs | Ski_Sno,SS | 2.01 |
| | 445808 | AV655234 | Hs.298083 | ESTs | sushi,TM,SS | 2.01 |
| | 435767 | H73505 | Hs.117874 | ESTs | Peptidase_S8,P,TM, | 2.01 |
| 65 | 430466 | AF052573 | Hs.241517 | polymerase (DNA | TM | 2.01 |
| | 422790 | AA809875 | Hs.25933 | ESTs | TM | 2.01 |
| | 443303 | U67319 | Hs.9216 | caspase 7, apop | ICE_p10,ICE_p20,TM, | 2.01 |
| | 410008 | AA079552 | | gb:zm20h12.s1 S | FG-GAP,TM,SS | 2.01 |
| | 440774 | AI420611 | Hs.127832 | ESTs | zf-MYND,TM,SS | 2.00 |
| 70 | 442961 | BE614474 | Hs.289074 | Homo sapiens cD | TM | 2.00 |
| | 424420 | BE614743 | Hs.146688 | prostaglandin E | MAPEG,TM,SS | 2.00 |
| | 410240 | AL157424 | Hs.61289 | synaplojanin 2 | TM | 2.00 |
| | 435014 | BE560898 | Hs.10026 | ribosomal prote | Ribosomal_L17,TM, | 2.00 |
| | 406752 | AI285598 | Hs.217493 | annexin A2 | TM | 2.00 |
| 75 | TABLE 41B: | | | | | |
| | Pkey: | Unique Eos probeset identifier number | | | | |
| | CAT number: | Gene cluster number | | | | |
| | Accession: | Genbank accession numbers | | | | |
| 80 | Pkey | CAT number | Accession | | | |
| | 410008 | 116812_1 | AA079552 BE142525 BE142527 | | | |
| | 418546 | 176677_1 | AA224827 T59708 T59843 BE156903 | | | |
| | 419546 | 185766_1 | AA244199 AA244272 H57440 | | | |

| | | | |
|----|--------|-----------|--|
| 5 | 419807 | 188252_1 | R77402 AA262462 AA250988 R06794 |
| | 422689 | 219896_1 | AW856665 AA315006 AW954733 |
| | 431120 | 328264_1 | AA492588 AA492498 AA492571 |
| | 433748 | 37385_1 | R12244 H71290 A110858 AF090916 AF075357 AA011531 |
| | 438223 | 452646_1 | AA781171 A1202139 A1202088 |
| | 438993 | 467651_1 | AA828995 AA834879 A1926361 |
| | 446995 | 702707_1 | A1355012 AW812856 |
| | 447197 | 711623_1 | R36075 A1366546 R36167 |
| 10 | 450190 | 827655_1 | T51387 AW191595 T51271 A1686285 |
| | 451237 | 863269_1 | AW600293 A1767468 |
| | 455778 | 1364506_1 | BE088746 BE088802 BE088755 BE088876 BE088947 BE088881 BE088952 |
| | 456157 | 158261_1 | AW979153 AA176967 AA826015 |

| | | |
|----|--------------|---|
| 15 | TABLE 41C: | |
| | Pkey: | Unique number corresponding to an Eos probeset |
| | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. |
| | Strand: | Indicates DNA strand from which exons were predicted. |
| 20 | NL_position: | Indicates nucleotide positions of predicted exons. |

| | | | | |
|----|--------|---------|--------|---|
| | Pkey | Ref | Strand | NL_position |
| | 400514 | 9796594 | Minus | 78844-79025,80850-80991,89754-89941,93750-93891 |
| | 401519 | 6649315 | Plus | 157315-157950 |
| 25 | 401708 | 2951946 | Plus | 154511-155298 |
| | 401866 | 8018106 | Plus | 73126-73623 |
| | 402075 | 8117407 | Plus | 121907-122035,122804-122921,124019-124161,124455-124610,125672-126076 |
| | 403055 | 8748904 | Minus | 109532-110225 |
| | 403208 | 7630829 | Minus | 147706-147903,148667-148804 |
| 30 | 403422 | 9665041 | Minus | 151169-151561 |
| | 403485 | 9966528 | Plus | 2888-3001,3198-3532,3655-4117 |
| | 403776 | 7770611 | Minus | 1414-1513,1624-1756 |
| | 404171 | 9930793 | Plus | 173667-173783,176876-177055 |
| | 404253 | 9367202 | Minus | 55675-56055 |
| 35 | 404519 | 8152000 | Plus | 12817-13000 |
| | 404567 | 7249169 | Minus | 101320-101501 |
| | 405484 | 5922025 | Plus | 199214-199579,199672-199920,200262-200495 |
| | 405545 | 1054740 | Plus | 118677-118807,119091-119296,121626-121823 |
| | 405818 | 4071056 | Plus | 29055-29196 |
| 40 | 406399 | 9256288 | Minus | 63448-63554 |

TABLE 42A: ABOUT 561 GENES UP-REGULATED IN STOMACH CANCER

Table 42A lists about 561 genes up-regulated in stomach cancer compared to normal stomach. These were selected as for Table 40A except using various non-malignant stomach specimens in determining the denominator value.

| | | | | | |
|----|----------------|---|-----------|--|------|
| 45 | Pkey: | Unique Eos probeset identifier number | | | |
| | ExAccn: | Exemplar Accession number, Genbank accession number | | | |
| | UnigeneID: | Unigene number | | | |
| | Unigene Title: | Unigene gene title | | | |
| | R1: | Ratio of tumor to normal tissue | | | |
| 50 | | | | | |
| | Pkey | ExAccn | UnigeneID | Unigene Title | R1 |
| | 428368 | BE440042 | Hs.83326 | matrix metalloproteinase 3 (stromelysin | 60.4 |
| | 448693 | AW004854 | Hs.228320 | Homo sapiens cDNA: FLJ23537 fis, clone L | 28.6 |
| 55 | 428664 | AK001666 | Hs.189095 | similar to SALL1 (sal (Drosophila)-like | 26.8 |
| | 422330 | D30783 | Hs.115263 | epiregulin | 22.0 |
| | 415989 | A1267700 | Hs.111128 | ESTs | 21.2 |
| | 439979 | AW600291 | Hs.6823 | hypothetical protein FLJ10430 | 19.0 |
| | 451099 | R52795 | Hs.25954 | interleukin 13 receptor, alpha 2 | 17.1 |
| | 403776 | | | | 14.9 |
| 60 | 424905 | NM_002497 | Hs.153704 | NIMA (never in mitosis gene a)-related k | 14.8 |
| | 414132 | A1801235 | Hs.48480 | ESTs | 14.2 |
| | 450375 | AA009647 | Hs.8850 | a disintegrin and metalloproteinase doma | 14.0 |
| | 453922 | AF053306 | Hs.36708 | budding uninhibited by benzimidazoles 1 | 13.8 |
| 65 | 436032 | AA150797 | Hs.109276 | latexin protein | 13.1 |
| | 427585 | D31152 | Hs.179729 | collagen, type X, alpha 1 (Schmid metaph | 12.5 |
| | 416661 | AA634543 | Hs.79440 | IGF-II mRNA-binding protein 3 | 12.2 |
| | 414972 | BE263782 | Hs.77695 | KIAA0008 gene product | 10.6 |
| | 445900 | AF070526 | Hs.13429 | Homo sapiens clone 24787 mRNA sequence | 10.5 |
| 70 | 446619 | AU076643 | Hs.313 | secreted phosphoprotein 1 (osteopontin, | 10.5 |
| | 441377 | BE218239 | Hs.202656 | ESTs | 10.2 |
| | 419423 | D26488 | Hs.90315 | KIAA0007 protein | 9.8 |
| | 415138 | C18356 | Hs.78045 | tissue factor pathway inhibitor 2 | 9.6 |
| | 424639 | A1917494 | Hs.131329 | ESTs | 9.4 |
| 75 | 412472 | AW975398 | Hs.293836 | ESTs | 9.2 |
| | 447048 | AW393080 | Hs.228320 | Homo sapiens cDNA: FLJ23537 fis, clone L | 8.9 |
| | 418379 | AA218940 | Hs.137516 | fidgetin-like 1 | 8.8 |
| | 423020 | AA383092 | Hs.1608 | replication protein A3 (14kD) | 8.6 |
| | 408908 | BE296227 | Hs.48915 | serine/threonine kinase 15 | 8.5 |
| 80 | 419948 | AB041035 | Hs.93847 | NADPH oxidase 4 | 8.3 |
| | 411750 | BE562298 | Hs.71827 | KIAA0112 protein; homolog of yeast ribos | 8.3 |
| | 411479 | AW848047 | | gb:IL3-CT0214-291299-052-A12 CT0214 Homo | 8.1 |
| | 420900 | AL045633 | Hs.44269 | ESTs | 8.0 |
| | 449347 | AV649748 | Hs.295901 | ESTs | 8.0 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 409041 | AB033025 | Hs.50081 | KIAA1199 protein | 8.0 |
| | 450480 | X82125 | Hs.25040 | zinc finger protein 239 | 7.6 |
| | 417655 | AA780791 | Hs.14014 | ESTs, Weakly similar to KIAA0973 protein | 7.6 |
| | 453878 | AW964440 | Hs.19025 | ESTs | 7.6 |
| 5 | 430403 | AF039390 | Hs.241382 | tumor necrosis factor (ligand) superfamily | 7.5 |
| | 427961 | AW293165 | Hs.143134 | ESTs | 7.4 |
| | 428330 | L25224 | Hs.2256 | matrix metalloproteinase 7 (matrilysin) | 7.3 |
| | 426235 | AI631964 | Hs.34447 | ESTs | 7.1 |
| | 452291 | AF015592 | Hs.28853 | CDCT (cell division cycle 7, S. cerevisiae) | 7.0 |
| 10 | 418205 | L21715 | Hs.83760 | troponin I, skeletal, fast | 7.0 |
| | 409757 | NM_001898 | Hs.123114 | cystatin SN | 6.9 |
| | 430044 | AA464510 | Hs.152812 | ESTs | 6.6 |
| | 444783 | AK001468 | Hs.62180 | anillin (Drosophila Scraps homolog), act | 6.5 |
| | 416209 | AA236776 | Hs.79078 | MAD2 (mitotic arrest deficient, yeast, h) | 6.5 |
| 15 | 449020 | AI621170 | Hs.192699 | ESTs | 6.3 |
| | 431958 | X53629 | Hs.2877 | cadherin 3, type 1; P-cadherin (placenta) | 5.8 |
| | 434699 | AA643687 | Hs.149425 | Homo sapiens cDNA FLJ11980 fis, clone HE | 5.7 |
| | 424345 | AK001380 | Hs.145479 | Homo sapiens cDNA FLJ10518 fis, clone NT | 5.6 |
| | 428227 | AA321649 | Hs.2248 | small inducible cytokine subfamily B (Cy | 5.4 |
| 20 | 434551 | BE387162 | Hs.280858 | ESTs, Highly similar to XPB_HUMAN DNA-RE | 5.3 |
| | 427660 | AI741320 | Hs.114121 | Homo sapiens cDNA: FLJ23228 fis, clone C | 5.0 |
| | 424960 | BE245380 | Hs.153952 | 5' nucleotidase (CD73) | 4.9 |
| | 400268 | | | | 4.8 |
| | 408427 | AW194270 | Hs.177236 | ESTs | 4.7 |
| 25 | 453785 | AI368236 | Hs.283732 | ESTs | 4.7 |
| | 411274 | NM_002776 | Hs.69423 | kallikrein 10 | 4.7 |
| | 424717 | H03754 | Hs.152213 | wingless-type MMTV integration site fami | 4.7 |
| | 415752 | BE314524 | Hs.78776 | putative transmembrane protein | 4.6 |
| | 434370 | AF130988 | Hs.58346 | downless (mouse) homolog | 4.6 |
| 30 | 431806 | AF186114 | Hs.270737 | tumor necrosis factor (ligand) superfamily | 4.6 |
| | 400205 | | | | 4.6 |
| | 422938 | NM_001809 | Hs.1594 | centromere protein A (17kD) | 4.5 |
| | 406687 | M31126 | Hs.272620 | pregnancy specific beta-1-glycoprotein 9 | 4.4 |
| | 453160 | AI263307 | Hs.146228 | ESTs | 4.4 |
| 35 | 423871 | AA331906 | | gb:EST35805 Embryo, 8 week 1 Homo sapien | 4.4 |
| | 431211 | M86849 | Hs.5566 | gap junction protein, beta 2, 26kD (conn | 4.4 |
| | 446638 | AL133063 | Hs.15783 | Homo sapiens mRNA; cDNA DKFZp434P1115 (f | 4.3 |
| | 406741 | AA058357 | Hs.74466 | carcinoembryonic antigen-related cell ad | 4.3 |
| | 411560 | AW851186 | | gb:IL3-CT0220-150200-071-H05 CT0220 Homo | 4.1 |
| 40 | 433159 | AB035898 | Hs.150587 | kinesin-like protein 2 | 4.1 |
| | 446142 | AI754693 | Hs.145968 | ESTs | 4.1 |
| | 414727 | BE466904 | | gb:hz28f03.x1 NC1_CGAP_GC6 Homo sapiens | 4.1 |
| | 422285 | AI803103 | | gb:tc14e06.x1 Soares_NhHMPu_S1 Homo sapi | 4.1 |
| 45 | 451807 | W52854 | Hs.27099 | DKFZP564J0863 protein | 4.1 |
| | 411558 | AA102670 | Hs.70725 | gamma-aminobutyric acid (GABA) A recepto | 4.0 |
| | 415701 | NM_003878 | Hs.78619 | gamma-glutamyl hydrolase (conjugase, fol | 4.0 |
| | 409420 | Z15008 | Hs.54451 | laminin, gamma 2 (nicein (100kD), kalini | 3.9 |
| | 452909 | NM_015368 | Hs.30985 | pannexin 1 | 3.9 |
| | 443211 | AI128388 | Hs.143655 | ESTs | 3.9 |
| 50 | 442896 | R37725 | Hs.261108 | ESTs | 3.8 |
| | 407788 | BE514982 | Hs.38991 | S100 calcium-binding protein A2 | 3.8 |
| | 406671 | AA129547 | Hs.285754 | met proto-oncogene (hepatocyte growth fa | 3.8 |
| | 421155 | H87879 | Hs.102267 | lysyl oxidase | 3.8 |
| | 420552 | AK000492 | Hs.98806 | hypothetical protein | 3.8 |
| 55 | 420727 | H75701 | Hs.99886 | complement component 4-binding protein, | 3.7 |
| | 422665 | AJ011812 | Hs.119018 | transcription factor NRF | 3.7 |
| | 447425 | AI963747 | Hs.18573 | acylphosphatase 1, erythrocyte (common) | 3.7 |
| | 417715 | AW969587 | Hs.86366 | ESTs | 3.7 |
| | 406076 | AL1390179 | Hs.137011 | Homo sapiens mRNA; cDNA DKFZp547P134 (fr | 3.6 |
| 60 | 452281 | T93500 | Hs.28792 | Homo sapiens cDNA FLJ11041 fis, clone PL | 3.6 |
| | 412723 | AA648459 | Hs.179912 | ESTs | 3.6 |
| | 452461 | J78223 | Hs.108106 | transcription factor | 3.6 |
| | 453331 | AI240665 | Hs.8895 | ESTs | 3.6 |
| | 406434 | | | | 3.6 |
| 65 | 417956 | AA210704 | Hs.190465 | ESTs | 3.6 |
| | 410102 | AW248508 | Hs.279727 | Homo sapiens cDNA FLJ14035 fis, clone HE | 3.6 |
| | 426471 | M22440 | Hs.170009 | transforming growth factor, alpha | 3.5 |
| | 425782 | U66468 | Hs.159525 | cell growth regulatory with EF-hand doma | 3.5 |
| 70 | 442556 | AL137761 | Hs.8379 | Homo sapiens mRNA; cDNA DKFZp586L2424 (f | 3.5 |
| | 426957 | AA393676 | Hs.97459 | ESTs, Weakly similar to KIAA0819 protein | 3.5 |
| | 448105 | AW591433 | Hs.170675 | ESTs, Weakly similar to TMS2_HUMAN TRANS | 3.5 |
| | 414998 | NM_002543 | Hs.77729 | oxidised low density lipoprotein (lectin | 3.5 |
| | 442942 | AW167087 | Hs.131562 | ESTs | 3.4 |
| | 416391 | AI878927 | Hs.79284 | mesoderm specific transcript (mouse) hom | 3.4 |
| 75 | 420230 | AL034344 | Hs.298020 | Homo sapiens cDNA FLJ11796 fis, clone HE | 3.4 |
| | 408243 | Y00787 | Hs.624 | interleukin 8 | 3.4 |
| | 412978 | AI431708 | Hs.820 | homeo box C6 | 3.4 |
| | 412851 | AI826502 | Hs.106149 | ESTs | 3.4 |
| 80 | 417720 | AA205625 | Hs.208067 | ESTs | 3.4 |
| | 414812 | X72755 | Hs.77367 | monokine induced by gamma interferon | 3.4 |
| | 453884 | AA355925 | Hs.36232 | KIAA0186 gene product | 3.4 |
| | 436396 | AI683487 | Hs.299112 | Homo sapiens cDNA FLJ11441 fis, clone HE | 3.4 |
| | 425921 | NM_007231 | Hs.162211 | solute carrier family 6 (neurotransmitte | 3.4 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 420092 | AA814043 | Hs.88045 | ESTs | 3.3 |
| | 423441 | R68649 | Hs.278359 | absent in melanoma 1 like | 3.3 |
| | 421787 | AA227068 | Hs.108301 | nuclear receptor subfamily 2, group C, m | 3.3 |
| 5 | 447342 | AI199268 | Hs.19322 | ESTs | 3.3 |
| | 430178 | AW449612 | Hs.152475 | ESTs | 3.3 |
| | 452826 | BE245286 | Hs.301636 | ESTs, Moderately similar to PEX6_HUMAN P | 3.3 |
| | 414821 | M53835 | Hs.77424 | Fc fragment of IgG, high affinity Ia, re | 3.3 |
| | 413339 | AI818080 | Hs.194290 | ESTs | 3.3 |
| 10 | 448756 | AI739241 | Hs.171480 | ESTs | 3.3 |
| | 421948 | L42583 | Hs.111758 | keratin 6A | 3.3 |
| | 431453 | AW753917 | | gb:RC0-CT0299-291199-031-F02 CT0299 Homo | 3.3 |
| | 438538 | AA832203 | Hs.291955 | ESTs | 3.3 |
| | 439759 | AL359055 | Hs.67709 | Homo sapiens mRNA full length insert cDN | 3.3 |
| 15 | 431721 | AB032996 | Hs.268044 | KIAA1170 protein | 3.3 |
| | 436391 | AJ227892 | Hs.146274 | ESTs | 3.3 |
| | 442025 | AW887434 | Hs.11810 | ESTs, Weakly similar to CD4.2 [C.elegans | 3.3 |
| | 418007 | M13509 | Hs.83169 | matrix metalloproteinase 1 (interstitial | 3.2 |
| | 411678 | AJ907114 | Hs.71465 | squalene epoxidase | 3.2 |
| 20 | 422956 | BE545072 | Hs.122579 | hypothetical protein FLJ10461 | 3.2 |
| | 450400 | AI694722 | Hs.279744 | ESTs | 3.2 |
| | 453857 | AL080235 | Hs.35861 | DKFZP586E1621 protein | 3.2 |
| | 423528 | AB011137 | Hs.129740 | KIAA0565 gene product | 3.2 |
| | 440659 | AF134160 | Hs.7327 | claudin 1 | 3.2 |
| 25 | 441085 | AW136551 | Hs.181245 | Homo sapiens cDNA FLJ12532 fis, clone NT | 3.2 |
| | 412022 | AI005043 | Hs.24143 | ESTs | 3.2 |
| | 418203 | X54942 | Hs.83758 | CDC28 protein kinase 2 | 3.1 |
| | 416111 | AA033813 | Hs.79018 | chromatin assembly factor 1, subunit A (| 3.1 |
| | 408633 | AW963372 | Hs.46677 | PRO2000 protein | 3.1 |
| 30 | 445808 | AV655234 | Hs.298083 | ESTs | 3.1 |
| | 414618 | AI204600 | Hs.96978 | ESTs | 3.1 |
| | 421340 | F07783 | Hs.1369 | decay accelerating factor for complement | 3.1 |
| | 422689 | AW856665 | | gb:RC3-CT0297-290100-013-d03 CT0297 Homo | 3.1 |
| | 456508 | AA502764 | Hs.123469 | ESTs, Weakly similar to AF208855 1 BM-01 | 3.1 |
| 35 | 420759 | T11832 | Hs.127797 | ESTs | 3.1 |
| | 452637 | AW971231 | Hs.291020 | ESTs | 3.1 |
| | 415857 | AA866115 | Hs.301646 | Homo sapiens cDNA FLJ11381 fis, clone HE | 3.1 |
| | 439451 | AF086270 | Hs.278554 | heterochromatin-like protein 1 | 3.1 |
| | 424051 | AL110203 | Hs.138411 | Homo sapiens mRNA: cDNA DKFZp586J1922 (f | 3.1 |
| 40 | 440138 | AB033023 | Hs.6982 | hypothetical protein FLJ10201 | 3.1 |
| | 454456 | AW850984 | | gb:IL3-CT0220-150200-068-H08 CT0220 Homo | 3.0 |
| | 429125 | AA446854 | Hs.271004 | ESTs | 3.0 |
| | 408031 | AA081395 | Hs.42173 | Homo sapiens cDNA FLJ10366 fis, clone NT | 3.0 |
| | 438394 | BE379623 | Hs.27693 | CGI-124 protein | 3.0 |
| 45 | 409361 | NM_005982 | Hs.54416 | sine oculis homeobox (Drosophila) homolo | 3.0 |
| | 439453 | BE264974 | Hs.6566 | thyroid hormone receptor interactor 13 | 3.0 |
| | 414696 | AF002020 | Hs.76918 | Niemann-Pick disease, type C1 | 3.0 |
| | 422746 | NM_004484 | Hs.119651 | glypican 3 | 3.0 |
| | 424947 | R77952 | Hs.239625 | integral membrane protein 2B | 3.0 |
| 50 | 453775 | NM_002916 | Hs.35120 | replication factor C (activator 1) 4 (37 | 3.0 |
| | 449386 | AA001308 | Hs.193213 | ESTs | 3.0 |
| | 430687 | BE274217 | Hs.249247 | heterogeneous nuclear protein similar to | 2.9 |
| | 428862 | NM_000346 | Hs.2316 | SRY (sex-determining region Y)-box 9 (ca | 2.9 |
| | 401747 | | | | 2.9 |
| 55 | 429682 | NM_006306 | Hs.211602 | SMC1 (structural maintenance of chromoso | 2.9 |
| | 444735 | BE019923 | Hs.243122 | hypothetical protein FLJ13057 similar to | 2.9 |
| | 413385 | M34455 | Hs.840 | indoleamine-pyrole 2,3 dioxygenase | 2.9 |
| | 436222 | AI208737 | Hs.122810 | Homo sapiens cDNA FLJ11489 fis, clone HE | 2.9 |
| | 442961 | BE614474 | Hs.289074 | Homo sapiens cDNA FLJ13986 fis, clone Y7 | 2.9 |
| 60 | 454798 | AW821295 | | gb:PM3-ST0307-241299-002-g03 ST0307 Homo | 2.9 |
| | 421650 | AA781795 | Hs.122587 | ESTs | 2.9 |
| | 434398 | AA121098 | Hs.3838 | serum-inducible kinase | 2.9 |
| | 420153 | N22120 | Hs.75277 | hypothetical protein FLJ13910 | 2.9 |
| | 435706 | W31254 | Hs.7045 | GL004 protein | 2.9 |
| 65 | 416065 | BE267931 | Hs.78996 | proliferating cell nuclear antigen | 2.9 |
| | 423250 | BE061916 | Hs.125849 | chromosome 8 open reading frame 2 | 2.8 |
| | 423493 | AI815965 | Hs.129683 | ubiquitin-conjugating enzyme E2D 1 (homo | 2.8 |
| | 430242 | U66569 | Hs.236642 | 3-hydroxyisobutyryl-Coenzyme A hydrolase | 2.8 |
| | 436411 | AW674352 | | gb:ba63c07.y1 NIH_MGC_12 Homo sapiens cD | 2.8 |
| 70 | 411770 | NM_014278 | Hs.71992 | heat shock protein (hsp110 family) | 2.8 |
| | 437834 | AA769294 | | gb:nz36g03.s1 NCI_CGAP_GCB1 Homo sapiens | 2.8 |
| | 400440 | X83957 | Hs.83870 | nebulin | 2.8 |
| | 444743 | AA045648 | Hs.11817 | nudix (nucleoside diphosphate linked moi | 2.8 |
| | 428725 | AI565937 | Hs.98692 | ESTs | 2.8 |
| 75 | 417771 | AA804698 | Hs.82547 | retinoic acid receptor responder (Iazaro | 2.8 |
| | 449420 | AI654852 | Hs.196562 | ESTs, Highly similar to TS24 MOUSE PROTE | 2.8 |
| | 433929 | AI375499 | Hs.27379 | ESTs | 2.8 |
| | 430287 | AW182459 | Hs.125759 | ESTs, Weakly similar to tumor suppressor | 2.8 |
| | 423346 | AI267677 | Hs.127416 | synaptotagmin 1 | 2.8 |
| 80 | 407824 | AA147884 | Hs.9812 | ESTs | 2.8 |
| | 408482 | NM_000676 | Hs.45743 | adenosine A2b receptor | 2.8 |
| | 425188 | AK002052 | Hs.155071 | hypothetical protein FLJ11190 | 2.8 |
| | 456999 | AA319798 | Hs.172247 | eukaryotic translation elongation factor | 2.8 |
| | 408875 | NM_015434 | Hs.48604 | DKFZP434B168 protein | 2.8 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| | 407839 | AA045144 | Hs.161566 | ESTs | 2.7 |
| | 409012 | AL117435 | Hs.49725 | DKFZP434I216 protein | 2.7 |
| | 410762 | AF226053 | Hs.66170 | HSKM-B protein | 2.7 |
| 5 | 426925 | NM_001196 | Hs.172894 | BH3 interacting domain death agonist | 2.7 |
| | 410116 | AW630671 | Hs.58636 | squamous cell carcinoma antigen recogniz | 2.7 |
| | 428398 | AI249368 | Hs.98558 | ESTs | 2.7 |
| | 400048 | | | AFFX control: YEL002c/WBP1 | 2.7 |
| | 412140 | AA219691 | Hs.73625 | RAB6 interacting, kinesin-like (rabkines | 2.7 |
| 10 | 435664 | AI032087 | Hs.269819 | ESTs | 2.7 |
| | 405695 | | | | 2.7 |
| | 456655 | AI376736 | Hs.111779 | secreted protein, acidic, cysteine-rich | 2.7 |
| | 408670 | AF160967 | Hs.46784 | potassium large conductance calcium-acti | 2.7 |
| | 422576 | BE548555 | Hs.118554 | CGI-83 protein | 2.7 |
| 15 | 431379 | AA504264 | Hs.182937 | peptidylprolyl isomerase A (cyclophilin | 2.7 |
| | 429540 | M85776 | | gb:EST02297 Fetal brain, Stratagene (cat | 2.7 |
| | 426874 | N67325 | Hs.247132 | ESTs | 2.7 |
| | 433183 | AF231338 | Hs.222024 | transcription factor BMAL2 | 2.7 |
| | 409902 | AI337658 | Hs.156351 | ESTs | 2.7 |
| 20 | 422336 | AI761322 | Hs.115285 | dihydrofolamide S-acetyltransferase (E2 | 2.7 |
| | 408434 | AW195317 | Hs.107716 | Homo sapiens cDNA: FLJ22344 fis, clone H | 2.7 |
| | 432328 | AI572739 | Hs.195471 | 6-phosphofructo-2-kinase/fructose-2,6-bi | 2.7 |
| | 407633 | NM_007069 | Hs.37189 | similar to rat HREV107 | 2.6 |
| | 419216 | AU076718 | Hs.164021 | small inducible cytokine subfamily B (Cy | 2.6 |
| 25 | 422363 | T55979 | Hs.115474 | replication factor C (activator 1) 3 (38 | 2.6 |
| | 445564 | AB028957 | Hs.12896 | KIAA1034 protein | 2.6 |
| | 401644 | | | | 2.6 |
| | 417479 | AI057052 | Hs.133554 | ESTs | 2.6 |
| | 434217 | AW014795 | Hs.23349 | ESTs | 2.6 |
| 30 | 426514 | BE616633 | Hs.301122 | bone morphogenetic protein 7 (osteogenic | 2.6 |
| | 414800 | BE538690 | | gb:601064676F1 NIH_MGC_10 Homo sapiens c | 2.6 |
| | 400289 | X07820 | Hs.2258 | matrix metalloproteinase 10 (stromelysin | 2.6 |
| | 418478 | U38945 | Hs.1174 | cyclin-dependent kinase inhibitor 2A (me | 2.6 |
| | 421246 | AW582962 | Hs.300961 | ESTs, Highly similar to AF151805 1 CGI-4 | 2.6 |
| 35 | 430397 | AI924533 | Hs.105607 | ESTs | 2.6 |
| | 428048 | AA705745 | Hs.185070 | ESTs | 2.6 |
| | 452092 | BE245374 | Hs.27842 | hypothetical protein FLJ11210 | 2.6 |
| | 440052 | AI633744 | Hs.195648 | ESTs | 2.6 |
| | 433077 | AA314262 | Hs.289008 | Homo sapiens cDNA: FLJ21814 fis, clone H | 2.6 |
| 40 | 432407 | AA221036 | Hs.285026 | HERV-H LTR-associating 1 | 2.6 |
| | 452401 | NM_007115 | Hs.29352 | tumor necrosis factor, alpha-induced pro | 2.6 |
| | 451813 | NM_016117 | Hs.27182 | phospholipase A2-activating protein | 2.6 |
| | 410889 | X91662 | Hs.66744 | twist (Drosophila) homolog (acrocephalos | 2.6 |
| | 440100 | BE382685 | Hs.158549 | ESTs | 2.6 |
| 45 | 413746 | AA133243 | Hs.171553 | ESTs | 2.6 |
| | 414737 | AI160386 | Hs.125087 | ESTs | 2.6 |
| | 422063 | BE156476 | | gb:QV0-HT0368-040100-082-c05 HT0368 Homo | 2.6 |
| | 418250 | U29926 | Hs.83918 | adenosine monophosphate deaminase (isofo | 2.6 |
| | 437641 | AA811452 | Hs.291911 | ESTs | 2.6 |
| 50 | 436027 | AI864053 | Hs.39972 | ESTs, Weakly similar to I38588 reverse t | 2.6 |
| | 444381 | BE387335 | Hs.283713 | ESTs, Weakly similar to CA54_HUMAN COLLA | 2.6 |
| | 452571 | W31518 | Hs.34665 | ESTs | 2.6 |
| | 452862 | AW378065 | Hs.8687 | ESTs | 2.6 |
| | 411984 | NM_005419 | Hs.72988 | signal transducer and activator of trans | 2.6 |
| 55 | 446440 | AV658411 | Hs.42656 | Homo sapiens cDNA FLJ12667 fis, clone NT | 2.6 |
| | 448663 | BE614599 | Hs.106823 | H.sapiens gene from PAC 42616, similar t | 2.6 |
| | 426427 | M86699 | Hs.169840 | TTK protein kinase | 2.6 |
| | 445848 | AA774824 | Hs.13377 | Homo sapiens clone 23649 and 23755 unkno | 2.6 |
| | 420022 | AA256253 | Hs.120817 | ESTs | 2.6 |
| 60 | 451418 | BE387790 | Hs.26369 | hypothetical protein FLJ20287 | 2.6 |
| | 428953 | AA306610 | Hs.194676 | DKFZP434C013 protein | 2.6 |
| | 424008 | R02740 | Hs.137555 | putative chemokine receptor; GTP-binding | 2.6 |
| | 417863 | AB000450 | Hs.82771 | vaccinia related kinase 2 | 2.6 |
| | 414987 | AA524394 | Hs.165544 | ESTs | 2.6 |
| | 440249 | AI246590 | Hs.125325 | ESTs | 2.6 |
| 65 | 407966 | AA295052 | Hs.38516 | ESTs | 2.5 |
| | 406685 | M18728 | | gb:Human nonspecific crossreacting antiq | 2.5 |
| | 403204 | | | | 2.5 |
| | 436961 | AW375974 | Hs.156704 | ESTs | 2.5 |
| 70 | 422260 | AA315993 | Hs.105484 | ESTs, Weakly similar to LITB_HUMAN LITB | 2.5 |
| | 444471 | AB020684 | Hs.11217 | KIAA0877 protein | 2.5 |
| | 430290 | AI734110 | Hs.136355 | ESTs | 2.5 |
| | 413670 | AB000115 | Hs.75470 | hypothetical protein, expressed in osteo | 2.5 |
| | 421928 | AF013758 | Hs.109643 | polyadenylate binding protein-interactin | 2.5 |
| 75 | 439580 | AF086401 | Hs.293847 | ESTs | 2.5 |
| | 439963 | AW247529 | Hs.6793 | platelet-activating factor acetylhydrola | 2.5 |
| | 457065 | AI476318 | Hs.192480 | ESTs | 2.5 |
| | 439521 | AI808955 | Hs.58248 | ESTs | 2.5 |
| | 426711 | AA383471 | Hs.180669 | conserved gene amplified in osteosarcoma | 2.5 |
| 80 | 422631 | BE218919 | Hs.118793 | hypothetical protein FLJ10688 | 2.5 |
| | 417866 | AW067903 | Hs.82772 | collagen, type XI, alpha 1 | 2.5 |
| | 416975 | NM_004131 | Hs.1051 | granzyme B (granzyme 2, cytotoxic T-lymp | 2.5 |
| | 415947 | U04045 | Hs.78934 | mutS (E. coli) homolog 2 (colon cancer, | 2.5 |
| | 454678 | AW813089 | | gb:RC3-ST0186-240400-111-b05 ST0186 Homo | 2.5 |

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|----|--------|-----------|-----------|--|-----|
| | 424080 | AW189983 | Hs.139119 | Homo sapiens cDNA FLJ10967 fis, clone PL | 2.5 |
| | 426572 | AB037783 | Hs.170623 | hypothetical protein FLJ11183 | 2.5 |
| | 440594 | AW445167 | Hs.126036 | ESTs | 2.5 |
| 5 | 428264 | AA424839 | Hs.98484 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.5 |
| | 408750 | BE294069 | Hs.93581 | hypothetical protein FLJ10512 | 2.5 |
| | 451177 | AI969716 | Hs.13034 | ESTs | 2.5 |
| | 449318 | AW236021 | Hs.108788 | ESTs, Weakly similar to zeste [D.melanog | 2.5 |
| | 434414 | AI798376 | | gb:tr34b07.x1 NCI_CGAP_Ov23 Homo sapiens | 2.5 |
| | 400240 | | | | 2.5 |
| 10 | 410519 | AW612264 | Hs.131705 | ESTs | 2.5 |
| | 440953 | AI683036 | Hs.124135 | KIAA1618 protein | 2.5 |
| | 421190 | U95031 | Hs.102482 | mucin 5, subtype B, tracheobronchial | 2.5 |
| | 444478 | W07318 | Hs.240 | M-phase phosphoprotein 1 | 2.5 |
| 15 | 442295 | AI827248 | Hs.224398 | Homo sapiens cDNA FLJ11469 fis, clone HE | 2.5 |
| | 420894 | AA744597 | Hs.88854 | ESTs | 2.5 |
| | 410094 | BE147897 | Hs.58593 | general transcription factor IIF, polype | 2.4 |
| | 413998 | AW103807 | Hs.243933 | ESTs | 2.4 |
| | 412281 | AI810054 | Hs.14119 | ESTs | 2.4 |
| | 418105 | AW937488 | Hs.178000 | ESTs | 2.4 |
| 20 | 447335 | BE617695 | Hs.286192 | protein phosphatase 1, regulatory (inhib | 2.4 |
| | 446852 | AW451643 | Hs.257479 | ESTs, Weakly similar to AF147747 1 BCG25 | 2.4 |
| | 408915 | NM_016651 | Hs.48950 | heptacellular carcinoma novel gene-3 pro | 2.4 |
| | 442991 | BE281238 | Hs.8886 | hypothetical protein FLJ20424 | 2.4 |
| 25 | 410193 | AJ132592 | Hs.59757 | zinc finger protein 281 | 2.4 |
| | 410664 | NM_006033 | Hs.65370 | lipase, endothelial | 2.4 |
| | 449264 | AI637649 | Hs.196105 | ESTs | 2.4 |
| | 423453 | AW450737 | Hs.128791 | CGI-09 protein | 2.4 |
| | 433757 | AI949974 | Hs.152670 | ESTs | 2.4 |
| 30 | 411598 | BE336654 | Hs.70937 | H3 histone family, member K | 2.4 |
| | 431657 | AI345227 | Hs.105448 | ESTs, Weakly similar to B34087 hypotheti | 2.4 |
| | 429663 | M68874 | Hs.211587 | phospholipase A2, group IVA (cytosolic, | 2.4 |
| | 428242 | H55709 | Hs.2250 | leukemia inhibitory factor (cholinergic | 2.4 |
| | 419559 | Y07828 | Hs.91096 | ring finger protein | 2.4 |
| 35 | 419839 | U24577 | Hs.93304 | phospholipase A2, group VII (platelet-ac | 2.4 |
| | 419713 | AW968058 | Hs.92381 | nudix (nucleoside diphosphate linked moi | 2.4 |
| | 413281 | AA861271 | Hs.34396 | ESTs | 2.4 |
| | 402819 | | | | 2.4 |
| | 431457 | NM_012211 | Hs.256297 | integrin, alpha 11 | 2.4 |
| 40 | 422564 | AI148006 | Hs.222120 | ESTs | 2.4 |
| | 443683 | BE241717 | Hs.9676 | uncharacterized hypothalamus protein HT0 | 2.4 |
| | 407242 | M18728 | | gb:Human nonspecific crossreacting antig | 2.4 |
| | 409235 | AA188827 | Hs.7988 | ESTs, Weakly similar to endo-alpha-D-man | 2.4 |
| | 408938 | AA059013 | Hs.22607 | ESTs | 2.4 |
| 45 | 422158 | L10343 | Hs.112341 | protease inhibitor 3, skin-derived (SKAL | 2.4 |
| | 423217 | NM_000094 | Hs.1640 | collagen, type VII, alpha 1 (epidermolys | 2.4 |
| | 408321 | AW405882 | Hs.44205 | cortistatin | 2.4 |
| | 419086 | NM_000216 | Hs.89591 | Kallmann syndrome 1 sequence | 2.4 |
| | 452945 | AW978187 | Hs.31086 | Homo sapiens mRNA for cytochrome b5, par | 2.4 |
| 50 | 452234 | AW084176 | Hs.223296 | ESTs | 2.4 |
| | 427722 | AK000123 | Hs.180479 | hypothetical protein FLJ20116 | 2.4 |
| | 430399 | AI916284 | Hs.199671 | ESTs | 2.4 |
| | 450737 | AW007152 | Hs.203330 | ESTs | 2.4 |
| | 428513 | BE220806 | Hs.184697 | Homo sapiens clone 23785 mRNA sequence | 2.4 |
| | 405454 | | | | 2.4 |
| 55 | 422168 | AA586894 | Hs.112408 | S100 calcium-binding protein A7 (psorias | 2.3 |
| | 421462 | AF016495 | Hs.104624 | aquaporin 9 | 2.3 |
| | 403416 | AI744626 | Hs.301506 | ESTs, Highly similar to KIAA0564 protein | 2.3 |
| | 422039 | BE567832 | Hs.82148 | hypothetical protein | 2.3 |
| 60 | 448988 | Y09763 | Hs.22785 | gamma-aminobutyric acid (GABA) A recepto | 2.3 |
| | 429145 | AI694923 | Hs.49031 | ESTs | 2.3 |
| | 423198 | M81933 | Hs.1634 | cell division cycle 25A | 2.3 |
| | 442914 | AW188551 | Hs.99519 | Homo sapiens cDNA FLJ14007 fis, clone Y7 | 2.3 |
| | 449042 | AW294985 | Hs.301148 | potassium voltage-gated channel, Isk-rel | 2.3 |
| 65 | 421308 | AA687322 | Hs.192843 | ESTs | 2.3 |
| | 419926 | AW900992 | Hs.93796 | DKFZP586D2223 protein | 2.3 |
| | 429992 | AL050053 | Hs.227397 | Homo sapiens mRNA; cDNA DKFZp566E103 (fr | 2.3 |
| | 440601 | N62409 | Hs.126688 | ESTs | 2.3 |
| | 445232 | AI281848 | Hs.165547 | ESTs | 2.3 |
| 70 | 410174 | AA306007 | Hs.59461 | DKFZP434C245 protein | 2.3 |
| | 452110 | T47667 | Hs.28005 | Homo sapiens mRNA; cDNA DKFZp564G2463 (f | 2.3 |
| | 422493 | AW474183 | Hs.233816 | ESTs | 2.3 |
| | 407047 | X65965 | | gb:H.sapiens SOD-2 gene for manganese su | 2.3 |
| | 411096 | U80034 | Hs.68583 | mitochondrial intermediate peptidase | 2.3 |
| 75 | 426457 | AW894667 | Hs.169965 | chimerin (chimaerin) 1 | 2.3 |
| | 442029 | AW956698 | Hs.14456 | neural precursor cell expressed, develop | 2.3 |
| | 446545 | AI431798 | Hs.164192 | ESTs, Weakly similar to Y161_HUMAN HYPOT | 2.3 |
| | 422094 | AF129535 | Hs.272027 | F-box only protein 5 | 2.3 |
| | 421933 | R88881 | Hs.109655 | sex comb on midleg (Drosophila)-like 1 | 2.3 |
| 80 | 430001 | AI580056 | Hs.98992 | ESTs | 2.3 |
| | 420802 | U22376 | Hs.1334 | v-myb avian myeloblastosis viral oncogen | 2.3 |
| | 402053 | | | | 2.3 |
| | 415666 | H72693 | | ghyru03c11.r1 Soares fetal liver spleen | 2.3 |
| | 432743 | AI146966 | Hs.101656 | ESTs | 2.3 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 433409 | AI278802 | Hs.25661 | ESTs | 2.3 |
| | 408330 | AW182602 | Hs.249954 | ESTs | 2.3 |
| | 407807 | AL031427 | Hs.40094 | Human DNA sequence from clone 167A19 on | 2.3 |
| | 436972 | AA284679 | Hs.25640 | claudin 3 | 2.3 |
| 5 | 436747 | AW977192 | Hs.291343 | ESTs | 2.3 |
| | 433730 | AK002135 | Hs.3542 | hypothetical protein FLJ11273 | 2.3 |
| | 414839 | X63692 | Hs.77462 | DNA (cytosine-5)-methyltransferase 1 | 2.3 |
| | 438192 | AI859065 | Hs.16808 | ESTs, Weakly similar to paraplegin-like | 2.3 |
| 10 | 415339 | NM_015156 | Hs.78398 | KIAA0071 protein | 2.3 |
| | 449539 | W80363 | Hs.58446 | ESTs | 2.2 |
| | 412651 | AA115333 | Hs.107968 | ESTs | 2.2 |
| | 450956 | AW193531 | Hs.205647 | ESTs, Moderately similar to ALU1_HUMAN A | 2.2 |
| | 430335 | D80007 | Hs.239499 | KIAA0185 protein | 2.2 |
| 15 | 417849 | AW291587 | Hs.82733 | nidogen 2 | 2.2 |
| | 454946 | AW846376 | Hs.73817 | gb:QV0-CT0179-090200-090-409 CT0179 Homo | 2.2 |
| | 412326 | R07566 | Hs.44276 | small inducible cytokine A3 (homologous | 2.2 |
| | 408349 | BE546947 | Hs.152096 | homeo box C10 | 2.2 |
| | 424704 | AI263293 | Hs.7395 | cytochrome P450, subfamily 11J (arachido | 2.2 |
| 20 | 419433 | AA814807 | Hs.55279 | hypothetical protein FLJ23182 | 2.2 |
| | 409632 | W74001 | Hs.949 | serine (or cysteine) proteinase inhibito | 2.2 |
| | 415323 | BE269352 | Hs.1087 | neutrophil cytosolic factor 2 (65kD, chr | 2.2 |
| | 417531 | NM_003157 | | serine/threonine kinase 2 | 2.2 |
| | 403137 | | | | 2.2 |
| 25 | 428479 | Y00272 | Hs.184572 | cell division cycle 2, G1 to S and G2 to | 2.2 |
| | 430200 | BE613337 | Hs.234896 | geminin | 2.2 |
| | 433745 | AF075320 | Hs.28980 | Homo sapiens clone HQ0270 | 2.2 |
| | 425390 | AI092634 | Hs.156114 | protein tyrosine phosphatase, non-receptl | 2.2 |
| | 408380 | AF123050 | Hs.44532 | diubiquitin | 2.2 |
| 30 | 422424 | AI186431 | Hs.116577 | prostate differentiation factor | 2.2 |
| | 431548 | AI834273 | Hs.9711 | Homo sapiens cDNA FLJ13018 fis, clone NT | 2.2 |
| | 400298 | AA032279 | Hs.61635 | six transmembrane epithelial antigen of | 2.2 |
| | 428771 | AB028992 | Hs.193143 | KIAA1069 protein | 2.2 |
| | 411571 | AA122393 | Hs.70811 | hypothetical protein FLJ20516 | 2.2 |
| 35 | 442573 | H93366 | Hs.7567 | Homo sapiens cDNA: FLJ21962 fis, clone H | 2.2 |
| | 412802 | U41518 | Hs.74602 | aquaporin 1 (channel-forming integral pr | 2.2 |
| | 412530 | AA766268 | Hs.266273 | Homo sapiens cDNA FLJ13346 fis, clone OV | 2.2 |
| | 414761 | AU077228 | Hs.77256 | enhancer of zeste (Drosophila) homolog 2 | 2.2 |
| | 408432 | AW195262 | | gb:xn67b05.x1 NCI_CGAP_CML1 Homo sapiens | 2.2 |
| 40 | 440283 | AI732892 | Hs.190489 | ESTs | 2.2 |
| | 429568 | AI088691 | Hs.208414 | Homo sapiens mRNA: cDNA DKFZp564D0472 (f | 2.2 |
| | 424003 | BE274717 | Hs.137506 | Homo sapiens BAC clone RP11-120J2 from 7 | 2.2 |
| | 425300 | AW601773 | Hs.270259 | ESTs | 2.2 |
| | 448568 | AA149121 | Hs.71947 | ESTs | 2.2 |
| 45 | 419229 | AI827237 | Hs.282884 | ESTs | 2.2 |
| | 420982 | AW576160 | Hs.100729 | KIAA0692 protein | 2.2 |
| | 403258 | | | | 2.2 |
| | 439653 | AW021103 | Hs.6631 | hypothetical protein FLJ20373 | 2.2 |
| | 426827 | AW067805 | Hs.172665 | methylenetetrahydrofolate dehydrogenase | 2.2 |
| 50 | 444514 | AI682905 | Hs.270431 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.2 |
| | 426298 | AW965058 | Hs.111583 | ESTs | 2.2 |
| | 425322 | U63630 | Hs.155637 | protein kinase, DNA-activated, catalytic | 2.2 |
| | 421662 | NM_014141 | Hs.106552 | cell recognition molecule Caspr2 | 2.2 |
| | 412505 | AA974491 | Hs.21734 | ESTs | 2.2 |
| 55 | 438788 | AA825716 | | gb:od29e10.s1 NCI_CGAP_GCB1 Homo sapiens | 2.2 |
| | 429058 | AF138863 | Hs.194827 | hypothetical protein FLB6421 | 2.2 |
| | 423104 | AJ005273 | Hs.123647 | antigenic determinant of recA protein (m | 2.2 |
| | 410406 | AI969703 | Hs.301842 | ESTs | 2.2 |
| | 443180 | R15875 | Hs.70945 | ESTs | 2.2 |
| 60 | 419235 | AW470411 | Hs.288433 | neurotrophin | 2.2 |
| | 421379 | Y15221 | Hs.103982 | small inducible cytokine subfamily B (Cy | 2.2 |
| | 422809 | AK001379 | Hs.121028 | hypothetical protein FLJ10549 | 2.2 |
| | 415058 | AW902848 | Hs.273829 | ESTs | 2.2 |
| | 418049 | AA211467 | Hs.190488 | hypothetical protein FLJ10120 | 2.2 |
| 65 | 436209 | AW850417 | Hs.254020 | ESTs, Moderately similar to unnamed prot | 2.2 |
| | 408042 | AL049233 | Hs.42244 | Homo sapiens mRNA: cDNA DKFZp564A023 (fr | 2.2 |
| | 425692 | D90041 | Hs.155956 | N-acetyltransferase 1 (arylamine N-acety | 2.2 |
| | 409665 | NM_006731 | Hs.55777 | Fukuyama type congenital muscular dystro | 2.2 |
| | 428157 | AJ738719 | Hs.298668 | ESTs | 2.2 |
| 70 | 410480 | R97457 | Hs.63984 | cadherin 13, H-cadherin (heart) | 2.2 |
| | 429732 | U20158 | Hs.2488 | lymphocyte cytosolic protein 2 (SH2 doma | 2.2 |
| | 414747 | U30872 | Hs.77204 | centromere protein F (350/400kD, mitotin | 2.2 |
| | 425843 | BE313280 | Hs.159627 | death associated protein 3 | 2.2 |
| | 445299 | AI910382 | Hs.118727 | Homo sapiens cDNA FLJ13692 fis, clone PL | 2.1 |
| 75 | 436251 | BE515065 | Hs.5092 | nucleolar protein (KKE/D repeat) | 2.1 |
| | 430066 | AI929659 | Hs.237825 | signal recognition particle 72kD | 2.1 |
| | 422516 | BE258862 | Hs.117950 | multifunctional polypeptide similar to S | 2.1 |
| | 407870 | AB032990 | Hs.40719 | hypothetical protein KIAA1164 | 2.1 |
| | 416109 | AI420311 | Hs.126550 | suppressor of K+ transport defect 1 | 2.1 |
| 80 | 427528 | AU077143 | Hs.179565 | minichromosome maintenance deficient (S. | 2.1 |
| | 448089 | AI467945 | Hs.173696 | ESTs | 2.1 |
| | 441790 | AW294909 | Hs.132208 | ESTs | 2.1 |
| | 400022 | | | AFFX control: STAT1 | 2.1 |
| | 428728 | NM_016625 | Hs.191381 | hypothetical protein | 2.1 |

| | | | | | |
|----|--------|-----------|-----------|---|-----|
| | 414366 | BE549143 | | gb:601076456F1 NIH_MGC_12 Homo sapiens c | 2.1 |
| | 409929 | R38772 | Hs.172619 | KIAA1106 protein | 2.1 |
| | 405264 | | | | 2.1 |
| 5 | 445625 | BE246743 | Hs.288529 | Homo sapiens cDNA: FLJ22635 fis, clone H | 2.1 |
| | 408949 | AF189011 | Hs.49163 | putative ribonuclease III | 2.1 |
| | 424513 | BE385864 | Hs.149894 | mitochondrial translational initiation f | 2.1 |
| | 433683 | AI817723 | Hs.22678 | hypothetical protein FLJ21832 | 2.1 |
| | 442952 | AI743261 | Hs.131860 | ESTs | 2.1 |
| 10 | 441020 | W79283 | Hs.35962 | ESTs | 2.1 |
| | 446770 | AV660309 | Hs.154986 | ESTs, Weakly similar to AF137386 1 plasm | 2.1 |
| | 432378 | AI493046 | Hs.146133 | ESTs | 2.1 |
| | 447769 | AW873704 | Hs.48764 | ESTs | 2.1 |
| | 412654 | AI093480 | Hs.29263 | Homo sapiens cDNA FLJ11896 fis, clone HE | 2.1 |
| 15 | 445669 | AI570830 | Hs.174870 | ESTs | 2.1 |
| | 417979 | AU077284 | Hs.83081 | GTP cyclohydrolase I feedback regulatory | 2.1 |
| | 433849 | BE465884 | Hs.280728 | ESTs | 2.1 |
| | 437928 | NM_005476 | Hs.5920 | UDP-N-acetylglucosamine-2-epimerase/N-ac | 2.1 |
| | 457341 | BE181716 | | gb:QV1-HT0639-150500-198-e03 HT0639 Homo | 2.1 |
| 20 | 452833 | BE559681 | Hs.30736 | KIAA0124 protein | 2.1 |
| | 403055 | | | | 2.1 |
| | 414581 | AA256213 | Hs.72010 | ESTs | 2.1 |
| | 432840 | AK001403 | Hs.279521 | hypothetical protein FLJ20530 | 2.1 |
| | 418994 | AA296520 | Hs.89546 | selectin E (endothelial adhesion molecu | 2.1 |
| 25 | 440908 | AI915225 | Hs.126735 | ESTs | 2.1 |
| | 417621 | AV654694 | Hs.82316 | interferon-induced, hepatitis C-associat | 2.1 |
| | 436895 | AF037335 | Hs.5338 | carbonic anhydrase XII | 2.1 |
| | 455716 | BE070263 | | gb:QV4-BT0407-280100-090-e07 BT0407 Homo | 2.1 |
| | 408420 | NM_006915 | Hs.299481 | Homo sapiens mRNA: cDNA DKFZp586B0118 (f | 2.1 |
| 30 | 435849 | BE305242 | Hs.112442 | ESTs, Weakly similar to CLDE_HUMAN CLAU | 2.1 |
| | 424308 | AW975531 | Hs.154443 | minichromosome maintenance deficient (S, | 2.1 |
| | 433644 | AW342028 | Hs.256112 | ESTs | 2.1 |
| | 400020 | | | AFFX control: STAT1 | 2.1 |
| | 434064 | AL049045 | Hs.180758 | hypothetical protein PRO0082 | 2.1 |
| 35 | 410660 | AI061118 | Hs.65328 | Fanconi anemia, complementation group F | 2.1 |
| | 404076 | | | | 2.1 |
| | 441362 | BE614410 | Hs.23044 | RAD51 (S. cerevisiae) homolog (E coli Re | 2.1 |
| | 422515 | AW500470 | Hs.117950 | multifunctional polypeptide similar to S | 2.1 |
| | 444863 | AW384082 | Hs.301323 | ESTs | 2.1 |
| 40 | 445867 | AF272663 | Hs.13405 | gephyrin | 2.1 |
| | 441021 | AW578716 | Hs.7644 | H1 histone family, member 2 | 2.1 |
| | 446595 | T57448 | Hs.15467 | hypothetical protein FLJ20725 | 2.1 |
| | 417515 | L24203 | Hs.82237 | ataxia-telangiectasia group D-associated | 2.1 |
| | 412429 | AV650262 | Hs.75765 | GRO2 oncogene | 2.1 |
| 45 | 449207 | AL044222 | Hs.23255 | nucleoporin 155kD | 2.1 |
| | 412095 | AI624707 | Hs.5921 | Homo sapiens cDNA: FLJ21592 fis, clone C | 2.1 |
| | 400861 | | | | 2.1 |
| | 448826 | AI580252 | Hs.293246 | ESTs, Weakly similar to putative p150 [H | 2.1 |
| | 440591 | AA431599 | Hs.132799 | Homo sapiens cDNA: FLJ23451 fis, clone H | 2.1 |
| 50 | 426181 | AA371422 | Hs.69844 | ESTs, Weakly similar to dJ191N21.1 [H.sa | 2.1 |
| | 452880 | AA029332 | Hs.87549 | ESTs | 2.1 |
| | 421878 | AA299652 | Hs.111496 | Homo sapiens cDNA FLJ11643 fis, clone HE | 2.1 |
| | 442104 | L20971 | Hs.188 | phosphodiesterase 4B, cAMP-specific (dun | 2.1 |
| | 427224 | AL135554 | Hs.101937 | sine oculis homeobox (Drosophila) homolo | 2.1 |
| 55 | 446921 | AB012113 | Hs.16530 | small inducible cytokine subfamily A (Cy | 2.1 |
| | 432487 | AA550988 | Hs.221472 | ESTs | 2.1 |
| | 429534 | AW976987 | Hs.163327 | ESTs | 2.1 |
| | 446051 | BE048061 | Hs.153315 | ESTs | 2.1 |
| | 447760 | AI431328 | Hs.291179 | ESTs, Weakly similar to topoisomerase I | 2.1 |
| 60 | 422675 | BE018517 | Hs.119140 | eukaryotic translation initiation factor | 2.1 |
| | 415173 | AW501735 | Hs.253015 | ESTs | 2.1 |
| | 425170 | AU077315 | Hs.154970 | transcription factor CP2 | 2.1 |
| | 453751 | R36762 | Hs.101282 | Homo sapiens mRNA: cDNA DKFZp434B102 (fr | 2.1 |
| | 426283 | NM_003937 | Hs.169139 | kynureninase (L-kynurenine hydrolase) | 2.1 |
| 65 | 417874 | BE616160 | Hs.82829 | protein tyrosine phosphatase, non-recept | 2.1 |
| | 449555 | AW450288 | Hs.195390 | ESTs | 2.1 |
| | 439699 | AF086534 | Hs.187561 | ESTs, Moderately similar to ALU1_HUMAN A | 2.1 |
| | 427413 | BE547647 | Hs.177781 | superoxide dismutase 2, mitochondrial | 2.1 |
| | 424673 | AA345051 | Hs.294092 | ESTs | 2.1 |
| 70 | 407802 | D84145 | Hs.39913 | novel RGD-containing protein | 2.0 |
| | 452834 | AI638627 | Hs.105685 | ESTs | 2.0 |
| | 438895 | AW007021 | Hs.82894 | ESTs | 2.0 |
| | 446035 | NM_006558 | Hs.13565 | Sam68-like phosphotyrosine protein, T-ST | 2.0 |
| | 406881 | S71129 | Hs.296844 | Acetylcholinesterase (14-E5 domain) [huma | 2.0 |
| 75 | 427001 | NM_006482 | Hs.173135 | dual-specificity tyrosine-(Y)-phosphoryl | 2.0 |
| | 439223 | AW238299 | Hs.23945 | ESTs | 2.0 |
| | 432343 | NM_002960 | Hs.2961 | S100 calcium-binding protein A3 | 2.0 |
| | 414890 | BE281095 | Hs.77573 | uridine phosphorylase | 2.0 |
| | 423019 | AI640185 | Hs.225816 | ESTs | 2.0 |
| 80 | 435905 | AW997484 | Hs.5003 | KIAA0456 protein | 2.0 |
| | 422278 | AF072873 | Hs.114218 | frizzled (Drosophila) homolog 6 | 2.0 |
| | 439608 | AW864696 | Hs.26198 | Homo sapiens cDNA: FLJ23363 fis, clone H | 2.0 |
| | 432114 | AL036021 | Hs.225597 | ESTs | 2.0 |
| | 405545 | | | | 2.0 |

| | | | | | |
|----|--------|-----------|-----------|--|-----|
| 5 | 418201 | AA214345 | Hs.98445 | Homo sapiens cDNA: FLJ21652 fis, clone C | 2.0 |
| | 442528 | AF150317 | Hs.134217 | ESTs | 2.0 |
| | 446237 | AW270515 | Hs.149596 | ESTs | 2.0 |
| | 428074 | BE387770 | Hs.182378 | colony stimulating factor 2 receptor, al | 2.0 |
| | 423430 | AF112481 | Hs.128501 | RAD54, S. cerevisiae, homolog of, B | 2.0 |
| | 435767 | H73505 | Hs.117874 | ESTs | 2.0 |
| | 432945 | AL043683 | Hs.271357 | ESTs, Weakly similar to unnamed protein | 2.0 |
| | 428792 | BE535955 | Hs.193602 | chromosome condensation protein G | 2.0 |
| 10 | 404170 | | | | 2.0 |
| | 410286 | AI739159 | Hs.61898 | DKFZP586N2124 protein | 2.0 |
| | 434565 | TS2172 | | gb:yb22d01.s1 Stratagene fetal spleen (9 | 2.0 |
| | 422610 | AF153820 | Hs.1547 | potassium inwardly-rectifying channel, s | 2.0 |
| | 417933 | X02308 | Hs.82962 | thymidylate synthetase | 2.0 |
| 15 | 441384 | AA447849 | Hs.288660 | protease, serine, 23 | 2.0 |
| | 437403 | AI208149 | Hs.121196 | ESTs | 2.0 |
| | 412673 | ALD42957 | Hs.31845 | ESTs | 2.0 |
| | 414020 | NM_002984 | Hs.75703 | small inducible cytokine A4 (homologous | 2.0 |
| | 438426 | AA835936 | Hs.269763 | ESTs | 2.0 |
| 20 | 413943 | AW294416 | Hs.144687 | ESTs | 2.0 |
| | 449001 | AI619957 | Hs.189854 | ESTs | 2.0 |
| | 427674 | NM_003528 | Hs.2178 | H2B histone family, member Q | 2.0 |
| | 435425 | H16263 | Hs.31416 | ESTs | 2.0 |
| | 433364 | AI075407 | Hs.296083 | ESTs | 2.0 |
| 25 | 429782 | NM_005754 | Hs.220689 | Ras-GTPase-activating protein SH3-domain | 2.0 |
| | 417366 | BE185289 | Hs.1076 | small proline-rich protein 1B (cornifin) | 2.0 |
| | 426746 | J03626 | Hs.2057 | uridine monophosphate synthetase (orotat | 2.0 |
| | 411943 | BE502436 | Hs.7962 | ESTs, Weakly similar to putative [C.eleg | 2.0 |
| | 414266 | BE267834 | | gb:601124428F1 NIH_MGC_8 Homo sapiens cD | 2.0 |
| 30 | 432677 | NM_004482 | Hs.278611 | UDP-N-acetyl-alpha-D-galactosamine:polyp | 2.0 |
| | 450534 | AI570189 | Hs.25132 | KIAA0470 gene product | 2.0 |
| | 446715 | AI337735 | Hs.173919 | ESTs | 2.0 |

TABLE 42B:

| | | |
|----|-------------|---------------------------------------|
| 35 | Pkey: | Unique Eos probeset identifier number |
| | CAT number: | Gene cluster number |
| | Accession: | Genbank accession numbers |

| | | | |
|----|--------|------------|---|
| 40 | Pkey | CAT number | Accession |
| | 408432 | 1058667_1 | AW195262 R27868 AW811262 |
| | 411479 | 1247077_1 | AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905 |
| | | | AW848214 |
| | 411560 | 1249443_1 | AW851186 AW996967 BE143456 |
| | 414266 | 1430984_1 | BE267834 BE514180 BE514096 |
| 45 | 414366 | 1438636_1 | BE549143 BE390613 BE277344 |
| | 414727 | 1481204_1 | BE466904 W28721 |
| | 414800 | 1491863_1 | BE538690 T40217 |
| | 415666 | 1543492_1 | H72693 R08673 H72694 F20990 R08580 |
| | 422063 | 210852_1 | BE156476 BE156473 BE156474 BE156475 AA302839 |
| 50 | 422285 | 214669_1 | AI803103 AI885143 AW470793 AW450703 AI090784 AW271587 AW236950 AW242783 |
| | 422689 | 219896_1 | AW856665 AA315006 AW954733 |
| | 423871 | 232749_1 | AA331906 AA332484 |
| | 429540 | 305828_1 | M85776 AA454535 AA456208 H90189 |
| | 431453 | 333457_1 | AW753917 BE152926 AA505333 BE155673 |
| 55 | 434414 | 38585_1 | AI798376 S46400 AW811617 AW811616 W00557 BE142245 AW858232 AW861851 AW858362 AA232351 AA218567 AA055556 AW858231 |
| | | | AW857541 AW814172 H66214 AW814398 AF134164 AA243093 AA173345 AA199942 AA223384 AA227092 AA227080 T12379 AA092174 T61139 |
| | | | AA149776 AA699829 AW879188 AW813567 AW813538 AI267168 AA157718 AA157719 AA100472 AA100774 AA130756 AA157705 AA157730 |
| | | | AA157715 AA053524 AW849581 AW854566 C05254 AW882836 T92637 AW812621 AA206583 AA209204 BE156909 AA226824 AI829309 AW991957 |
| | | | N66951 AA527374 H66215 AA045564 AI694265 H60808 AA149726 AW195620 BE081333 BE073424 AW817662 AW817705 AW817703 AW817659 |
| | | | BE081531 H59570 |
| 60 | 434565 | 38898_1 | TS2172 AF147324 TS2248 |
| | 436411 | 419334_1 | AW674352 AA715374 Z25205 |
| | 437834 | 443674_1 | AA769294 AW749299 AW749302 AW749295 AW749304 AW749293 AW749298 AW749294 AW749288 AW749291 AW749297 AW749292 AW749296 |
| | | | AW749289 AW749287 BE535498 |
| 65 | 438788 | 465159_1 | AA825716 AW978859 AA828841 |
| | 454456 | 1207088_1 | AW850984 AW752836 M86124 |
| | 454678 | 1228915_1 | AW813089 W28102 |
| | 454798 | 1235104_1 | AW821295 AW821272 AW821282 |
| | 454946 | 1245753_1 | AW846376 AW846375 AW846434 AW846287 AW846365 AW846554 AW846384 AW846290 AW846356 AW846474 |
| 70 | 455716 | 1352695_1 | BE070263 BE070195 BE070265 BE070202 BE070233 BE070399 BE070203 |
| | 457341 | 322221_1 | BE181716 AW948314 AW801848 AW948320 AW983981 AA484444 |

TABLE 42C:

| | | |
|----|--------------|---|
| 75 | Pkey: | Unique number corresponding to an Eos probeset |
| | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. |
| | Strand: | Indicates DNA strand from which exons were predicted. |
| | Nt_position: | Indicates nucleotide positions of predicted exons. |

| | | | | |
|----|--------|---------|--------|---|
| 80 | Pkey | Ref | Strand | Nt_position |
| | 400861 | 9757506 | Plus | 163855-164016 |
| | 401644 | 8576138 | Plus | 82655-83959 |
| | 401747 | 9789672 | Minus | 118596-118816, 119119-119244, 119609-119761, 120422-120990, 130161-130381, 130468-130593, 131097-131258, 131866-31932, 132451-132575, 133580-134011 |

| | | | | |
|----|--------|---------|-------|---|
| 5 | 402053 | 8083229 | Plus | 62703-63179 |
| | 402819 | 6729581 | Plus | 29217-29422 |
| | 403055 | 8748904 | Minus | 109532-110225 |
| | 403137 | 9211494 | Minus | 92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337 |
| | 403204 | 7622392 | Plus | 16214-16439 |
| 10 | 403258 | 7770439 | Minus | 156251-156619 |
| | 403776 | 7770611 | Minus | 1414-1513,1624-1756 |
| | 404076 | 9931752 | Minus | 3848-3967 |
| | 404170 | 9930793 | Plus | 168836-169248 |
| | 405264 | 7329374 | Plus | 28556-28684 |
| 15 | 405454 | 7656675 | Plus | 133807-134053 |
| | 405545 | 1054740 | Plus | 118677-118807,119091-119296,121626-121823 |
| | 405695 | 4309958 | Plus | 51860-52162 |
| | 406434 | 9256651 | Minus | 17803-17931 |
| | | | | |

TABLE 43A: ABOUT 339 GENES UP-REGULATED IN STOMACH CANCER

Table 43A lists about 339 genes up-regulated in stomach cancer compared to normal stomach that are likely to be extracellular or cell-surface proteins. These were selected as for Table 42A and the predicted protein contained a structural domain that is indicative of surface or extracellular localization (e.g. ig, ln3, egr, 7tm domains). Predicted protein domains are noted.

| | | | | | | |
|----|----------------|---|-----------|-----------------|--------------------------------|------|
| | Pkey: | Unique Eos probeset identifier number | | | | |
| | ExAccn: | Exemplar Accession number, Genbank accession number | | | | |
| | UnigenelD: | Unigene number | | | | |
| 25 | Unigene Title: | Unigene gene title | | | | |
| | PSDomain: | Protein Structural Domain | | | | |
| | R1: | Ratio of tumor to normal tissue | | | | |
| | Pkey | ExAccn | UnigenelD | Unigene Title | PSDomain | R1 |
| 30 | 428368 | BE440042 | Hs.83326 | matrix metallo | hemopexin,Peptidase_M10,SS | 60.4 |
| | 428664 | AK001666 | Hs.189095 | similar to SALL | zf-C2H2,TM,SS | 26.8 |
| | 422330 | D30783 | Hs.115263 | epiregulin | EGF,TM,SS | 22.0 |
| | 439979 | AW600291 | Hs.6823 | hypothetical pr | TM | 19.0 |
| | 451099 | RS2795 | Hs.25954 | interleukin 13 | ln3,TM,SS | 17.1 |
| | 403776 | | | | IL8,TM,SS | 14.9 |
| 35 | 424905 | NM_002497 | Hs.153704 | NIMA (never in | pkinae,TM, | 14.8 |
| | 453922 | AF053306 | Hs.36708 | budding uninhib | TM | 13.8 |
| | 436032 | AA150797 | Hs.109276 | latexin protein | TM | 13.1 |
| | 427585 | D31152 | Hs.179729 | collagen, type | C1q,Collagen,TM,SS | 12.5 |
| 40 | 416661 | AA634543 | Hs.79440 | IGF-II mRNA-bin | KH-domain,TM, | 12.2 |
| | 414972 | BE263782 | Hs.77695 | KIAA0008 gene p | TM | 10.6 |
| | 446619 | AU076643 | Hs.313 | secreted phosph | Osteopontin,TM,SS | 10.5 |
| | 415138 | C18356 | Hs.78045 | tissue factor p | Kunitz_BPTI,G-gamma,TM,SS | 9.6 |
| | 423020 | AA383092 | Hs.1608 | replication pro | TM | 8.6 |
| 45 | 408908 | BE296227 | Hs.48915 | serine/threonin | pkinae,TM,SS | 8.5 |
| | 419948 | AB041035 | Hs.93847 | NADPH oxidase 4 | Ferric_reduct,TM,SS | 8.3 |
| | 411750 | BE562298 | Hs.71827 | KIAA0112 protei | SS | 8.3 |
| | 420900 | AL045633 | Hs.44269 | ESTs | Ald_Xan_dh_C,FAD_binding_5,TM, | 8.0 |
| | 450480 | X82125 | Hs.25040 | zinc finger pro | zf-C2H2,TM,SS | 7.6 |
| 50 | 417655 | AA780791 | Hs.14014 | ESTs, Weakly si | TM | 7.6 |
| | 430403 | AF039390 | Hs.241382 | tumor necrosis | TM,SS | 7.5 |
| | 428330 | L22524 | Hs.2256 | matrix metallo | Peptidase_M10,SS | 7.3 |
| | 452291 | AF015592 | Hs.28853 | CDC7 (cell divi | pkinae,TM, | 7.0 |
| | 418205 | L21715 | Hs.83760 | troponin I, ske | Troponin_SS | 7.0 |
| 55 | 409757 | NM_001898 | Hs.123114 | cystatin SN | cystatin_SS | 6.9 |
| | 444783 | AK001468 | Hs.62180 | anilin (Drosop | PH,TM, | 6.5 |
| | 416209 | AA236776 | Hs.79078 | MAD2 (mitotic a | HORMA_SS | 6.5 |
| | 431958 | X63629 | Hs.2877 | cadherin 3, typ | cadherin,Cadherin_C_term,TM,SS | 5.8 |
| | 424345 | AK001380 | Hs.145479 | Homo sapiens cD | TM,SS | 5.6 |
| 60 | 428227 | AA321649 | Hs.2248 | small inducible | IL8,TM,SS | 5.4 |
| | 424960 | BE245380 | Hs.153952 | 5' nucleotidase | 5_nucleotidase,TM,SS | 4.9 |
| | 400268 | | | | Myosin_tail_SS | 4.8 |
| | 411274 | NM_002776 | Hs.69423 | kallikrein 10 | trypsin,TM, | 4.7 |
| | 415752 | BE314524 | Hs.78776 | putative transm | TM | 4.6 |
| 55 | 431806 | AF186114 | Hs.270737 | tumor necrosis | TM,SS | 4.6 |
| | 400205 | | | | SS | 4.6 |
| | 422938 | NM_001809 | Hs.1594 | centromere prot | histone,TM, | 4.5 |
| | 406687 | M31126 | Hs.272620 | pregnancy speci | hemopexin,TM, | 4.4 |
| | 423871 | AA331906 | | gb:EST35805 Emb | TM | 4.4 |
| 70 | 431211 | M86849 | Hs.5566 | gap junction pr | connexin,TM, | 4.4 |
| | 446638 | AL133063 | Hs.15783 | Homo sapiens mR | TM | 4.3 |
| | 406741 | AA058357 | Hs.74466 | carcinoembryoni | ig,TM,SS | 4.3 |
| | 411560 | AW851186 | | gb:IL3-CT0220-1 | TM | 4.1 |
| | 433159 | AB035898 | Hs.150587 | kinesin-like pr | kinesin,Myosin_tail,TM,SS | 4.1 |
| 75 | 422285 | AI803103 | | gb:tc14e06.x1 S | TM,SS | 4.1 |
| | 451807 | W52854 | Hs.27099 | DKFZP564J0863 p | TM | 4.1 |
| | 411558 | AA102670 | Hs.70725 | gamma-aminobuty | neur_chan,TM,SS | 4.0 |
| | 415701 | NM_003878 | Hs.78619 | gamma-glutamyl | TM,SS | 4.0 |
| | 409420 | Z15008 | Hs.54451 | laminin, gamma | laminin_EGF,laminin_B_SS | 3.9 |
| | 452909 | NM_015368 | Hs.30985 | pannexin 1 | TM | 3.9 |
| 80 | 407788 | BE514982 | Hs.38991 | S100 calcium-bi | efhand_S_100,TM,SS | 3.8 |
| | 421155 | H87879 | Hs.102267 | lysyl oxidase | Lysyl_oxidase_SS | 3.8 |
| | 420552 | AK000492 | Hs.98806 | hypothetical pr | SS | 3.8 |
| | 420727 | H175701 | Hs.99886 | complement comp | sushi, | 3.7 |

| | | | | | | |
|----|--------|-----------|-----------|-----------------|----------------------------|-----|
| | 422665 | AJ011812 | Hs.119018 | transcription f | R3H,G-patch,GTP_CDC,TM,SS | 3.7 |
| | 447425 | AI963747 | Hs.18573 | acylphosphatase | Acylphosphatase,TM, | 3.7 |
| | 406076 | AL390179 | Hs.137011 | Homo sapiens mR | TM | 3.6 |
| 5 | 406434 | | | | heme_1,TM, | 3.6 |
| | 417956 | AA210704 | Hs.190465 | ESTs | sushi,SS | 3.6 |
| | 410102 | AW248508 | Hs.279727 | Homo sapiens cD | TM,SS | 3.6 |
| | 426471 | M22440 | Hs.170009 | transforming gr | EGF,TM,SS | 3.5 |
| | 425782 | U66468 | Hs.159525 | cell growth reg | SS | 3.5 |
| 10 | 426957 | AA393676 | Hs.97459 | ESTs, Weakly si | SS | 3.5 |
| | 448105 | AW591433 | Hs.170675 | ESTs, Weakly si | trypsin,TM, | 3.5 |
| | 414998 | NM_002543 | Hs.77729 | oxidised low de | TM | 3.5 |
| | 442942 | AW167087 | Hs.131562 | ESTs | pkinese,TM,SS | 3.4 |
| | 416391 | AI878927 | Hs.79284 | mesoderm specif | abhydrolase,TM,SS | 3.4 |
| 15 | 420230 | AL034344 | Hs.298020 | Homo sapiens cD | Fork_head,TM, | 3.4 |
| | 408243 | Y00787 | Hs.624 | interleukin 8 | IL8,TM,SS | 3.4 |
| | 412978 | AA431708 | Hs.820 | homeo box C6 | homeobox,TM, | 3.4 |
| | 412851 | AI826502 | Hs.106149 | ESTs | TM,SS | 3.4 |
| | 414812 | X72755 | Hs.77367 | monokine induca | IL8,SS | 3.4 |
| 20 | 453884 | AA355925 | Hs.36232 | KIAA0186 gene p | TM | 3.4 |
| | 425921 | NM_007231 | Hs.162211 | solute carrier | SNF,TM, | 3.4 |
| | 421787 | AA227068 | Hs.108301 | nuclear recepto | TM | 3.3 |
| | 447342 | AI199268 | Hs.19322 | ESTs | TM,SS | 3.3 |
| | 452826 | BE245286 | Hs.301636 | ESTs, Moderatel | AAA,TM, | 3.3 |
| 25 | 414821 | M63835 | Hs.77424 | Fc fragment of | ig,TM,SS | 3.3 |
| | 448756 | AI739241 | Hs.171480 | ESTs | TM | 3.3 |
| | 421948 | L42583 | Hs.111758 | keratin 6A | filament,TM, | 3.3 |
| | 438538 | AA832203 | Hs.291955 | ESTs | TM | 3.3 |
| | 436391 | AJ227892 | Hs.146274 | ESTs | SS | 3.3 |
| 30 | 418007 | M13509 | Hs.83169 | matrix metallo | hemopexin,Peptidase_M10,SS | 3.2 |
| | 411678 | AF907114 | Hs.71465 | squalene epoxid | Monooxygenase,TM, | 3.2 |
| | 422956 | BE545072 | Hs.122579 | hypothetical pr | TM | 3.2 |
| | 450400 | AI694722 | Hs.279744 | ESTs | TM | 3.2 |
| | 440659 | AF134160 | Hs.7327 | claudin 1 | PMP22_Claudin,TM,SS | 3.2 |
| 35 | 418203 | X54942 | Hs.83758 | CDC28 protein k | CKS,TM, | 3.1 |
| | 416111 | AA033813 | Hs.79018 | chromatin assem | TM,SS | 3.1 |
| | 445808 | AV655234 | Hs.298083 | ESTs | sushi,TM,SS | 3.1 |
| | 421340 | F07783 | Hs.1369 | decay accelerat | sushi,SS | 3.1 |
| | 422689 | AW856665 | | gb:RC3-CT0297-2 | SNF2_N,TM, | 3.1 |
| 40 | 439451 | AF086270 | Hs.278554 | heterochromatin | chromo,Chromo_shadow,SS | 3.1 |
| | 454456 | AW850984 | | gb:IL3-CT0220-1 | fn3,TM,SS | 3.0 |
| | 429125 | AA446854 | Hs.271004 | ESTs | TM | 3.0 |
| | 409361 | NM_005982 | Hs.54416 | sine oculis hom | homeobox,SS | 3.0 |
| | 439453 | BE264974 | Hs.6566 | thyroid hormone | AAA,TM, | 3.0 |
| 45 | 414696 | AF002020 | Hs.76918 | Niemann-Pick di | Patched,TM,SS | 3.0 |
| | 422746 | NM_004484 | Hs.119651 | glypican 3 | Glypican,TM,SS | 3.0 |
| | 453775 | NM_002916 | Hs.35120 | replication fac | AAA,TM,SS | 3.0 |
| | 428862 | NM_000346 | Hs.2316 | SRY (sex-determ | HMG_box,TM, | 2.9 |
| | 401747 | | | | filament,TM, | 2.9 |
| 50 | 429682 | NM_006306 | Hs.211602 | SMC1 (structura | SMC_C,SMC_N,TM, | 2.9 |
| | 413385 | M34455 | Hs.840 | indoleamine-pyr | IDO,TM, | 2.9 |
| | 442961 | BE614474 | Hs.289074 | Homo sapiens cD | TM | 2.9 |
| | 421650 | AA781795 | Hs.122587 | ESTs | TM | 2.9 |
| | 434398 | AA121098 | Hs.3838 | serum-inducible | pkinese,POLO_box,TM, | 2.9 |
| 55 | 435706 | W31254 | Hs.7045 | GL004 protein | PDEase,TM, | 2.9 |
| | 416065 | BE267931 | Hs.78996 | proliferating c | TM | 2.9 |
| | 423493 | AI815965 | Hs.129683 | ubiquitin-conju | UQ_con,SS | 2.8 |
| | 430242 | U66669 | Hs.236642 | 3-hydroxyisobut | TM | 2.8 |
| | 411770 | NM_014278 | Hs.71992 | heat shock prot | HSP70,TM, | 2.8 |
| 60 | 400440 | X83957 | Hs.83870 | nebulin | TM | 2.8 |
| | 444743 | AA045648 | Hs.11817 | nudix (nucleosi | nuIT,TM, | 2.8 |
| | 417771 | AA804698 | Hs.82547 | retinoic acid r | TM | 2.8 |
| | 430287 | AW182459 | Hs.125759 | ESTs, Weakly si | TM,SS | 2.8 |
| | 408482 | NM_000676 | Hs.45743 | adenosine A2b r | 7tm_1,TM,SS | 2.8 |
| 65 | 425188 | AK002052 | Hs.155071 | hypothetical pr | TM | 2.8 |
| | 456999 | AA319798 | Hs.172247 | eukaryotic tran | SS | 2.8 |
| | 408875 | NM_015434 | Hs.48604 | DKFZP434B168 pr | TM | 2.8 |
| | 409012 | AL117435 | Hs.49725 | DKFZP434I216 pr | RhoGEF,TM, | 2.7 |
| | 410762 | AF226053 | Hs.66170 | HSKM-B protein | zf-MYND,SS | 2.7 |
| 70 | 426925 | NM_001196 | Hs.172894 | BH3 interacting | TM | 2.7 |
| | 410116 | AW630671 | Hs.58636 | squamous cell c | TM,SS | 2.7 |
| | 428398 | AI249368 | Hs.98558 | ESTs | SS | 2.7 |
| | 412140 | AA219691 | Hs.73625 | RAB6 interactin | kinesin,TM,SS | 2.7 |
| | 456655 | AI376736 | Hs.111779 | secreted protei | kazal,SS | 2.7 |
| 75 | 408670 | AF160967 | Hs.46784 | potassium large | TM,SS | 2.7 |
| | 422576 | BE548555 | Hs.118554 | CGI-83 protein | lactamase_B,SS | 2.7 |
| | 431379 | AA504264 | Hs.182937 | peptidylprolyl | TM | 2.7 |
| | 433183 | AF231338 | Hs.222024 | transcription f | HLH,PAS,TM,SS | 2.7 |
| | 432328 | AI572739 | Hs.195471 | 6-phosphofructo | PGAM,6PF2K,TM, | 2.7 |
| 80 | 407633 | NM_007069 | Hs.37189 | similar to rat | TM,SS | 2.6 |
| | 419216 | AU076718 | Hs.164021 | small inducible | IL8,TM,SS | 2.6 |
| | 422363 | T55979 | Hs.115474 | replication fac | TM | 2.6 |
| | 401644 | | | | zf-C2H2,TM, | 2.6 |
| | 417479 | AI057052 | Hs.133554 | ESTs | CARD,TM, | 2.6 |

| | | | | | | |
|----|--------|-----------|-----------|-----------------|----------------------------------|-----|
| | 426514 | BE616633 | Hs.301122 | bone morphogene | TGF-beta,TGFb_propeptide,TM,SS | 2.6 |
| | 400289 | X07820 | Hs.2258 | matrix metallo | hemopexin,,SS | 2.6 |
| | 418478 | U38945 | Hs.1174 | cyclin-dependen | ank,TM,SS | 2.6 |
| 5 | 421246 | AW582962 | Hs.300961 | ESTs, Highly si | PolyA_pol,TM, | 2.6 |
| | 428048 | AA705745 | Hs.185070 | ESTs | AMP-binding,TM, | 2.6 |
| | 452092 | BE245374 | Hs.27842 | hypothetical pr | Acyltransferase,TM,SS | 2.6 |
| | 440052 | AI633744 | Hs.195648 | ESTs | PAC,TM,SS | 2.6 |
| | 452401 | NM_007115 | Hs.29352 | tumor necrosis | Xlink,CUB,TM,SS | 2.6 |
| 10 | 451813 | NM_016117 | Hs.27182 | phospholipase A | WD40,,SS | 2.6 |
| | 410889 | X91662 | Hs.66744 | twist (Drosophi | HLH,TM, | 2.6 |
| | 422063 | BE156476 | | gb:QV0-HT0368-0 | SS | 2.6 |
| | 418250 | U29926 | Hs.83918 | adenosine monop | A_deaminase,TM, | 2.6 |
| | 437641 | AA811452 | Hs.291911 | ESTs | TM | 2.6 |
| 15 | 452571 | W31518 | Hs.34665 | ESTs | TM | 2.6 |
| | 411984 | NM_005419 | Hs.72988 | signal transduc | SH2,STAT,,SS | 2.6 |
| | 426427 | M86699 | Hs.169840 | TTK protein kin | ptkinase,TM, | 2.6 |
| | 445848 | AA774824 | Hs.13377 | Homo sapiens cl | TM | 2.6 |
| | 420022 | AA256253 | Hs.120817 | ESTs | SS | 2.6 |
| 20 | 451418 | BE387790 | Hs.26369 | hypothetical pr | TM | 2.6 |
| | 428953 | AA306610 | Hs.194676 | DKFZP434C013 pr | arf,TNFR_c6,DEAD,Statmin,TM,SS | 2.6 |
| | 424008 | R02740 | Hs.137555 | putative chemok | 7tm_1,TM, | 2.6 |
| | 417863 | AB000450 | Hs.82771 | vaccinia relate | ptkinase,TM,SS | 2.6 |
| | 436961 | AW375974 | Hs.156704 | ESTs | TM | 2.6 |
| 25 | 413670 | AB000115 | Hs.75470 | hypothetical pr | TM | 2.5 |
| | 421928 | AF013758 | Hs.109643 | polyadenylate b | SS | 2.5 |
| | 439963 | AW247529 | Hs.6793 | platelet-activa | PAF-AH,HMG_box,ptkinase,TM, | 2.5 |
| | 426711 | AA383471 | Hs.180669 | conserved gene | TM | 2.5 |
| | 422631 | BE218919 | Hs.118793 | hypothetical pr | TM | 2.5 |
| 30 | 417866 | AW067903 | Hs.82772 | collagen, type | TSPN,Collagen,COLFI,,SS | 2.5 |
| | 416975 | NM_004131 | Hs.1051 | granzyme B (gra | trypsin,,SS | 2.5 |
| | 415947 | U04045 | Hs.78934 | mutS (E. coli) | MutS_C,MutS_N,TM, | 2.5 |
| | 454678 | AW813089 | | gb:RC3-ST0186-2 | TPR,Ribosomal_SS,TM,SS | 2.5 |
| 35 | 426572 | AB037783 | Hs.170623 | hypothetical pr | PH,FYVE,TM, | 2.5 |
| | 428264 | AA424839 | Hs.98484 | ESTs, Weakly si | TM | 2.5 |
| | 444478 | W07318 | Hs.240 | M-phase phospho | kinesin,,SS | 2.5 |
| | 442295 | AI827248 | Hs.224398 | Homo sapiens cD | Collagen,COLFI,vwc,TM,SS | 2.5 |
| | 410094 | BE147897 | Hs.58593 | general transcr | TFIIF_beta,TM, | 2.5 |
| | 413998 | AW103807 | Hs.243933 | ESTs | TPR,TM,SS | 2.4 |
| 40 | 412281 | AI810054 | Hs.14119 | ESTs | Ribosomal_S7e,TM, | 2.4 |
| | 446852 | AW451643 | Hs.257479 | ESTs, Weakly si | TM | 2.4 |
| | 408915 | NM_016651 | Hs.48950 | heptacellular c | TM,SS | 2.4 |
| | 442991 | BE281238 | Hs.8886 | hypothetical pr | TM | 2.4 |
| | 410193 | AJ132592 | Hs.59757 | zinc finger pro | zf-C2H2,TM, | 2.4 |
| 45 | 410664 | NM_006033 | Hs.65370 | lipase, endothe | Ribosomal_L22,lipase,PLAT,TM,SS | 2.4 |
| | 423453 | AW450737 | Hs.128791 | CGI-09 protein | Granin,COP-OH_P_transf,TM, | 2.4 |
| | 411598 | BE336654 | Hs.70937 | H3 histone fami | histone,,SS | 2.4 |
| | 429663 | M68874 | Hs.211587 | phospholipase A | C2,PLA2_B,TM, | 2.4 |
| | 428242 | H55709 | Hs.2250 | leukemia inhibi | LIF_OSM,,SS | 2.4 |
| 50 | 419559 | Y07828 | Hs.91096 | ring finger pro | zf-C3HC4,zf-B_box,TM, | 2.4 |
| | 419839 | U24577 | Hs.93304 | phospholipase A | SS | 2.4 |
| | 402819 | | | | IBR,TM, | 2.4 |
| | 431457 | NM_012211 | Hs.256297 | integrin, alpha | FG-GAP,vwa,TM,SS | 2.4 |
| 55 | 443683 | BE241717 | Hs.9676 | uncharacterized | DUF157,TM, | 2.4 |
| | 422158 | L10343 | Hs.112341 | protease inhibi | wap,,SS | 2.4 |
| | 423217 | NM_000094 | Hs.1640 | collagen, type | fn3,Collagen,Kunitz_BPTI,vwa,,SS | 2.4 |
| | 408321 | AW405882 | Hs.44205 | coristatin | TM | 2.4 |
| | 419086 | NM_000216 | Hs.89591 | Kallmann syndro | fn3,wap,,SS | 2.4 |
| | 427722 | AK000123 | Hs.180479 | hypothetical pr | PH,,SS | 2.4 |
| 60 | 405454 | | | | TM | 2.4 |
| | 422168 | AA586894 | Hs.112408 | S100 calcium-bi | efhand,TM, | 2.4 |
| | 421462 | AF016495 | Hs.104624 | aquaporin 9 | MIP,TM, | 2.3 |
| | 403416 | AI744626 | Hs.301506 | ESTs, Highly si | SS | 2.3 |
| 65 | 448988 | Y09763 | Hs.22785 | gamma-aminobuty | neur_chan,TM,SS | 2.3 |
| | 423198 | M81933 | Hs.1634 | cell division c | Rhodanese,,SS | 2.3 |
| | 419926 | AW900992 | Hs.93796 | DKFZP586D2223 p | SS | 2.3 |
| | 429992 | AL050053 | Hs.227397 | Homo sapiens mR | fn3,TM,SS | 2.3 |
| | 446232 | AI281848 | Hs.165547 | ESTs | 7tm_3,TM, | 2.3 |
| | 422493 | AW474183 | Hs.233816 | ESTs | TM | 2.3 |
| 70 | 407047 | X65965 | | gb:H.sapiens SO | sodfe,TM, | 2.3 |
| | 411096 | U80034 | Hs.68583 | mitochondrial i | Peptidase_M3,, | 2.3 |
| | 426457 | AW894667 | Hs.169965 | chimerin (chima | DAG_PE-bind,RhoGAP,TM, | 2.3 |
| | 446545 | AI431798 | Hs.164192 | ESTs, Weakly si | TM | 2.3 |
| | 422094 | AF129535 | Hs.272027 | F-box only prot | TM | 2.3 |
| 75 | 421933 | R98881 | Hs.109655 | sex comb on mid | SAM,TM, | 2.3 |
| | 430001 | AI580056 | Hs.98992 | ESTs | TM | 2.3 |
| | 420802 | U22376 | Hs.1334 | v-myb avian mye | TM | 2.3 |
| | 402053 | | | | gpdh,,SS | 2.3 |
| 80 | 432743 | AI146966 | Hs.101656 | ESTs | SS | 2.3 |
| | 433409 | AI278802 | Hs.25661 | ESTs | PWWP,PHD,bromodomain,TM, | 2.3 |
| | 408330 | AW182602 | Hs.249954 | ESTs | TM,SS | 2.3 |
| | 407807 | AL031427 | Hs.40094 | Human DNA seque | T4_deiodinase,TM, | 2.3 |
| | 436972 | AA284679 | Hs.25640 | claudin 3 | PMP22_Claudin,TM,SS | 2.3 |
| | 433730 | AK002135 | Hs.3542 | hypothetical pr | TM,SS | 2.3 |

| | | | | | | |
|----|--------|-----------|-----------|------------------|--|-----|
| 5 | 414839 | X63692 | Hs.77462 | DNA (cytosine-5 | zf-CXXC,BAH,TM,SS | 2.3 |
| | 438192 | AJ859065 | Hs.16808 | ESTs, Weakly si | TM,SS | 2.3 |
| | 415339 | NM_015156 | Hs.78398 | KJAA0071 protei | ELM2,TM, | 2.3 |
| | 449539 | W80363 | Hs.58446 | ESTs | kinase,Furin-like,Recep_L_domain,TM,SS | 2.2 |
| | 450956 | AW193531 | Hs.205647 | ESTs, Moderatel | kinase,TM,SS | 2.2 |
| | 430335 | D60007 | Hs.239499 | KJAA0185 protei | S1,TM, | 2.2 |
| | 417849 | AW291587 | Hs.82733 | nidogen 2 | EGF,Idl_recept_b,thyroglobulin_1,TM,SS | 2.2 |
| | 412326 | R07566 | Hs.73817 | small inducible | IL8,SS | 2.2 |
| 10 | 408349 | BE546947 | Hs.44276 | homeo box C10 | homeobox,TM, | 2.2 |
| | 424704 | AI263293 | Hs.152096 | cytochrome P450 | p450,SS | 2.2 |
| | 409632 | W74001 | Hs.55279 | serine (or cyst | serpin,TM, | 2.2 |
| | 415323 | BE269352 | Hs.949 | neutrophil cyto | SH3,TPR,TM, | 2.2 |
| | 417531 | NM_003157 | Hs.1087 | serine/threonin | kinase,TM, | 2.2 |
| | 403137 | | | | rm,TM,SS | 2.2 |
| 15 | 428479 | Y00272 | Hs.184572 | cell division c | kinase,TM,SS | 2.2 |
| | 430200 | BE613337 | Hs.234896 | geminin | TM,SS | 2.2 |
| | 425390 | AI092634 | Hs.156114 | protein tyrosin | ig.Opioids_neuropep,TM,SS | 2.2 |
| | 408380 | AF123050 | Hs.44532 | diubiquitin | ubiquitin,7tm_3,ANF_receptor,sushi,7tm_1,TM, | 2.2 |
| | 422424 | AI186431 | Hs.116577 | prostate differ | TGF-beta,SS | 2.2 |
| 20 | 400298 | AA032279 | Hs.61635 | six transmembra | TM | 2.2 |
| | 411571 | AA122393 | Hs.70811 | hypothetical pr | SS | 2.2 |
| | 412802 | U41518 | Hs.74602 | aquaporin 1 (ch | MIP,TM, | 2.2 |
| | 414761 | AU077228 | Hs.77256 | enhancer of zes | SET,TM, | 2.2 |
| | 408432 | AW195262 | | gb:xn67b05.x1 N | TM,SS | 2.2 |
| 25 | 429558 | AI088691 | Hs.208414 | Homo sapiens mR | mito_carr,TM, | 2.2 |
| | 425300 | AW601773 | Hs.270259 | ESTs | TM | 2.2 |
| | 439653 | AW021103 | Hs.6631 | hypothetical pr | TM,SS | 2.2 |
| | 426827 | AW067805 | Hs.172655 | methylene tetrah | THF_DHG_CYH,FTHFS,TM, | 2.2 |
| 30 | 444514 | AI682905 | Hs.270431 | ESTs, Weakly si | cnMP_binding,TM,SS | 2.2 |
| | 425322 | U63630 | Hs.155637 | protein kinase, | MCM,TM, | 2.2 |
| | 421662 | NM_014141 | Hs.106552 | cell recognitio | laminin_G,TM,SS | 2.2 |
| | 438788 | AA825716 | | gb:od29e10.s1 N | ank,death,RHD,TM, | 2.2 |
| | 429058 | AF138863 | Hs.194827 | hypothetical pr | TM | 2.2 |
| 35 | 423104 | AJ005273 | Hs.123647 | antigenic deter | TM | 2.2 |
| | 410406 | AJ969703 | Hs.301842 | ESTs | FGGY,TM, | 2.2 |
| | 421379 | Y15221 | Hs.103982 | small inducible | IL8,TM,SS | 2.2 |
| | 422809 | AK001379 | Hs.121028 | hypothetical pr | IQ,TM, | 2.2 |
| | 418049 | AA211467 | Hs.190488 | hypothetical pr | TM | 2.2 |
| 40 | 436209 | AW850417 | Hs.254020 | ESTs, Moderatel | TM,SS | 2.2 |
| | 408042 | AL049233 | Hs.42244 | Homo sapiens mR | TM | 2.2 |
| | 425692 | D90041 | Hs.155956 | N-acetyltransfe | Acetyltransf2,TM, | 2.2 |
| | 409665 | NM_006731 | Hs.55777 | Fukuyama type c | SS | 2.2 |
| | 428157 | AJ738719 | Hs.298668 | ESTs | hexokinase,TM, | 2.2 |
| 45 | 410480 | R97457 | Hs.63984 | cadherin 13, H- | cadherin,TM,SS | 2.2 |
| | 429732 | U20158 | Hs.2488 | lymphocyte cyto | SH2,TM, | 2.2 |
| | 414747 | U30872 | Hs.77204 | centromere prot | SS | 2.2 |
| | 425843 | BE313280 | Hs.159627 | death associate | TM | 2.2 |
| | 445299 | AI910382 | Hs.118727 | Homo sapiens cD | HLH,TM, | 2.1 |
| | 436251 | BE515065 | Hs.5092 | nucleolar prote | Nop,TM,SS | 2.1 |
| 50 | 430066 | AI929659 | Hs.237825 | signal recognit | TPR,SS | 2.1 |
| | 427528 | AU077143 | Hs.179565 | minichromosome | MCM,TM,SS | 2.1 |
| | 448089 | AI467945 | Hs.173696 | ESTs | TM,SS | 2.1 |
| | 428728 | NM_016625 | Hs.191381 | hypothetical pr | TM | 2.1 |
| | 409929 | R38772 | Hs.172619 | KJAA1106 protei | TM | 2.1 |
| 55 | 405264 | | | | SS | 2.1 |
| | 445625 | BE246743 | Hs.288529 | Homo sapiens cD | TM | 2.1 |
| | 408949 | AF189011 | Hs.49163 | putative ribonu | Ribonuclease_3,TM,SS | 2.1 |
| | 424513 | BE385864 | Hs.149894 | mitochondrial t | GTP_EFTU,IF2,TM, | 2.1 |
| 60 | 433683 | AI817723 | Hs.22678 | hypothetical pr | SS | 2.1 |
| | 442952 | AI743261 | Hs.131860 | ESTs | TM | 2.1 |
| | 432378 | AI493046 | Hs.146133 | ESTs | TM | 2.1 |
| | 417979 | AU077284 | Hs.83081 | GTP cyclohydrol | TM,SS | 2.1 |
| | 433849 | BE465884 | Hs.280728 | ESTs | SS | 2.1 |
| 65 | 437928 | NM_005476 | Hs.5920 | UDP-N-acetylglu | ROK,Epimerase_2,TM, | 2.1 |
| | 403055 | | | | filament,TM,SS | 2.1 |
| | 432840 | AK001403 | Hs.279521 | hypothetical pr | TM | 2.1 |
| | 418994 | AA296520 | Hs.89546 | selectin E (end | EGF,lectin_c,sushi,TM,SS | 2.1 |
| | 440908 | AI915225 | Hs.126735 | ESTs | TM | 2.1 |
| 70 | 417621 | AV654694 | Hs.82316 | interferon-indu | TM | 2.1 |
| | 436895 | AF037335 | Hs.5338 | carbonic anhydr | carb_anhydrase,TM,SS | 2.1 |
| | 408420 | NM_006915 | Hs.299481 | Homo sapiens mR | TM | 2.1 |
| | 434064 | AL049045 | Hs.180758 | hypothetical pr | cadherin,TM,SS | 2.1 |
| | 404076 | | | | RmaAD,TM, | 2.1 |
| 75 | 422515 | AW500470 | Hs.117950 | multifunctional | AIRC,SAICAR_synt,TM, | 2.1 |
| | 445867 | AF272663 | Hs.13405 | gephyrin | MoCF_biosynth,TM, | 2.1 |
| | 441021 | AW578716 | Hs.7644 | H1 histone fami | linker_histone,TM, | 2.1 |
| | 446595 | T57448 | Hs.15467 | hypothetical pr | TM,SS | 2.1 |
| | 417515 | L24203 | Hs.82237 | ataxia-telangie | zf-B_box,SS | 2.1 |
| 80 | 412429 | AV650262 | Hs.75765 | GRO2 oncogene | IL8,TM,SS | 2.1 |
| | 449207 | AL044222 | Hs.23255 | nucleoporin 155 | TM,SS | 2.1 |
| | 412095 | AI624707 | Hs.5921 | Homo sapiens cD | TM,SS | 2.1 |
| | 400861 | | | | kinase,TM, | 2.1 |
| | 440591 | AA431599 | Hs.132799 | Homo sapiens cD | TM | 2.1 |

| | | | | | |
|--------|-----------|-----------|-------------------|------------------------------------|-----|
| 442104 | L20971 | Hs.188 | phosphodiesterase | PDEase,TM, | 2.1 |
| 446921 | AB012113 | Hs.16530 | small inducible | IL8,SS | 2.1 |
| 446051 | BE048061 | Hs.153315 | ESTs | Reprolysin,Pep_M12B_propep,TM,SS | 2.1 |
| 422675 | BE018517 | Hs.119140 | eukaryotic tran | elfF-5a,TM, | 2.1 |
| 425170 | AU077315 | Hs.154970 | transcription f | TM | 2.1 |
| 453751 | R36762 | Hs.101282 | Homo sapiens mR | TM | 2.1 |
| 426283 | NM_003937 | Hs.169139 | kyureninase (L | TM | 2.1 |
| 417874 | BE516160 | Hs.82829 | protein tyrosin | Y_phosphatase,TM, | 2.1 |
| 449555 | AW450288 | Hs.195390 | ESTs | TM | 2.1 |
| 439699 | AF086534 | Hs.187561 | ESTs, Moderate | TM | 2.1 |
| 427413 | BE547647 | Hs.177781 | superoxide dism | sodie,TM, | 2.1 |
| 407802 | D84145 | Hs.39913 | novel RGD-conta | hexapep,TM,SS | 2.0 |
| 446035 | NM_006558 | Hs.13565 | Sam68-like phos | TM | 2.0 |
| 406981 | S71129 | Hs.296844 | Acetylcholinest | COesterase,TM,SS | 2.0 |
| 432343 | NM_002960 | Hs.2961 | S100 calcium-bi | S_100,efhand,TM,SS | 2.0 |
| 414890 | BE281095 | Hs.77573 | uridine phospho | PNP_UDP_1,TM,SS | 2.0 |
| 423019 | AI640185 | Hs.225816 | ESTs | SS | 2.0 |
| 422278 | AF072873 | Hs.114218 | fizzled (Droso | Fz,Fizzled,TM,SS | 2.0 |
| 405545 | | | | ABC_tran,ABC_membrane,TM,SS | 2.0 |
| 446237 | AW270515 | Hs.149596 | ESTs | bZIP,TM, | 2.0 |
| 428074 | BE387770 | Hs.182378 | colony stimulat | SS | 2.0 |
| 423430 | AF112481 | Hs.128501 | RAD54, S. cerev | SNF2_N,helicase_C,TM, | 2.0 |
| 435767 | H73505 | Hs.117874 | ESTs | Peptidase_S8,P,TM, | 2.0 |
| 432945 | AL043683 | Hs.271357 | ESTs, Weakly si | PK_SS | 2.0 |
| 404170 | | | | sodie,TM, | 2.0 |
| 422610 | AF153820 | Hs.1547 | potassium inwar | IRK,TM, | 2.0 |
| 417933 | X02308 | Hs.82962 | thymidylate syn | thymidylat_synt,SS | 2.0 |
| 441384 | AA447849 | Hs.288660 | protease, serin | TM | 2.0 |
| 414020 | NM_002984 | Hs.75703 | small inducible | IL8,SS | 2.0 |
| 427674 | NM_003528 | Hs.2178 | H2B histone fam | histone,TM,SS | 2.0 |
| 435425 | H16263 | Hs.31416 | ESTs | TM | 2.0 |
| 429782 | NM_005754 | Hs.220689 | Ras-GTPase-acti | rm,NTF2,SS | 2.0 |
| 417366 | BE185289 | Hs.1076 | small proline-r | Corinfin,TM, | 2.0 |
| 426746 | J03626 | Hs.2057 | uridine monopho | Pribosyltran,OMPdecase,TM, | 2.0 |
| 432677 | NM_004482 | Hs.278611 | UDP-N-acetyl-al | Glycos_transf_2,Ricin_B_lectin,TM, | 2.0 |

TABLE 43B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

| Pkey | CAT number | Accession |
|--------|------------|---|
| 408432 | 1058667_1 | AW195262 R27868 AW811262 |
| 411560 | 1249443_1 | AW851186 AW996967 BE143456 |
| 422063 | 210852_1 | BE156476 BE156473 BE156474 BE156475 AA302839 |
| 422285 | 214669_1 | AI803103 AI885143 AW470793 AW450703 AI090784 AW271587 AW236950 AW242783 |
| 422689 | 219896_1 | AW856665 AA315006 AW954733 |
| 423871 | 232749_1 | AA331906 AA332484 |
| 438788 | 465159_1 | AA825716 AW978859 AA828841 |
| 454456 | 1207088_1 | AW850984 AW752836 M86124 |
| 454678 | 1228915_1 | AW813089 W28102 |

TABLE 43C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

| Pkey | Ref | Strand | NL_position |
|--------|---------|--------|---|
| 400861 | 9757506 | Plus | 163855-164016 |
| 401644 | 8576138 | Plus | 82655-83959 |
| 401747 | 9789672 | Minus | 118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011 |
| 402053 | 8083229 | Plus | 62703-63179 |
| 402819 | 6729581 | Plus | 29217-29422 |
| 403055 | 8748904 | Minus | 109532-110225 |
| 403137 | 9211494 | Minus | 92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337 |
| 403776 | 7770611 | Minus | 1414-1513,1624-1756 |
| 404076 | 9931752 | Minus | 3848-3967 |
| 404170 | 9930793 | Plus | 168836-169248 |
| 405264 | 7329374 | Plus | 28556-28684 |
| 405454 | 7656675 | Plus | 133807-134053 |
| 405545 | 1054740 | Plus | 118677-118807,119091-119296,121626-121823 |
| 406434 | 9256651 | Minus | 17803-17931 |

TABLE 44A: ABOUT 314 GENES DOWN-REGULATED IN STOMACH CANCER

Table 44A lists about 314 genes significantly down-regulated in stomach cancer compared to normal stomach. These were selected as for Table 42A, except that the numerator and denominator were switched.

Pkey: Unique Eos probeset identifier number
 ExAccon: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number

| Unigene Title: R1: | | Unigene gene title Ratio of tumor to normal tissue | | |
|-----------------------|--------|---|-----------|---|
| | Pkey | ExAccn | UnigeneID | Unigene Title |
| 5 | 412859 | NM_000705 | Hs.813 | ATPase, H ⁺ /K ⁺ exchanging, beta polypepti |
| | 415447 | Z97171 | Hs.78454 | myocilin, trabecular meshwork inducible |
| | 427469 | AA403084 | Hs.269347 | ESTs |
| | 407486 | S69741 | | gb:hSCG-3=stomach cancer gene-3 (oncogen |
| | 428602 | AL137479 | Hs.186655 | Homo sapiens mRNA; cDNA DKFZp434M0223 (f |
| 10 | 402761 | BE387621 | Hs.108809 | chaperonin containing TCP1, subunit 7 (e |
| | 443547 | AW271273 | Hs.23767 | Homo sapiens cDNA FLJ12666 fis, clone NT |
| | 430130 | AL137311 | Hs.234074 | Homo sapiens mRNA; cDNA DKFZp761G02121 (|
| | 435473 | N53550 | Hs.260881 | ESTs |
| | 455826 | BE144228 | | gb:MR0-HT0165-140200-009-d04 HT0165 Homo |
| 15 | 402015 | | | ESTs |
| | 430664 | AW969834 | | gb:EST381912 MAGE resequences, MAGK Homo |
| | 444515 | AW204908 | Hs.169979 | ESTs |
| | 429201 | X03178 | Hs.198246 | group-specific component (vitamin D bind |
| | 434424 | AI811202 | Hs.125365 | Homo sapiens cDNA: FLJ23523 fis, clone L |
| 20 | 450940 | AI744943 | Hs.300744 | ESTs, Moderately similar to ALU7_HUMAN A |
| | 400811 | AF219139 | Hs.87726 | KIAA0154 protein; ADP-ribosylation facto |
| | 424596 | AB020639 | Hs.151017 | estrogen-related receptor gamma |
| | 403670 | | | ESTs |
| | 410234 | NM_003837 | Hs.61255 | fructose-1,6-bisphosphatase 2 |
| 25 | 407462 | AJ252011 | | gb:Homo sapiens partial mRNA for amilor |
| | 405110 | | | ESTs |
| | 402760 | | | ESTs |
| | 408947 | AL080093 | Hs.49117 | Homo sapiens mRNA; cDNA DKFZp564N1662 (f |
| | 413724 | AA131466 | Hs.23767 | Homo sapiens cDNA FLJ12666 fis, clone NT |
| 30 | 431514 | AW972363 | | gb:EST384454 MAGE resequences, MAGL Homo |
| | 451103 | R52804 | Hs.25956 | DKFZP564D206 protein |
| | 452033 | AW273741 | Hs.246977 | ESTs |
| | 440058 | AJ932662 | Hs.164073 | ESTs |
| | 405645 | | | ESTs |
| 35 | 429093 | NM_000253 | Hs.195799 | microsomal triglyceride transfer protein |
| | 445627 | AW818475 | Hs.7363 | ESTs |
| | 425679 | X05997 | Hs.159177 | lipase, gastric |
| | 417296 | L36196 | Hs.81884 | sulfotransferase family, cytosolic, 2A, |
| | 443537 | D13305 | Hs.203 | cholecystokinin B receptor |
| 40 | 435654 | AW139612 | Hs.131041 | ESTs |
| | 406326 | | | ESTs |
| | 454120 | AB032990 | Hs.40719 | hypothetical protein KIAA1164 |
| | 455541 | AW993005 | | gb:RC2-BN0032-160200-013-d04 BN0032 Homo |
| | 453989 | M63962 | Hs.36992 | ATPase, H ⁺ /K ⁺ exchanging, alpha polypept |
| 45 | 407261 | L03172 | | gb:Homo sapiens cell-type T-cell immunog |
| | 451062 | AL110125 | Hs.25910 | Homo sapiens mRNA; cDNA DKFZp564C1416 (f |
| | 429350 | AJ754634 | Hs.131987 | ESTs |
| | 411021 | F00055 | Hs.172004 | titin |
| | 441212 | AW242447 | Hs.146182 | ESTs, Weakly similar to lactase phlorizi |
| 50 | 450572 | AJ700863 | Hs.202494 | Homo sapiens cDNA FLJ13245 fis, clone OV |
| | 444922 | AJ921750 | Hs.144871 | Homo sapiens cDNA FLJ13752 fis, clone PL |
| | 421562 | AA530994 | Hs.105803 | ghrelin precursor |
| | 457432 | NM_005136 | Hs.268538 | potassium voltage-gated channel, Isk-rel |
| | 418421 | R58620 | Hs.85050 | phospholamban |
| 55 | 424104 | AA669515 | Hs.144950 | ESTs |
| | 422582 | AA312660 | | gb:EST183335 Jurkat T-cells VI Homo sapi |
| | 417332 | AW972717 | Hs.288462 | Homo sapiens cDNA: FLJ21511 fis, clone C |
| | 432440 | X63597 | Hs.2996 | sucrase-isomaltase |
| | 448520 | AB002367 | Hs.21355 | doublecortin and CaM kinase-like 1 |
| 60 | 401989 | | | ESTs |
| | 452528 | AA742457 | Hs.291479 | ESTs |
| | 412569 | H63789 | Hs.296288 | ESTs, Weakly similar to KIAA0638 protein |
| | 434779 | AF153815 | Hs.50151 | potassium inwardly-rectifying channel, s |
| | 406255 | | | ESTs |
| 65 | 419293 | AA746282 | Hs.255659 | ESTs |
| | 428649 | AL045716 | Hs.188228 | Homo sapiens cDNA FLJ11003 fis, clone PL |
| | 410036 | R57171 | Hs.57975 | calsequestrin 2, cardiac muscle |
| | 414502 | AL133721 | Hs.224680 | ESTs |
| | 432113 | AA935065 | Hs.152385 | ESTs |
| 70 | 413808 | J00287 | Hs.182183 | caldesmon 1 |
| | 451406 | AJ694320 | Hs.6295 | ESTs, Weakly similar to T17248 hypotheti |
| | 434745 | AW974445 | Hs.185155 | ESTs, Weakly similar to HuEMAP [H.sapien |
| | 420444 | AJ905985 | Hs.111805 | ESTs |
| | 445200 | AA084460 | Hs.12409 | somatostatin |
| 75 | 415314 | N88802 | Hs.5422 | glycoprotein M6B |
| | 427019 | AA001732 | Hs.173233 | hypothetical protein FLJ10970 |
| | 431152 | AW970998 | | gb:EST383083 MAGE resequences, MAGK Homo |
| | 432306 | Y18207 | Hs.274315 | protein phosphatase 1, regulatory (inhib |
| | 401775 | | | ESTs |
| 80 | 440059 | AW467335 | Hs.257676 | ESTs |
| | 436089 | AA804957 | Hs.119840 | ESTs |
| | 447071 | AW236867 | Hs.244376 | ESTs |
| | 435604 | AA625279 | Hs.26892 | uncharacterized bone marrow protein BM04 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| 5 | 423968 | AF098277 | Hs.136529 | solute carrier family 23 (nucleobase tra | 0.32 |
| | 445487 | AI806287 | Hs.201217 | ESTs | 0.32 |
| | 421296 | NM_002666 | Hs.103253 | perilipin | 0.32 |
| | 427138 | N77624 | Hs.173717 | phosphatidic acid phosphatase type 2B | 0.33 |
| | 449916 | T60525 | Hs.299221 | ESTs | 0.33 |
| 10 | 446393 | AW014174 | Hs.151707 | ESTs | 0.33 |
| | 446632 | AI333565 | Hs.159073 | diacylglycerol kinase, eta | 0.33 |
| | 428070 | T63918 | Hs.182313 | retinol-binding protein 2, cellular | 0.33 |
| | 421451 | AA291377 | Hs.50831 | ESTs | 0.33 |
| | 405817 | | | | 0.33 |
| 15 | 454790 | AW820852 | | gb:RC2-ST0301-120200-011-f12 ST0301 Homo | 0.33 |
| | 413679 | BE156765 | | gb:RC1-HT0370-120100-012-c09 HT0370 Homo | 0.34 |
| | 404121 | | | | 0.34 |
| | 433084 | M18079 | Hs.282265 | fatty acid binding protein 2, intestinal | 0.34 |
| | 413079 | BE064382 | | gb:RC4-BT0310-110300-015-c12 BT0310 Homo | 0.34 |
| 20 | 403059 | | | | 0.35 |
| | 458987 | AW750067 | Hs.205386 | ESTs | 0.35 |
| | 429609 | AF002246 | Hs.210863 | cell adhesion molecule with homology to | 0.35 |
| | 423371 | AU076819 | Hs.1650 | solute carrier family 26, member 3 | 0.35 |
| | 424765 | AA428211 | Hs.284256 | hypothetical protein FLJ14033 similar to | 0.35 |
| 25 | 451818 | AI819018 | | gb:ts54f01.x1 NCI_CGAP_Kd8 Homo sapiens | 0.35 |
| | 438380 | T06430 | Hs.6194 | chondroitin sulfate proteoglycan BEHAB/b | 0.35 |
| | 405742 | | | | 0.35 |
| | 403429 | | | | 0.35 |
| | 443622 | AI911527 | Hs.11805 | ESTs | 0.36 |
| 30 | 404973 | | | | 0.36 |
| | 444567 | AV654020 | Hs.184261 | ESTs, Weakly similar to putative type II | 0.36 |
| | 412228 | AW503785 | Hs.73792 | complement component (3d/Epstein Barr vi | 0.36 |
| | 407110 | AA018042 | Hs.95078 | ESTs | 0.36 |
| | 411671 | BE049094 | Hs.278567 | ESTs | 0.36 |
| 35 | 430800 | NM_000805 | Hs.2681 | gastrin | 0.36 |
| | 454560 | AW807281 | | gb:MR4-ST0062-240300-003-g01 ST0062 Homo | 0.36 |
| | 444536 | AI161068 | Hs.14780 | ESTs | 0.36 |
| | 454042 | H22570 | Hs.172572 | hypothetical protein FLJ20093 | 0.37 |
| | 444102 | AV647953 | Hs.282379 | ESTs | 0.37 |
| 40 | 424122 | AA335593 | Hs.116147 | ESTs | 0.37 |
| | 452093 | AA447453 | Hs.27860 | Homo sapiens mRNA; cDNA DKFZp586M0723 (f | 0.37 |
| | 436277 | R88520 | Hs.120917 | ESTs | 0.37 |
| | 456350 | BE246762 | Hs.89499 | arachidonate 5-lipoxygenase | 0.37 |
| | 451027 | AW519204 | Hs.40808 | ESTs | 0.37 |
| 45 | 426784 | U03749 | Hs.172216 | chromogranin A (parathyroid secretory pr | 0.38 |
| | 410023 | AB017169 | Hs.57929 | silt (Drosophila) homolog 3 | 0.38 |
| | 436802 | N34486 | Hs.170504 | ESTs | 0.38 |
| | 448142 | AI521768 | Hs.164586 | ESTs | 0.38 |
| | 442378 | R54033 | Hs.21245 | ESTs | 0.38 |
| 50 | 446406 | AI553681 | Hs.25248 | ESTs | 0.38 |
| | 455753 | BE075124 | | gb:PM1-BT0585-110200-003-h02 BT0585 Homo | 0.38 |
| | 424903 | T26477 | Hs.22883 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 0.38 |
| | 406714 | AI219304 | Hs.283108 | hemoglobin, gamma G | 0.39 |
| | 434340 | AI193043 | Hs.128685 | ESTs | 0.39 |
| 55 | 406036 | | | | 0.39 |
| | 431078 | U82827 | Hs.249195 | homeo box A13 | 0.39 |
| | 457663 | AW371946 | Hs.116119 | ESTs | 0.39 |
| | 451880 | AI821032 | Hs.209387 | ESTs | 0.39 |
| | 419219 | AW583139 | Hs.89717 | carboxypeptidase A2 (pancreatic) | 0.39 |
| 60 | 446414 | W93246 | Hs.59187 | ESTs | 0.39 |
| | 442317 | AI915599 | Hs.129225 | ESTs | 0.39 |
| | 447261 | NM_006691 | Hs.17917 | lymphatic vessel endothelial hyaluronan | 0.39 |
| | 439569 | AW602166 | Hs.222399 | CEGP1 protein | 0.39 |
| | 433485 | AI493076 | Hs.78183 | aldo-keto reductase family 1, member C1 | 0.40 |
| 65 | 432753 | NM_014075 | Hs.278915 | PRO0593 protein | 0.40 |
| | 420200 | AI271429 | Hs.88142 | ESTs | 0.40 |
| | 421863 | AI952677 | Hs.108972 | Homo sapiens mRNA; cDNA DKFZp434P228 (fr | 0.40 |
| | 453950 | AA156998 | Hs.211568 | eukaryotic translation initiation factor | 0.40 |
| | 407408 | AF054830 | | gb:Homo sapiens interleukin-1 type I rec | 0.40 |
| 70 | 410732 | AW984328 | | gb:PM3-HN0010-050400-001-h12 HN0010 Homo | 0.40 |
| | 458272 | AI797360 | Hs.264899 | ESTs, Weakly similar to ALU3_HUMAN ALU S | 0.40 |
| | 401514 | AF147186 | | gb:AF147186 Homo sapiens library (Schere | 0.40 |
| | 436363 | AA843926 | Hs.124434 | ESTs | 0.40 |
| | 434445 | AI349306 | Hs.11782 | ESTs | 0.40 |
| 75 | 413272 | AA127923 | Hs.293256 | ESTs | 0.40 |
| | 409681 | N51508 | Hs.143718 | ESTs | 0.40 |
| | 454554 | AW847505 | | gb:RC0-CT0210-280999-021-c10 CT0210 Homo | 0.40 |
| | 450891 | AI743118 | Hs.238914 | ESTs, Weakly similar to neuregulin-4 sho | 0.40 |
| | 452078 | AA022620 | Hs.52170 | ESTs | 0.41 |
| 80 | 419278 | AU076799 | Hs.1247 | apolipoprotein A-IV | 0.41 |
| | 433637 | AW024214 | Hs.135405 | ESTs | 0.41 |
| | 449923 | BE258051 | | gb:601111034F1 NIH_MGC_16 Homo sapiens c | 0.41 |
| | 416982 | J05401 | Hs.80691 | creatine kinase, mitochondrial 2 (sarcos | 0.41 |
| | 453139 | AA330620 | Hs.240659 | ESTs | 0.41 |
| | 408614 | AL137698 | Hs.46531 | Homo sapiens mRNA; cDNA DKFZp434C1915 (f | 0.41 |
| | 437931 | AI249468 | Hs.145274 | ESTs | 0.41 |
| | 402759 | | | | 0.41 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| 5 | 450888 | AW021446 | Hs.80714 | ESTs | 0.41 |
| | 417318 | AW953937 | Hs.12891 | ESTs | 0.41 |
| | 407244 | M10014 | Hs.75431 | fibrinogen, gamma polypeptide | 0.41 |
| | 424884 | AW299437 | Hs.225717 | ESTs | 0.41 |
| | 439024 | R95696 | Hs.35598 | ESTs | 0.42 |
| | 423732 | AF058056 | Hs.132183 | solute carrier family 16 (monocarboxylic | 0.42 |
| | 409300 | AA126190 | | gb:zm78f03.r1 Stratagene neuroepithelium | 0.42 |
| | 444237 | AA336878 | Hs.9842 | Human DNA sequence from clone RP4-788L20 | 0.42 |
| 10 | 425860 | L29339 | Hs.1964 | solute carrier family 5 (sodium/glucose | 0.42 |
| | 447021 | AI356564 | Hs.161406 | ESTs | 0.42 |
| | 422270 | AF114494 | Hs.114062 | protein tyrosine phosphatase-like (profi | 0.42 |
| | 407850 | AW086230 | Hs.244912 | ESTs | 0.42 |
| | 449884 | AI673110 | Hs.222195 | ESTs | 0.42 |
| 15 | 436327 | AA813075 | Hs.120181 | ESTs | 0.42 |
| | 415972 | H11436 | Hs.260201 | ESTs | 0.42 |
| | 400917 | | | | 0.43 |
| | 435309 | AW089050 | Hs.187993 | ESTs | 0.43 |
| | 424410 | W79027 | Hs.271762 | ESTs | 0.43 |
| 20 | 445577 | N40696 | Hs.146077 | ESTs | 0.43 |
| | 411069 | AL133092 | Hs.68055 | hypothetical protein DKFZp434i0428 | 0.43 |
| | 440286 | U29589 | Hs.7138 | cholinergic receptor, muscarinic 3 | 0.43 |
| | 451123 | AI927224 | Hs.213480 | ESTs | 0.43 |
| | 457151 | AW206116 | Hs.253538 | ESTs | 0.43 |
| 25 | 459185 | AI908222 | | gb:RC-BT165-300399-020 BT165 Homo sapien | 0.43 |
| | 411607 | AW853498 | | gb:RC1-CT0252-170200-025-h02 CT0252 Homo | 0.43 |
| | 424815 | AA347287 | Hs.104573 | ESTs | 0.43 |
| | 429704 | AA584440 | Hs.185812 | ESTs | 0.43 |
| | 411067 | AI681006 | Hs.301543 | ESTs | 0.43 |
| 30 | 430172 | AA468591 | Hs.161889 | ESTs | 0.43 |
| | 435124 | AA725362 | Hs.120456 | ESTs | 0.43 |
| | 445966 | L17330 | Hs.280 | pre-T/NK cell associated protein | 0.43 |
| | 443741 | AW451759 | Hs.145420 | ESTs | 0.43 |
| | 416275 | H42823 | Hs.155742 | glyoxylate reductase/hydroxypyruvate red | 0.44 |
| 35 | 451138 | W92287 | Hs.40268 | ESTs | 0.44 |
| | 409038 | T97490 | Hs.50002 | small inducible cytokine subfamily A (Cy | 0.44 |
| | 426730 | AL040738 | | gb:DKFZp434B1615_r1 434 (synonym: hles3) | 0.44 |
| | 410066 | AL117664 | Hs.58419 | DKFZP586L2024 protein | 0.44 |
| | 427965 | D00306 | Hs.183864 | elastase 3B | 0.44 |
| 40 | 418026 | BE379727 | Hs.83213 | fatty acid binding protein 4, adipocyte | 0.44 |
| | 408479 | BE047329 | Hs.144483 | ESTs | 0.44 |
| | 457994 | AW136239 | Hs.132922 | ESTs | 0.44 |
| | 435564 | AF210652 | Hs.16614 | 5(3)-deoxynucleotidase (dNT-2); nucl | 0.45 |
| | 435869 | AF255910 | Hs.54650 | vascular endothelial junction-associated | 0.45 |
| 45 | 434399 | AA878845 | Hs.125769 | ESTs | 0.45 |
| | 415797 | AI291896 | Hs.72800 | ESTs | 0.45 |
| | 430264 | AA470519 | | gb:nc71f10.s1 NCI_CGAP_Pr1 Homo sapiens | 0.45 |
| | 409435 | AI810721 | Hs.95424 | ESTs | 0.45 |
| | 433542 | AA598869 | Hs.173770 | ESTs | 0.45 |
| 50 | 455400 | AW936342 | | gb:QV4-DT0021-281299-070-h12 DT0021 Homo | 0.45 |
| | 412047 | AA934589 | Hs.49696 | ESTs | 0.45 |
| | 443948 | T56148 | Hs.9997 | Homo sapiens mRNA full length insert cDN | 0.45 |
| | 450307 | AW450336 | Hs.201783 | ESTs | 0.45 |
| | 434500 | AF143877 | Hs.215047 | Homo sapiens clone IMAGE:113431 mRNA seq | 0.45 |
| 55 | 420460 | AA262331 | Hs.135503 | ESTs | 0.45 |
| | 450752 | AA012986 | Hs.60466 | ESTs | 0.45 |
| | 418138 | AA213626 | Hs.136204 | EST | 0.45 |
| | 441088 | AA916546 | Hs.126546 | ESTs | 0.46 |
| | 410990 | AW812929 | | gb:RC3-ST0186-250200-018-c05 ST0186 Homo | 0.46 |
| 60 | 438211 | T08401 | | gb:EST06292 Infant Brain, Bento Soares H | 0.46 |
| | 434349 | NM_015678 | Hs.3821 | neurobeachin | 0.46 |
| | 409824 | AW501063 | | gb:UI-HF-BP0p-aiz-c-01-0-UI.r1 NIH_MGC_5 | 0.46 |
| | 403279 | | | | 0.46 |
| | 434882 | AW974752 | Hs.269497 | ESTs | 0.46 |
| 65 | 404629 | | | | 0.46 |
| | 427393 | AB029018 | Hs.177635 | KIAA1095 protein | 0.46 |
| | 454651 | AW812091 | | gb:RC4-ST0173-191099-032-b04 ST0173 Homo | 0.46 |
| | 401992 | | | | 0.46 |
| | 457275 | AA463422 | Hs.209431 | ESTs | 0.46 |
| 70 | 403710 | | | | 0.46 |
| | 419728 | L36861 | Hs.92858 | guanylate cyclase activator 1A (retina) | 0.46 |
| | 401075 | | | | 0.46 |
| | 421387 | AF059566 | Hs.103983 | solute carrier family 5 (sodium iodide s | 0.46 |
| | 453404 | AA035446 | Hs.261224 | ESTs | 0.46 |
| 75 | 407208 | T10695 | Hs.102948 | enigma (LJM domain protein) | 0.46 |
| | 440681 | AW449696 | Hs.166547 | ESTs | 0.46 |
| | 454206 | AW810279 | | gb:MR4-ST0125-151299-029-a09 ST0125 Homo | 0.47 |
| | 402466 | | | | 0.47 |
| | 429936 | N90822 | Hs.48969 | ESTs | 0.47 |
| 80 | 403680 | | | | 0.47 |
| | 428151 | AA422028 | | gb:zv26g06.r1 Soares_NhHMPu_S1 Homo sapi | 0.47 |
| | 410495 | N95428 | | gb:zb60d09.s1 Soares_senescent_fibroblas | 0.47 |
| | 402851 | | | | 0.47 |
| | 438421 | AA806907 | Hs.194451 | ESTs | 0.47 |

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|----|--------|-----------|-----------|--|------|
| 5 | 454661 | BE244138 | | gb:TCBAP1E1218 Pediatric pre-B cell acut | 0.47 |
| | 408753 | AI337192 | Hs.47438 | SH3 domain binding glutamic acid-rich pr | 0.47 |
| | 409106 | AW337854 | Hs.177386 | ESTs | 0.47 |
| | 413199 | M82843 | Hs.75236 | ELAV (embryonic lethal, abnormal vision, | 0.47 |
| | 442799 | AI564739 | Hs.68505 | ESTs | 0.47 |
| | 457955 | AI208986 | Hs.143945 | ESTs | 0.47 |
| | 458147 | AW752597 | | gb:IL3-CT0214-161299-045-B06 CT0214 Homo | 0.47 |
| | 407938 | AA905097 | Hs.85050 | phospholamban | 0.47 |
| 10 | 414141 | BE255083 | | gb:601111390F1 NIH_MGC_16 Homo sapiens c | 0.47 |
| | 448869 | AI792798 | Hs.12496 | ESTs | 0.47 |
| | 400749 | | | | 0.47 |
| | 458745 | AW207347 | Hs.211101 | ESTs | 0.48 |
| | 418437 | AA771738 | Hs.295351 | ESTs | 0.48 |
| 15 | 452286 | AI358570 | Hs.123933 | ESTs | 0.48 |
| | 430369 | AA477631 | Hs.119484 | ESTs | 0.48 |
| | 453572 | AA382590 | Hs.31848 | ESTs, Weakly similar to hypothetical pro | 0.48 |
| | 455175 | AW993247 | | gb:RC2-BN0033-180200-014-h09 BN0033 Homo | 0.48 |
| | 445765 | AV655102 | Hs.117266 | ESTs | 0.48 |
| 20 | 400322 | AF045576 | Hs.247758 | olfactory receptor, family 5, subfamily | 0.48 |
| | 412526 | M90366 | Hs.73982 | zona pellucida glycoprotein 2 (sperm rec | 0.48 |
| | 407986 | U32659 | Hs.41724 | interleukin 17 (cytotoxic T-lymphocyte-a | 0.48 |
| | 455479 | AW948312 | | gb:RC0-MT0015-280300-021-h04 MT0015 Homo | 0.48 |
| | 450308 | AI692571 | Hs.201681 | ESTs | 0.48 |
| 25 | 411149 | N68715 | Hs.269128 | ESTs | 0.48 |
| | 453982 | AW014252 | Hs.252637 | ESTs | 0.48 |
| | 410971 | AW812258 | | gb:RC0-ST0174-191099-031-b02 ST0174 Homo | 0.48 |
| | 410839 | NM_006849 | Hs.66581 | protein disulfide isomerase | 0.48 |
| | 421553 | AA536080 | Hs.97302 | ESTs | 0.48 |
| 30 | 442376 | W95588 | Hs.129982 | Homo sapiens cDNA FLJ12228 fis, clone MA | 0.48 |
| | 454754 | AW819191 | | gb:CM1-ST0283-071299-061-d08 ST0283 Homo | 0.48 |
| | 447858 | AW080339 | Hs.211911 | ESTs | 0.49 |
| | 422639 | AI929377 | Hs.173724 | creatine kinase, brain | 0.49 |
| | 402449 | | | | 0.49 |
| 35 | 420440 | NM_002407 | Hs.97644 | mammaglobin 2 | 0.49 |
| | 435056 | AW023337 | Hs.5422 | glycoprotein M68 | 0.49 |
| | 419543 | AA244170 | Hs.188719 | ESTs | 0.49 |
| | 407033 | U78628 | | gb:Human leukemia inhibitory factor rece | 0.49 |
| | 437468 | AA457619 | | gb:aa89d11.1 Stratagene fetal retina 93 | 0.49 |
| 40 | 412639 | AW961284 | Hs.296235 | ESTs | 0.49 |
| | 406109 | | | | 0.49 |
| | 404519 | | | | 0.49 |
| | 410285 | AA083609 | | gb:zm63d05.r1 Stratagene fibroblast (937 | 0.49 |
| | 406014 | | | | 0.49 |
| 45 | 400938 | | | | 0.49 |
| | 414290 | AI568801 | Hs.71721 | ESTs | 0.49 |
| | 432433 | AW014734 | Hs.157969 | ESTs | 0.49 |
| | 405273 | | | | 0.49 |
| 50 | 454738 | BE072139 | | gb:PM1-BT0533-291299-002-b05 BT0533 Homo | 0.49 |
| | 414383 | BE279406 | | gb:601157981F1 NIH_MGC_21 Homo sapiens c | 0.49 |
| | 445911 | AI985987 | Hs.145645 | ESTs, Moderately similar to ALU1_HUMAN A | 0.49 |
| | 451241 | AI767545 | Hs.209572 | ESTs | 0.49 |
| | 428336 | AA503115 | Hs.183752 | microseminoprotein, beta- | 0.49 |
| | 418310 | AA814100 | Hs.86693 | ESTs | 0.49 |
| 55 | 452152 | AL046755 | Hs.28219 | protein phosphatase 2 (formerly 2A), reg | 0.49 |
| | 454869 | AW836004 | | gb:PM0-LT0019-170200-001-d11 LT0019 Homo | 0.49 |
| | 400332 | S66407 | Hs.248032 | FLT4 | 0.49 |
| | 425280 | U31519 | Hs.1872 | phosphoenolpyruvate carboxykinase 1 (sol | 0.49 |
| | 408221 | AA912183 | Hs.47447 | ESTs | 0.49 |
| 60 | 440179 | AI990151 | Hs.125904 | ESTs | 0.50 |
| | 425360 | BE547704 | | gb:601076309F1 NIH_MGC_12 Homo sapiens c | 0.50 |
| | 406600 | | | | 0.50 |
| | 418594 | AI732083 | Hs.187619 | ESTs | 0.50 |
| | 432128 | AA127221 | Hs.117037 | ESTs | 0.50 |
| 65 | 458611 | AI268407 | Hs.211458 | ESTs | 0.50 |
| | 426495 | NM_001151 | Hs.2043 | solute carrier family 25 (mitochondrial | 0.50 |
| | 441068 | AA913897 | Hs.233559 | ESTs | 0.50 |
| | 428108 | AA421452 | Hs.164851 | ESTs | 0.50 |
| | 400803 | | | | 0.50 |
| 70 | 439996 | AA916565 | Hs.221675 | ESTs | 0.50 |

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|-------------|---------------------------------------|---|--|
| TABLE 44B: | | | |
| Pkey: | Unique Eos probeset identifier number | | |
| CAT number: | Gene cluster number | | |
| Accession: | Genbank accession numbers | | |
| Pkey | CAT number | Accession | |
| 409300 | 111676_1 | AA126190 AA074486 AA074707 AA070059 AA084886 | |
| 409824 | 1155499_1 | AW501063 AW503034 AW501523 | |
| 410285 | 119128_1 | AA083609 AA083790 AA112048 | |
| 410495 | 1205826_1 | N95428 W24040 AW751366 H81987 | |
| 410732 | 1218556_1 | AW984328 AW984322 AW984318 AW984330 R58427 AW984332 AW799807 AW984321 | |
| 410971 | 1228216_1 | AW812258 AW812252 AW812261 AW812263 AW812285 AW812277 AW812264 | |
| 410990 | 1228649_1 | AW812929 AW812779 AW813088 | |

| | | | |
|----|--------|-----------|--|
| | 411607 | 1251251_1 | AW853498 AW853442 AW853590 AW853433 AW853592 |
| | 413079 | 1348528_1 | BE064382 BE064387 BE064385 BE064381 BE153367 BE153366 BE153401 BE153385 BE064372 |
| | 413679 | 1382784_1 | BE156765 BE156770 BE156767 BE156769 BE156803 BE156802 BE156847 BE156853 BE156780 BE156836 BE156792 BE156834 BE156779 |
| 5 | 414141 | 1420715_1 | BE156789 BE156833 BE156844 BE156831 BE156849 BE156797 BE156784 BE156801 BE156843 BE156793 BE156852 |
| | 414383 | 1440279_1 | BE255083 BE257634 |
| | 422582 | 218132_1 | BE279406 BE280100 |
| | 425360 | 250631_1 | AA312660 AJ474863 |
| | 426730 | 271055_1 | BE547704 AA355909 |
| 10 | 428151 | 287658_1 | AL040738 AA383683 |
| | 430264 | 315008_1 | AA422028 W79191 |
| | 430664 | 321423_1 | AA470519 BE303010 BE302954 BE384120 |
| | 431152 | 328675_1 | AW969834 AA528493 AA483165 AW969842 |
| | 431514 | 334213_1 | AW970998 AW971004 AA574217 AA493538 |
| 15 | 437468 | 43743_1 | AW972363 AA506335 AJ077445 |
| | 438211 | 45225_1 | AA457619 AL390167 |
| | 449923 | 81926_1 | T08401 ZB3934 T16897 |
| | 451818 | 887271_1 | BE258051 R45758 AA004732 BE256126 |
| 20 | 454206 | 1050848_1 | AJ819018 RD5492 W27615 |
| | | | AW810279 BE146684 BE146693 BE146694 BE146679 AW810472 AW810208 AW810356 AW810193 AW178838 AW178837 AW178857 AW810515 |
| | | | AW810330 AW810514 AW810441 AW810358 AW178852 AW810359 AW810322 AW810327 AW810211 AW178835 AW810635 AW810288 AW810263 |
| | | | AW810325 AW810443 AW810198 AW810321 AW810265 AW810567 AW810447 AW810328 AW810513 BE146674 AW810257 AW810185 AW810281 |
| | | | AW810258 BE062400 AW810323 AW810293 BE146652 AW810516 BE146689 AW810289 AW810566 AW810636 AW178842 BE062434 BE146653 |
| | | | AW810536 AW846649 |
| 25 | 454554 | 1223842_1 | AW847505 AW811792 BE061442 BE061433 AW847506 AW806999 AW806996 BE061436 BE061430 BE142460 BE146499 AW806994 AW809156 |
| | | | AW806991 AW814082 AW806992 BE061669 AW807002 BE146659 AW806995 AW807000 AW845743 AW845747 AW847504 BE142458 BE061431 |
| | | | BE061435 AW847507 BE146650 BE142470 AW814096 AW807012 BE061438 AW807011 AW806993 BE142465 BE142459 BE142462 AW854330 |
| | | | AW854331 BE061434 BE061731 BE142464 AW847501 AW807001 BE142463 AW811800 BE061437 AW811802 BE061440 AW806997 AW806998 |
| | | | BE061745 BE061753 |
| 30 | 454560 | 1223940_1 | AW807281 AW807092 AW807425 AW807330 AW807174 AW807171 AW807274 AW807278 AW807367 |
| | 454561 | 1228069_1 | AW812091 AW812228 AW812106 AW938581 AW812080 |
| | 454561 | 1228527_1 | BE244138 BE244727 AW812636 AW812647 |
| | 454738 | 1232449_1 | BE072139 BE157977 BE157974 AW857974 AW817778 |
| | 454754 | 1233580_1 | AW819191 AW819252 AW819183 AW819175 AW819177 AW819186 AW819180 BE158470 AW819242 AW819269 AW819244 AW819190 AW819265 |
| | | | AW819268 AW819246 BE152602 AW819249 AW819251 AW819263 AW819194 |
| 35 | 454790 | 1234752_1 | AW820852 AW820773 AW821088 |
| | 454869 | 1238137_1 | AW836004 AW836087 AW836163 AW836162 AW836085 AW836084 AW836079 AW836083 AW836082 AW836086 AW836088 AW836166 AW836164 |
| | | | AW836002 AW836078 AW836161 AW862135 AW836165 AW836003 |
| | 455175 | 1257335_1 | AW993247 AW861464 |
| 40 | 455400 | 1288135_1 | AW936342 AW936366 |
| | 455479 | 1293163_1 | AW948312 AW948286 AW948289 AW948297 AW948279 AW948295 |
| | 455541 | 1323705_1 | AW993005 AW993285 AW993290 |
| | 455753 | 1356070_1 | BE075124 BE075229 BE075278 |
| | 455826 | 1373392_1 | BE144228 BE144291 |
| 45 | 458147 | 488021_1 | AW752597 AW848781 AW849062 AW848490 AW752699 AW752604 AW752700 |
| | 459185 | 922823_1 | AJ908222 AJ908224 AJ908217 |

TABLE 44C:

Pkey: Unique number corresponding to an Eos probeset

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

NI_position: Indicates nucleotide positions of predicted exons.

| | | | | |
|----|--------|---------|--------|---|
| 55 | Pkey | Ref | Strand | NI_position |
| | 400749 | 7331445 | Minus | 9162-9293 |
| | 400803 | 8567875 | Minus | 18267-19088 |
| | 400917 | 7283186 | Minus | 173258-173631 |
| | 400938 | 7652890 | Minus | 92074-92423 |
| | 401075 | 3687273 | Plus | 81218-81395 |
| 60 | 401514 | 7622355 | Plus | 93224-93292,94913-95065,95163-95334 |
| | 401775 | 9966311 | Minus | 110228-110340 |
| | 401989 | 4309964 | Minus | 118611-118821 |
| | 401992 | 4153858 | Plus | 31452-31649 |
| | 402015 | 7417802 | Minus | 48791-49043,50038-50205,51530-51672,54448-54565,55933-56073 |
| 65 | 402449 | 9796674 | Plus | 59867-60039,62588-62828,63465-63623,64923-65108 |
| | 402466 | 9796919 | Plus | 57659-57866,58839-58908 |
| | 402759 | 9213869 | Plus | 134117-134281 |
| | 402760 | 9213869 | Plus | 136829-136952,137336-137521 |
| | 402851 | 9650753 | Minus | 63022-63136,63683-63783 |
| 70 | 403059 | 8954192 | Minus | 69553-69702 |
| | 403279 | 8072597 | Plus | 162569-162768,163918-164168 |
| | 403429 | 9719566 | Minus | 52789-52917 |
| | 403670 | 7259739 | Minus | 88377-88537 |
| | 403680 | 7331517 | Minus | 157184-157415 |
| 75 | 403710 | 6437516 | Plus | 27413-28978 |
| | 404121 | 9796219 | Plus | 59256-59401 |
| | 404519 | 8152000 | Plus | 12817-13000 |
| | 404629 | 9796665 | Plus | 55584-55796 |
| | 404973 | 3213020 | Plus | 101602-102591 |
| 80 | 405110 | 8096688 | Minus | 118940-119100 |
| | 405273 | 4156137 | Minus | 98141-98754 |
| | 405645 | 4926864 | Minus | 92231-92380,92724-92869 |
| | 405742 | 7283744 | Minus | 54424-55488 |

| | | | |
|--------|---------|-------|-------------------------|
| 405817 | 4071056 | Plus | 19914-20112,25655-25810 |
| 406014 | 6758904 | Minus | 23738-24076 |
| 406036 | 6758919 | Plus | 17942-18163 |
| 406109 | 9127147 | Minus | 58328-58485 |
| 406255 | 7417729 | Plus | 2959-3200 |
| 406326 | 9212385 | Plus | 84508-84655 |
| 406600 | 8248616 | Minus | 36296-36610 |

TABLE 45A: ABOUT 947 GENES UP-REGULATED IN STOMACH CANCER COMPARED TO NORMAL ADULT TISSUES
Table 45A lists about 947 genes up-regulated in stomach cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" stomach cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" stomach cancer level was set to the 90th percentile amongst various stomach cancers. The "average" normal adult tissue level was set to the 90th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 15th percentile value amongst various non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of stomach cancer compared to normal stomach

| Pkey | ExAccn | UnigeneID | Unigene Title | R1 |
|--------|-----------|-----------|--|-------|
| 418007 | M13509 | Hs.83169 | matrix metalloproteinase 1 (interstitial | 66.80 |
| 411243 | AB039886 | Hs.69319 | CA11 | 61.16 |
| 428368 | BE440042 | Hs.83326 | matrix metalloproteinase 3 (stromelysin | 42.36 |
| 427585 | D31152 | Hs.179729 | collagen, type X, alpha 1 (Schmid metaph | 35.80 |
| 425679 | X05997 | Hs.159177 | lipase, gastric | 28.34 |
| 409041 | AB033025 | Hs.50081 | KIAA1199 protein | 26.91 |
| 452121 | NM_004081 | Hs.70936 | deleted in azoospermia | 26.22 |
| 403776 | | | NA | 25.00 |
| 444783 | AK001468 | Hs.62180 | anilin (Drosophila Scraps homolog), act | 23.90 |
| 422956 | BE545072 | Hs.122579 | hypothetical protein FLJ10461 | 23.90 |
| 409187 | AF154830 | Hs.50966 | carbamoyl-phosphate synthetase 1, mitoch | 23.35 |
| 424252 | AK000520 | Hs.143811 | hypothetical protein FLJ20513 | 22.26 |
| 439759 | AL359055 | Hs.67709 | Homo sapiens mRNA full length insert cDN | 21.06 |
| 415989 | AI267700 | Hs.317584 | ESTs | 20.72 |
| 416209 | AA236776 | Hs.79078 | MAD2 (mitotic arrest deficient, yeast, h | 19.84 |
| 452401 | NM_007115 | Hs.29352 | tumor necrosis factor, alpha-induced pro | 15.50 |
| 438639 | AI278360 | Hs.31409 | ESTs | 15.16 |
| 426427 | M86699 | Hs.169840 | TTK protein kinase | 14.54 |
| 449032 | AA045573 | Hs.22900 | nuclear factor (erythroid-derived 2)-lik | 14.26 |
| 443211 | AI128388 | Hs.143655 | ESTs | 14.22 |
| 421470 | R27496 | Hs.1378 | annexin A3 | 13.96 |
| 400792 | AA635062 | Hs.50094 | Homo sapiens mRNA; cDNA DKFZp434O0515 (f | 13.94 |
| 424086 | AI351010 | Hs.102267 | lysyl oxidase | 13.73 |
| 437789 | AI581344 | Hs.127812 | ESTs, Weakly similar to T17330 hypotheti | 13.38 |
| 409757 | NM_001898 | Hs.123114 | cystatin SN | 13.33 |
| 447033 | AI357412 | Hs.157601 | ESTs | 13.20 |
| 447164 | AF026941 | Hs.17518 | Homo sapiens cig5 mRNA, partial sequence | 12.80 |
| 420159 | AI572490 | Hs.99785 | Homo sapiens cDNA: FLJ21245 fs, clone C | 12.66 |
| 432596 | AJ224741 | Hs.278461 | matrilin 3 | 12.64 |
| 424905 | NM_002497 | Hs.153704 | NIMA (never in mitosis gene a)-related k | 12.46 |
| 413582 | AW295647 | Hs.71331 | hypothetical protein MGC5350 | 12.32 |
| 423020 | AA383092 | Hs.1608 | replication protein A3 (14kD) | 12.18 |
| 448693 | AW004854 | Hs.228320 | hypothetical protein FLJ23537 | 11.74 |
| 442660 | AW138174 | Hs.130651 | ESTs | 11.73 |
| 441693 | AA384673 | Hs.7943 | RPB5-mediating protein | 11.16 |
| 450221 | AA328102 | Hs.24641 | cytoskeleton associated protein 2 | 11.08 |
| 414142 | AW368397 | Hs.150042 | Homo sapiens cDNA FLJ14438 fs, clone HE | 10.90 |
| 424717 | H03754 | Hs.152213 | wingless-type MMTV integration site fami | 10.48 |
| 443715 | AI583187 | Hs.9700 | cyclin E1 | 10.44 |
| 420900 | AL045633 | Hs.44269 | ESTs | 10.38 |
| 453922 | AF053306 | Hs.36708 | budding uninhibited by benzimidazoles 1 | 10.36 |
| 415076 | NM_000857 | Hs.77890 | guanylate cyclase 1, soluble, beta 3 | 10.20 |
| 452291 | AF015592 | Hs.28853 | CDC7 (cell division cycle 7, S. cerevisi | 10.18 |
| 410566 | AA373210 | Hs.43047 | Homo sapiens cDNA FLJ13585 fs, clone PL | 10.14 |
| 414422 | AA147224 | Hs.337232 | ESTs | 10.12 |
| 409269 | AA576953 | Hs.22972 | hypothetical protein FLJ13352 | 10.02 |
| 414972 | BE263782 | Hs.77695 | KIAA0008 gene product | 10.02 |
| 418882 | NM_004996 | Hs.89433 | ATP-binding cassette, sub-family C (CFTR | 9.80 |
| 428365 | AA295331 | Hs.183861 | Homo sapiens cDNA FLJ20042 fs, clone CO | 9.72 |
| 416661 | AA634543 | Hs.79440 | IGF-II mRNA-binding protein 3 | 9.68 |
| 400195 | NA | | NA | 9.66 |
| 418738 | AW388633 | Hs.6682 | solute carrier family 7, (cationic amino | 9.64 |
| 420170 | U43374 | Hs.95631 | Human normal keratinocyte mRNA | 9.60 |
| 414259 | W44633 | Hs.301296 | Homo sapiens cDNA: FLJ23131 fs, clone L | 9.58 |
| 417517 | AF001176 | Hs.82238 | POP4 (processing of precursor, S. cerev | 9.34 |
| 446998 | N99013 | Hs.16762 | Homo sapiens mRNA; cDNA DKFZp56482062 (f | 9.26 |
| 429486 | AF155827 | Hs.203963 | hypothetical protein FLJ10339 | 9.16 |
| 428227 | AA321649 | Hs.2248 | small inducible cytokine subfamily B (Cy | 8.95 |
| 431810 | X67155 | Hs.270845 | kinesin-like 5 (mitotic kinesin-like pro | 8.84 |
| 419261 | X07876 | Hs.89791 | wingless-type MMTV integration site fami | 8.80 |
| 425921 | NM_007231 | Hs.162211 | solute carrier family 6 (neurotransmitte | 8.78 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 424834 | AK001432 | Hs.153408 | Homo sapiens cDNA FLJ10570 fs, clone NT | 8.69 |
| | 413268 | AL039079 | Hs.75256 | regulator of G-protein signalling 1 | 8.68 |
| | 417801 | AA417383 | Hs.82582 | integrin, beta-like 1 (with EGF-like rep | 8.68 |
| 5 | 452461 | N78223 | Hs.108106 | transcription factor | 8.68 |
| | 425916 | NM_006786 | Hs.162200 | urotensin 2 | 8.64 |
| | 422805 | AA436989 | Hs.121017 | H2A histone family, member A | 8.54 |
| | 438394 | BE379623 | Hs.27693 | peptidylprolyl isomerase (cyclophilin)-I | 8.52 |
| | 441377 | BE218239 | Hs.202656 | ESTs | 8.41 |
| 10 | 445891 | AW391342 | Hs.199460 | ESTs | 8.31 |
| | 408771 | AW732573 | Hs.47584 | potassium voltage-gated channel, delayed | 8.30 |
| | 439521 | AI808955 | Hs.58248 | ESTs | 8.30 |
| | 425087 | R62424 | Hs.126059 | ESTs | 8.28 |
| | 424653 | AW977534 | Hs.151469 | calcium/calmodulin-dependent serine prot | 8.22 |
| 15 | 441795 | N58115 | Hs.21137 | AD024 protein | 8.02 |
| | 427878 | C05766 | Hs.181022 | CGI-07 protein | 8.00 |
| | 413583 | AL120806 | Hs.5888 | ESTs | 7.98 |
| | 407853 | AA336797 | Hs.40499 | dickkopf (Xenopus laevis).homolog 1 | 7.98 |
| | 426269 | H15302 | Hs.168950 | Homo sapiens mRNA; cDNA DKFp566A1046 (f | 7.97 |
| 20 | 404996 | | | NA | 7.96 |
| | 400289 | X07820 | Hs.2258 | matrix metalloproteinase 10 (stromelysin | 7.96 |
| | 410044 | BE566742 | Hs.58169 | highly expressed in cancer, rich in leuc | 7.94 |
| | 417655 | AA780791 | Hs.14014 | hypothetical protein FLJ14813 | 7.92 |
| | 452838 | U65011 | Hs.30743 | preferentially expressed antigen in mela | 7.91 |
| 25 | 418895 | AA894638 | Hs.14600 | ESTs | 7.90 |
| | 446155 | AI553695 | Hs.159422 | Homo sapiens cDNA FLJ13997 fs, clone Y7 | 7.86 |
| | 423123 | NM_012247 | Hs.124027 | SELENOPHOSPHATE SYNTHETASE ; Human selen | 7.82 |
| | 434539 | AW748078 | Hs.214410 | ESTs, Weakly similar to MUC2_HUMAN MUCIN | 7.80 |
| | 447505 | AL049266 | Hs.18724 | Homo sapiens mRNA; cDNA DKFp564F093 (fr | 7.72 |
| 30 | 418763 | AK000219 | Hs.88367 | hypothetical protein FLJ20212 | 7.70 |
| | 447289 | AW247017 | Hs.36978 | melanoma antigen, family A, 3 | 7.70 |
| | 443354 | AW970672 | Hs.9247 | protein kinase, AMP-activated, alpha 1 c | 7.69 |
| | 427718 | AI798680 | Hs.25933 | ESTs | 7.66 |
| | 434032 | AW009951 | Hs.206892 | ESTs | 7.60 |
| 35 | 427738 | NM_000318 | Hs.180612 | peroxisomal membrane protein 3 (35kD, Ze | 7.58 |
| | 450480 | X82125 | Hs.25040 | zinc finger protein 239 | 7.51 |
| | 418678 | NM_001327 | Hs.167379 | cancer/testis antigen | 7.49 |
| | 431494 | AA991355 | Hs.298312 | hypothetical protein DKFp434A1315 | 7.44 |
| | 452705 | H49805 | Hs.246005 | ESTs | 7.36 |
| 40 | 443646 | AI085198 | Hs.164226 | ESTs | 7.32 |
| | 425420 | BE536911 | Hs.234545 | hypothetical protein NUF2R | 7.30 |
| | 420617 | AK001652 | Hs.99423 | ATP-dependent RNA helicase | 7.28 |
| | 421155 | H87879 | Hs.102267 | lysyl oxidase | 7.24 |
| | 450715 | AI266484 | Hs.31570 | ESTs, Weakly similar to KIAA1324 protein | 7.24 |
| 45 | 447254 | NM_004153 | Hs.17908 | origin recognition complex, subunit 1 (y | 7.22 |
| | 435473 | N53550 | Hs.260881 | ESTs | 7.20 |
| | 413293 | AL047483 | Hs.302498 | GTP-binding protein homologous to Saccha | 7.14 |
| | 449347 | AV649748 | Hs.295901 | KIAA0493 protein | 7.11 |
| | 452281 | T93500 | Hs.28792 | Homo sapiens cDNA FLJ11041 fs, clone PL | 7.11 |
| 50 | 408908 | BE296227 | Hs.250822 | serine/threonine kinase 15 | 7.11 |
| | 408660 | AA525775 | Hs.292523 | ESTs, Moderately similar to PC4259 ferri | 7.10 |
| | 453688 | AW381270 | Hs.194110 | hypothetical protein PRO2730 | 7.02 |
| | 426890 | AA393167 | Hs.41294 | ESTs | 6.98 |
| | 404440 | | | NA | 6.97 |
| 55 | 426642 | AW068223 | Hs.171581 | ubiquitin C-terminal hydrolase UCH37 | 6.96 |
| | 431723 | AW058350 | Hs.16762 | Homo sapiens mRNA; cDNA DKFp564B2062 (f | 6.95 |
| | 413833 | Z15005 | Hs.75573 | centromere protein E (312kD) | 6.94 |
| | 426249 | F05422 | Hs.168352 | nucleoporin-like protein 1 | 6.94 |
| | 441421 | AA356792 | Hs.334824 | hypothetical protein FLJ14825 | 6.92 |
| 60 | 400298 | AA032279 | Hs.61635 | six transmembrane epithelial antigen of | 6.85 |
| | 423903 | M57765 | Hs.1721 | interleukin 11 | 6.84 |
| | 431041 | AA490967 | Hs.197955 | KIAA0704 protein | 6.74 |
| | 417256 | U94332 | Hs.81791 | tumor necrosis factor receptor superfam | 6.74 |
| | 426921 | AA037145 | Hs.172865 | cleavage stimulation factor, 3' pre-RNA, | 6.70 |
| | 407771 | AL138272 | Hs.62713 | ESTs | 6.69 |
| 65 | 433393 | AF038564 | Hs.98074 | itchy (mouse homolog) E3 ubiquitin prote | 6.66 |
| | 407162 | N63855 | Hs.142634 | zinc finger protein | 6.64 |
| | 411343 | U77949 | Hs.69563 | CDC6 (cell division cycle 6, S. cerevisi | 6.64 |
| | 427920 | Z11502 | Hs.181107 | annexin A13 | 6.59 |
| 70 | 450159 | AI702416 | Hs.200771 | ESTs, Moderately similar to A Chain A, T | 6.58 |
| | 427401 | U20582 | Hs.2149 | actin like protein | 6.55 |
| | 447102 | BE167434 | Hs.98471 | ESTs, Weakly similar to T18712 hypotheti | 6.54 |
| | 431806 | AF186114 | Hs.270737 | tumor necrosis factor (ligand) superfam | 6.54 |
| | 435159 | AA668879 | Hs.116649 | ESTs | 6.54 |
| 75 | 440209 | H05049 | Hs.22269 | neurexin 3 | 6.54 |
| | 418134 | AA397769 | Hs.86617 | ESTs | 6.50 |
| | 451807 | W52854 | Hs.27099 | hypothetical protein FLJ23293 similar to | 6.47 |
| | 434894 | AW977850 | Hs.23856 | hypothetical protein MGC5297 | 6.40 |
| | 422505 | AL120862 | Hs.124165 | ESTs | 6.34 |
| 80 | 426010 | AA136563 | Hs.1975 | hypothetical protein FLJ21007 | 6.32 |
| | 414696 | AF002020 | Hs.76918 | Niemann-Pick disease, type C1 | 6.31 |
| | 408380 | AF123050 | Hs.44532 | diubiquitin | 6.31 |
| | 420218 | AW958037 | Hs.286 | ribosomal protein L4 | 6.29 |
| | 405817 | NA | | NA | 6.28 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| 5 | 406747 | AJ925153 | Hs.217493 | annexin A2 | 6.24 |
| | 448743 | AB032962 | Hs.21896 | KIAA1136 protein | 6.24 |
| | 434636 | AA083764 | Hs.6101 | hypothetical protein MGC3178 | 6.20 |
| | 424602 | AK002055 | Hs.151046 | hypothetical protein FLJ11193 | 6.17 |
| | 412661 | N32860 | Hs.24611 | ESTs, Weakly similar to I54374 gene NF2 | 6.17 |
| | 401644 | | | NA | 6.16 |
| | 423248 | AA380177 | Hs.125845 | ribulose-5-phosphate-3-epimerase | 6.13 |
| | 427335 | AA448542 | Hs.251677 | G antigen 7B | 6.12 |
| 10 | 450375 | AA009647 | Hs.8850 | a disintegrin and metalloproteinase doma | 6.07 |
| | 422420 | U03398 | Hs.1524 | tumor necrosis factor (ligand) superfam | 6.06 |
| | 419752 | AA249573 | Hs.152618 | ESTs, Moderately similar to ZN91_HUMAN Z | 6.06 |
| | 413573 | AJ733859 | Hs.149089 | ESTs | 6.06 |
| | 408758 | NM_003686 | Hs.47504 | exonuclease 1 | 6.02 |
| 15 | 444188 | AJ393165 | Hs.699 | peptidylprolyl isomerase B (cyclophilin | 6.02 |
| | 407746 | AK001962 | Hs.38114 | hypothetical protein FLJ11100 | 6.00 |
| | 446364 | AB006624 | Hs.14912 | KIAA0286 protein | 5.98 |
| | 418939 | AW630803 | Hs.89497 | lamin B1 | 5.90 |
| | 424639 | AJ917494 | Hs.9812 | Homo sapiens cDNA FLJ14388 fis, clone HE | 5.88 |
| 20 | 434377 | AW137148 | Hs.306593 | Homo sapiens cDNA FLJ11382 fis, clone HE | 5.86 |
| | 419863 | AW952691 | Hs.93485 | Homo sapiens mRNA; cDNA DKFZp761D191 (fr | 5.84 |
| | 430849 | AJ940727 | Hs.270556 | ESTs, Highly similar to AF156779 1 ASB-4 | 5.82 |
| | 428822 | W28418 | Hs.30715 | potassium voltage-gated channel, Isk-rel | 5.80 |
| | 448776 | BE302464 | Hs.30057 | MRS2 (S. cerevisiae)-like, magnesium hom | 5.74 |
| 25 | 442957 | AJ949952 | Hs.49397 | ESTs | 5.72 |
| | 444577 | AJ207721 | Hs.11393 | RAD51 (S. cerevisiae) homolog C | 5.72 |
| | 424565 | AW102723 | Hs.75295 | guanylate cyclase 1, soluble, alpha 3 | 5.71 |
| | 433330 | AW207084 | Hs.132816 | hypothetical protein MGC14801 | 5.68 |
| | 428618 | AA885360 | Hs.160199 | NADPH oxidase, EF hand calcium-binding d | 5.68 |
| 30 | 432867 | AW016936 | Hs.233364 | ESTs | 5.64 |
| | 412140 | AA219691 | Hs.73625 | RAB6 interacting, kinesin-like (rabkines | 5.63 |
| | 433133 | AB027249 | Hs.104741 | PDZ-binding kinase; T-cell originated pr | 5.62 |
| | 418379 | AA218940 | Hs.137516 | fidgetin-like 1 | 5.57 |
| | 434551 | BE387162 | Hs.280858 | ESTs, Highly similar to A35661 DNA excis | 5.57 |
| 35 | 442353 | BE379594 | Hs.49136 | ESTs, Moderately similar to ALU7_HUMAN A | 5.56 |
| | 427386 | AW836261 | Hs.337717 | ESTs | 5.54 |
| | 425650 | NM_001944 | Hs.1925 | desmoglein 3 (pemphigus vulgaris antigen | 5.52 |
| | 428479 | Y00272 | Hs.184572 | cell division cycle 2, G1 to S and G2 to | 5.51 |
| | 449370 | AK002114 | Hs.23495 | hypothetical protein FLJ11252 | 5.50 |
| 40 | 431118 | BE264901 | Hs.250502 | carbonic anhydrase VIII | 5.50 |
| | 423673 | BE003054 | Hs.1695 | matrix metalloproteinase 12 (macrophage | 5.50 |
| | 453931 | AL121278 | Hs.25144 | ESTs | 5.49 |
| | 409044 | AI129586 | Hs.33033 | hypothetical protein FLJ14623 | 5.48 |
| | 436291 | BE568452 | Hs.5101 | protein regulator of cytokinesis 1 | 5.45 |
| 45 | 448336 | RS3848 | Hs.44976 | ESTs | 5.44 |
| | 454018 | AW016892 | Hs.100855 | ESTs | 5.42 |
| | 457030 | AJ301740 | Hs.173381 | dihydropyrimidinase-like 2 | 5.42 |
| | 412246 | AI160873 | Hs.69233 | zinc finger protein | 5.40 |
| | 432193 | AA372264 | Hs.273193 | hypothetical protein FLJ10706 | 5.40 |
| 50 | 437319 | BE410958 | Hs.56406 | Homo sapiens cDNA FLJ13549 fis, clone PL | 5.40 |
| | 427660 | AI741320 | Hs.114121 | Homo sapiens cDNA: FLJ23228 fis, clone C | 5.40 |
| | 452862 | AW378065 | Hs.8587 | ESTs | 5.38 |
| | 409327 | L41162 | Hs.53563 | collagen, type IX, alpha 3 | 5.36 |
| | 412811 | H06382 | Hs.21400 | ESTs | 5.34 |
| 55 | 448390 | AL035414 | Hs.21068 | hypothetical protein | 5.32 |
| | 428187 | AI687303 | Hs.285529 | G protein-coupled receptor 49 | 5.30 |
| | 450434 | AA166950 | Hs.195870 | hypothetical protein FLJ14991 | 5.29 |
| | 434265 | AA846811 | Hs.130554 | Homo sapiens cDNA: FLJ23089 fis, clone L | 5.28 |
| | 407811 | AW190902 | Hs.40098 | cysteine knot superfamily 1, BMP antagon | 5.27 |
| 60 | 446638 | AL133063 | Hs.15783 | Homo sapiens mRNA; cDNA DKFZp434P1115 (f | 5.26 |
| | 444743 | AA045648 | Hs.301957 | nudix (nucleoside diphosphate linked moi | 5.25 |
| | 424902 | NM_003866 | Hs.153687 | inositol polyphosphate-4-phosphatase, ty | 5.24 |
| | 452150 | W42490 | Hs.260844 | ESTs | 5.24 |
| | 432865 | AJ753709 | Hs.152484 | ESTs, Weakly similar to I38022 hypotheti | 5.22 |
| 65 | 453382 | AA709285 | Hs.5997 | hypothetical protein FLJ13078 | 5.22 |
| | 447048 | AW393080 | Hs.228320 | hypothetical protein FLJ23537 | 5.22 |
| | 426518 | Z43039 | Hs.170198 | KIAA0009 gene product | 5.22 |
| | 453884 | AA355925 | Hs.36232 | KIAA0186 gene product | 5.20 |
| | 429625 | AA455568 | Hs.193814 | ESTs | 5.20 |
| 70 | 413472 | BE242870 | Hs.75379 | solute carrier family 1 (glial high affi | 5.20 |
| | 449318 | AW236021 | Hs.78531 | Homo sapiens, Similar to RIKEN cDNA 5730 | 5.19 |
| | 444059 | R69743 | Hs.116774 | integrin, alpha 1 | 5.18 |
| | 409432 | D49372 | Hs.54460 | small inducible cytokine subfamily A (Cy | 5.17 |
| | 412719 | AW016610 | Hs.129911 | ESTs | 5.15 |
| 75 | 444342 | NM_014398 | Hs.10887 | similar to lysosome-associated membrane | 5.14 |
| | 425739 | T19016 | Hs.159410 | molybdopter synthase sulfurylase | 5.12 |
| | 452198 | AJ097560 | Hs.61210 | ESTs, Weakly similar to I38022 hypotheti | 5.12 |
| | 445657 | AW612141 | Hs.279575 | Homo sapiens G-protein coupled receptor | 5.10 |
| | 434699 | AA643687 | Hs.149425 | Homo sapiens cDNA FLJ11980 fis, clone HE | 5.09 |
| 80 | 424296 | AI631874 | Hs.155140 | casein kinase 2, alpha 1 polypeptide | 5.08 |
| | 441645 | AI222279 | Hs.201555 | ESTs, Weakly similar to T23406 hypotheti | 5.06 |
| | 412723 | AA648459 | Hs.335951 | hypothetical protein AF301222 | 5.06 |
| | 448811 | AI590371 | Hs.174759 | ESTs | 5.05 |
| | 447342 | AI199268 | Hs.19322 | Homo sapiens, Similar to RIKEN cDNA 2010 | 5.04 |

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|----|--------|-----------|-----------|---|------|
| | 411835 | U29343 | Hs.72550 | hyaluronan-mediated motility receptor (R | 5.04 |
| | 421373 | AA808229 | Hs.167771 | ESTs | 5.04 |
| | 448991 | AW771565 | Hs.189594 | ESTs | 5.02 |
| | 429370 | C19097 | Hs.89709 | glutamate-cysteine ligase, modifier subu | 5.00 |
| 5 | 454036 | AA374756 | Hs.93560 | Homo sapiens mRNA for KIAA1771 protein, | 4.98 |
| | 405770 | | | NA | 4.96 |
| | 421110 | AJ250717 | Hs.1355 | cathepsin E | 4.96 |
| | 452588 | AA889120 | Hs.110637 | homeo box A10 | 4.92 |
| 10 | 433159 | AB035898 | Hs.150587 | kinesin-like protein 2 | 4.91 |
| | 420952 | AA282067 | Hs.88972 | ESTs, Moderately similar to A46010 X-in | 4.88 |
| | 408321 | AW405882 | Hs.44205 | coristatin | 4.87 |
| | 441801 | AW242799 | Hs.86366 | ESTs | 4.84 |
| | 450568 | AL050078 | Hs.25159 | Homo sapiens cDNA FLJ10784 fs, clone NT | 4.83 |
| 15 | 452909 | NM_015368 | Hs.30985 | pannexin 1 | 4.82 |
| | 409799 | D11928 | Hs.76845 | phosphoserine phosphatase-like | 4.82 |
| | 451105 | AJ761324 | | gb:wf60b11.x1 NCL_CGAP_Co16 Homo sapiens | 4.80 |
| | 417168 | AL133117 | Hs.81376 | Homo sapiens mRNA; cDNA DKFZp586L1121 (f | 4.80 |
| | 418203 | X54942 | Hs.83758 | CDC28 protein kinase 2 | 4.80 |
| 20 | 418994 | AA296520 | Hs.89546 | selectin E (endothelial adhesion molecucl | 4.78 |
| | 436982 | AB018305 | Hs.5378 | spondin 1, (I-spondin) extracellular mat | 4.78 |
| | 432874 | W94322 | Hs.279651 | melanoma inhibitory activity | 4.78 |
| | 440351 | AF030933 | Hs.7179 | RAD1 (S. pombe) homolog | 4.78 |
| | 431956 | AK002032 | Hs.272245 | Homo sapiens cDNA FLJ11170 fs, clone PL | 4.77 |
| 25 | 442980 | AA857025 | Hs.8878 | kinesin-like 1 | 4.76 |
| | 432437 | W07088 | Hs.293685 | ESTs | 4.76 |
| | 414869 | AA157291 | Hs.21479 | ubiquitin 1 | 4.74 |
| | 446254 | BE179829 | Hs.179852 | Homo sapiens cDNA FLJ12832 fs, clone NT | 4.74 |
| | 418380 | AA425473 | Hs.84429 | KIAA0971 protein | 4.74 |
| 30 | 419343 | AA456245 | Hs.85603 | down-regulated by Ctnnb1, a | 4.74 |
| | 418478 | U38945 | Hs.1174 | cyclin-dependent kinase inhibitor 2A (me | 4.72 |
| | 425813 | AA364136 | Hs.210553 | hypothetical protein DKFZp7611172 | 4.71 |
| | 425071 | NM_013989 | Hs.154424 | deiodinase, iodothyronine, type II | 4.71 |
| | 412733 | AA984472 | Hs.74554 | KIAA0080 protein | 4.68 |
| 35 | 444325 | AW152618 | Hs.16757 | ESTs | 4.66 |
| | 407638 | AJ404672 | Hs.334483 | hypothetical protein FLJ23571 | 4.66 |
| | 430345 | AK000282 | Hs.239681 | hypothetical protein FLJ20275 | 4.66 |
| | 428330 | L22524 | Hs.2256 | matrix metalloproteinase 7 (matrilysin, | 4.64 |
| | 449448 | D60730 | Hs.57471 | ESTs | 4.62 |
| 40 | 409732 | NM_016122 | Hs.56148 | NY-REN-58 antigen | 4.62 |
| | 432415 | T16971 | Hs.289014 | ESTs, Weakly similar to A43932 mucin 2 p | 4.62 |
| | 421987 | AJ133161 | Hs.286131 | CGI-101 protein | 4.60 |
| | 430217 | N47863 | Hs.336901 | ribosomal protein S24 | 4.58 |
| | 429597 | NM_003816 | Hs.2442 | a disintegrin and metalloproteinase doma | 4.57 |
| 45 | 425932 | M81650 | Hs.1968 | semenogelin I | 4.57 |
| | 408728 | AL137379 | Hs.47125 | hypothetical protein FLJ13912 | 4.56 |
| | 428434 | AW363590 | Hs.65551 | Homo sapiens, Similar to DNA segment, Ch | 4.55 |
| | 451254 | AI571016 | Hs.172967 | ESTs | 4.54 |
| | 422426 | W79117 | Hs.58559 | ESTs | 4.54 |
| 50 | 439483 | T69980 | Hs.58323 | Homo sapiens cDNA FLJ11613 fs, clone HE | 4.53 |
| | 435420 | AI928513 | Hs.59203 | ESTs | 4.53 |
| | 447519 | U46258 | Hs.339665 | ESTs | 4.52 |
| | 424176 | AL137273 | Hs.142307 | hypothetical protein | 4.52 |
| | 414812 | X72755 | Hs.77367 | monokine induced by gamma interferon | 4.51 |
| 55 | 438069 | N80701 | Hs.33790 | ESTs | 4.50 |
| | 450096 | AI682088 | Hs.79375 | holocarboxylase synthetase (biotin-[prop | 4.50 |
| | 438159 | Z83947 | | gb:H.sapiens mRNA; clone CD 117 | 4.50 |
| | 433925 | AI183551 | Hs.26481 | SBB126 protein | 4.48 |
| | 417866 | AW067903 | Hs.82772 | collagen, type XI, alpha 1 | 4.48 |
| 60 | 433384 | AI021992 | Hs.124244 | ESTs | 4.47 |
| | 421863 | AI952677 | Hs.108972 | Homo sapiens mRNA; cDNA DKFZp434P228 (fr | 4.47 |
| | 453941 | U39817 | Hs.36820 | Bloom syndrome | 4.45 |
| | 423401 | NM_001992 | Hs.128087 | coagulation factor II (thrombin) recepto | 4.44 |
| | 430510 | AW162916 | Hs.241576 | hypothetical protein PRO2577 | 4.43 |
| | 424084 | AI940675 | Hs.20914 | hypothetical protein FLJ23056 | 4.42 |
| 65 | 459587 | AA031956 | | gb:zk15e04.s1 Soares_pregnant_uterus_NbH | 4.42 |
| | 417956 | AA210704 | Hs.190465 | ESTs | 4.42 |
| | 449433 | AI672096 | Hs.9012 | ESTs, Weakly similar to S26650 DNA-bindi | 4.42 |
| | 421477 | AI904743 | Hs.104650 | hypothetical protein FLJ10292 | 4.42 |
| 70 | 406687 | M31126 | Hs.272620 | pregnancy specific beta-1-glycoprotein 9 | 4.41 |
| | 451813 | NM_016117 | Hs.27182 | phospholipase A2-activating protein | 4.41 |
| | 415091 | AL044872 | Hs.77910 | 3-hydroxy-3-methylglutaryl-Coenzyme A sy | 4.40 |
| | 425142 | AW954397 | Hs.154762 | HIV-1 rev binding protein 2 | 4.40 |
| | 441720 | AI346487 | Hs.28739 | ESTs | 4.40 |
| 75 | 409683 | U33317 | Hs.711 | defensin, alpha 6, Paneth cell-specific | 4.39 |
| | 411571 | AA122393 | Hs.70811 | hypothetical protein FLJ20516 | 4.38 |
| | 430044 | AA464510 | Hs.152812 | ESTs | 4.37 |
| | 436246 | AW450963 | Hs.119991 | ESTs | 4.37 |
| | 409582 | R27430 | Hs.271565 | ESTs | 4.37 |
| 80 | 453652 | AW009640 | Hs.28368 | ESTs, Moderately similar to S65657 alpha | 4.35 |
| | 425211 | M18667 | Hs.1867 | progastricsin (pepsinogen C) | 4.34 |
| | 448692 | AW013907 | Hs.167531 | methylcrotonoyl-Coenzyme A carboxylase 2 | 4.34 |
| | 409459 | D86407 | Hs.54481 | low density lipoprotein receptor-related | 4.34 |
| | 442470 | AW273860 | Hs.5759 | ESTs | 4.33 |

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|----|--------|-----------|-----------|--|------|
| | 441894 | AA134329 | Hs.24170 | Homo sapiens, clone IMAGE:3685398, mRNA, | 4.32 |
| | 422867 | L32137 | Hs.1584 | cartilage oligomeric matrix protein (pse | 4.31 |
| | 436396 | AI683487 | Hs.152213 | wingless-type MMTV integration site fami | 4.31 |
| 5 | 433397 | AW079766 | Hs.134880 | ESTs, Weakly similar to unnamed protein | 4.30 |
| | 417576 | AA339449 | Hs.82285 | phosphoribosylglycinamide formyltransfer | 4.29 |
| | 413278 | BE563085 | Hs.833 | interferon-stimulated protein, 15 kDa | 4.29 |
| | 451592 | AI805416 | Hs.213897 | ESTs | 4.28 |
| | 453900 | AW003582 | Hs.226414 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 4.28 |
| 10 | 422892 | AA988176 | Hs.121553 | hypothetical protein FLJ20641 | 4.26 |
| | 431699 | NM_001173 | Hs.267831 | Rho GTPase activating protein 5 | 4.26 |
| | 428389 | AW135714 | Hs.283127 | ESTs, Weakly similar to T19201 hypotheti | 4.24 |
| | 410361 | BE391804 | Hs.62661 | guanylate binding protein 1, interferon- | 4.23 |
| | 409913 | BE243842 | Hs.283077 | centrosomal P4.1-associated protein; unc | 4.22 |
| 15 | 445537 | AJ245671 | Hs.12844 | EGF-like-domain, multiple 6 | 4.21 |
| | 445640 | AW969626 | Hs.31704 | ESTs, Weakly similar to KIAA0227 [H.sapi | 4.20 |
| | 422232 | D43945 | Hs.113274 | transcription factor EC | 4.18 |
| | 442655 | AW027457 | Hs.30323 | ESTs, Weakly similar to B34087 hypotheti | 4.18 |
| | 444381 | BE387335 | Hs.283713 | ESTs, Weakly similar to S64054 hypotheti | 4.16 |
| 20 | 434217 | AW014795 | Hs.23349 | ESTs | 4.16 |
| | 413384 | NM_000401 | Hs.75334 | exostoses (multiple) 2 | 4.14 |
| | 407768 | AW002841 | Hs.29475 | ESTs | 4.14 |
| | 419168 | AI336132 | Hs.33718 | Homo sapiens cDNA FLJ12641 fis, clone NT | 4.13 |
| | 408165 | AL137573 | Hs.43143 | Homo sapiens mRNA; cDNA DKFZp564A2463 (f | 4.12 |
| 25 | 443691 | AJ081724 | Hs.17267 | ESTs | 4.12 |
| | 409640 | U78722 | Hs.55481 | zinc finger protein 165 | 4.12 |
| | 438176 | AW138970 | Hs.122113 | ESTs | 4.10 |
| | 435532 | AW291488 | Hs.117305 | Homo sapiens, clone IMAGE:3682908, mRNA | 4.10 |
| | 419606 | AW294795 | Hs.198529 | ESTs | 4.08 |
| 30 | 452824 | W27643 | Hs.73965 | splicing factor, arginine/serine-rich 2 | 4.08 |
| | 414152 | NM_003248 | Hs.75774 | thrombospondin 4 | 4.08 |
| | 418688 | T85017 | Hs.1192 | KIAA0074 protein | 4.07 |
| | 404253 | | | NA | 4.06 |
| | 421741 | AK001879 | Hs.107527 | hypothetical protein FLJ11017 | 4.06 |
| 35 | 428218 | AA424266 | Hs.123642 | EphA3 | 4.06 |
| | 428858 | AA436760 | | gb:zv67d11.r1 Soares fetal_fetus_Nb2HF8_ | 4.06 |
| | 428336 | AA503115 | Hs.183752 | microseminoprotein, beta- | 4.05 |
| | 442875 | BE623003 | Hs.23625 | Homo sapiens clone TCCCTA00142 mRNA sequ | 4.04 |
| | 421841 | AA908197 | Hs.108850 | MAK-related kinase | 4.04 |
| 40 | 451177 | AI969716 | Hs.13034 | ESTs | 4.04 |
| | 425188 | AK002052 | Hs.155071 | hypothetical protein FLJ11190 | 4.04 |
| | 421262 | AA286746 | Hs.9343 | Homo sapiens cDNA FLJ14265 fis, clone PL | 4.03 |
| | 424634 | NM_003613 | Hs.151407 | cartilage intermediate layer protein, nu | 4.02 |
| | 438777 | AA825487 | Hs.142179 | ESTs | 4.02 |
| 45 | 423343 | AA324643 | Hs.246106 | ESTs | 4.02 |
| | 425788 | BE466417 | Hs.231899 | ESTs, Weakly similar to rab3 effector-li | 4.02 |
| | 409928 | AL137163 | Hs.57549 | hypothetical protein dJ47384 | 4.01 |
| | 406671 | AA129547 | Hs.285754 | met proto-oncogene (hepatocyte growth fa | 4.01 |
| | 442973 | BE567665 | Hs.288550 | Homo sapiens cDNA: FLJ23156 fis, clone L | 4.00 |
| 50 | 433225 | AW816515 | Hs.173540 | ATPase, Class V, type 10D | 4.00 |
| | 411765 | H43346 | | gb:yp09a04.r1 Soares breast 3NbHBst Homo | 4.00 |
| | 452022 | AW072330 | Hs.293875 | ESTs | 4.00 |
| | 451806 | NM_003729 | Hs.27076 | RNA 3'-terminal phosphate cyclase | 3.99 |
| | 423541 | AA295922 | Hs.129778 | gastrointestinal peptide | 3.99 |
| 55 | 414132 | AI801235 | Hs.48480 | ESTs | 3.99 |
| | 452453 | AI902519 | | gb:QV-BT009-101198-051 BT009 Homo sapien | 3.98 |
| | 418454 | AA315308 | Hs.195870 | hypothetical protein FLJ14931 | 3.98 |
| | 430134 | BE380149 | Hs.105223 | ESTs, Weakly similar to T33188 hypotheti | 3.98 |
| | 453160 | AI263307 | Hs.239884 | H2B histone family, member L | 3.97 |
| 60 | 417235 | AA810278 | Hs.24250 | ESTs | 3.96 |
| | 425398 | AL049689 | Hs.156369 | hypothetical protein similar to tenascin | 3.95 |
| | 414136 | AA812434 | Hs.119023 | SMC2 (structural maintenance of chromoso | 3.94 |
| | 436608 | AA628980 | Hs.192371 | down syndrome critical region protein DS | 3.94 |
| | 431753 | X76029 | Hs.2841 | neuromedin U | 3.94 |
| 65 | 453161 | AA628608 | Hs.61656 | ESTs | 3.94 |
| | 454821 | AW833504 | | gb:QV4-TT0008-091199-025-03 TT0008 Homo | 3.94 |
| | 427961 | AW293165 | Hs.143134 | ESTs | 3.94 |
| | 439453 | BE264974 | Hs.6566 | thyroid hormone receptor interactor 13 | 3.93 |
| | 409564 | AA045857 | Hs.54943 | fracture callus 1 (rat) homolog | 3.93 |
| 70 | 418396 | AI765805 | Hs.26691 | ESTs | 3.92 |
| | 451411 | AA017492 | Hs.135655 | EST | 3.92 |
| | 445885 | AI734009 | Hs.127699 | KIAA1603 protein | 3.92 |
| | 407698 | AA058900 | Hs.32646 | hypothetical protein FLJ21901 | 3.91 |
| | 442896 | R37725 | Hs.261108 | ESTs | 3.90 |
| 75 | 433361 | AW469373 | Hs.300141 | ribosomal protein L39 | 3.90 |
| | 419926 | AW900992 | Hs.93796 | DKFZP586D2223 protein | 3.89 |
| | 413775 | AW409934 | Hs.75528 | nucleolar GTPase | 3.88 |
| | 452943 | BE247449 | Hs.31082 | hypothetical protein FLJ10525 | 3.86 |
| | 428549 | AA430064 | Hs.220929 | Homo sapiens cDNA FLJ14369 fis, clone HE | 3.86 |
| 80 | 456120 | AA535244 | Hs.78305 | RAB2, member RAS oncogene family | 3.86 |
| | 452194 | AI694413 | Hs.332649 | olfactory receptor, family 2, subfamily | 3.85 |
| | 421247 | BE391727 | Hs.102910 | general transcription factor IIH, polype | 3.85 |
| | 417720 | AA205625 | Hs.208067 | ESTs | 3.85 |
| | 418811 | AK001407 | Hs.88663 | hypothetical protein FLJ10545 | 3.84 |

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|----|--------|-----------|-----------|--|------|
| | 430899 | BE018217 | Hs.183528 | hypothetical protein FLJ14906 | 3.84 |
| | 421246 | AW582962 | Hs.102897 | CGI-47 protein | 3.83 |
| | 407366 | AF026942 | | gb:Homo sapiens cig33 mRNA, partial sequ | 3.83 |
| | 428698 | AA852773 | Hs.334838 | KIAA1866 protein | 3.82 |
| 5 | 435202 | AI971313 | Hs.170204 | KIAA0551 protein | 3.82 |
| | 454074 | R63503 | Hs.28419 | ESTs | 3.82 |
| | 448917 | AI683598 | Hs.201615 | ESTs | 3.82 |
| | 410507 | AA355288 | Hs.40834 | transitional epithelia response protein | 3.82 |
| | 452571 | W31518 | Hs.34665 | ESTs | 3.82 |
| 10 | 445663 | AI247343 | Hs.149232 | ESTs | 3.82 |
| | 450701 | H39960 | Hs.288467 | Homo sapiens cDNA FLJ12280 fis, clone MA | 3.80 |
| | 423025 | AA831267 | Hs.12244 | hypothetical protein FLJ20097 | 3.80 |
| | 425656 | AB018284 | Hs.158688 | KIAA0741 gene product | 3.80 |
| | 407168 | RA5175 | Hs.117183 | ESTs | 3.79 |
| 15 | 403422 | NA | | NA | 3.79 |
| | 425492 | AL021918 | Hs.158174 | zinc finger protein 184 (Kruppel-like) | 3.79 |
| | 432239 | X81334 | Hs.2936 | matrix metalloproteinase 13 (collagenase | 3.79 |
| | 457325 | AA744550 | Hs.136345 | ESTs | 3.78 |
| | 433800 | AI034361 | Hs.135150 | lung type-I cell membrane-associated gly | 3.77 |
| 20 | 428865 | BE544095 | Hs.164960 | BarH-like homeobox 1 | 3.76 |
| | 424188 | AW954552 | Hs.142634 | zinc finger protein | 3.75 |
| | 424638 | AI472106 | Hs.49303 | Homo sapiens cDNA FLJ11663 fis, clone HE | 3.75 |
| | 451099 | R52795 | Hs.25954 | interleukin 13 receptor, alpha 2 | 3.75 |
| | 448105 | AW581433 | Hs.298241 | Transmembrane protease, serine 3 | 3.74 |
| 25 | 452785 | AL359942 | Hs.296434 | erythroid differentiation and denucleati | 3.74 |
| | 459000 | AA903705 | Hs.4190 | Homo sapiens cDNA: FLJ23269 fis, clone C | 3.74 |
| | 432653 | N62096 | Hs.293185 | ESTs, Weakly similar to JC7328 amino aci | 3.73 |
| | 409632 | W74001 | Hs.55279 | serine (or cysteine) proteinase inhibito | 3.73 |
| | 414883 | AA926960 | Hs.334883 | CDC28 protein kinase 1 | 3.73 |
| 30 | 415064 | AA159840 | Hs.149305 | hypothetical protein MGC2603 | 3.72 |
| | 432198 | AI475306 | Hs.50458 | ESTs | 3.72 |
| | 458194 | AW383618 | Hs.265459 | ESTs, Moderately similar to ALU2_HUMAN A | 3.72 |
| | 415263 | AA948033 | Hs.130853 | ESTs | 3.71 |
| | 408296 | AL117452 | Hs.44155 | DKFZP586G1517 protein | 3.71 |
| 35 | 408460 | AA054726 | Hs.285574 | ESTs | 3.71 |
| | 437496 | AA452378 | Hs.170144 | Homo sapiens mRNA: cDNA DKFZp547J125 (fr | 3.70 |
| | 443486 | NM_003428 | Hs.9450 | zinc finger protein 84 (HPF2) | 3.68 |
| | 432021 | AA524470 | Hs.58753 | ESTs | 3.68 |
| | 420092 | AA814043 | Hs.88045 | ESTs | 3.68 |
| 40 | 414923 | AW445008 | Hs.77637 | homeo box A4 | 3.68 |
| | 429432 | AI678059 | Hs.202676 | synaptonemal complex protein 2 | 3.68 |
| | 435496 | AW840171 | Hs.265398 | ESTs, Weakly similar to transformation-r | 3.67 |
| | 430544 | AA481066 | Hs.105153 | Homo sapiens, clone IMAGE:3461987, mRNA, | 3.67 |
| | 432542 | AW083920 | Hs.16098 | claudin 2 | 3.67 |
| 45 | 410782 | AW504860 | Hs.288836 | hypothetical protein FLJ12673 | 3.66 |
| | 421106 | AA877124 | Hs.172844 | ESTs | 3.64 |
| | 439107 | AL046134 | Hs.13944 | adrenergic, beta, receptor kinase 2 | 3.64 |
| | 418735 | N48769 | Hs.44609 | ESTs | 3.64 |
| 50 | 411598 | BE336654 | Hs.70937 | H3 histone family, member A | 3.63 |
| | 424687 | J05070 | Hs.151738 | matrix metalloproteinase 9 (gelatinase B | 3.63 |
| | 436411 | AW674352 | | gb:ba63c07.y1 NIH_MGC_12 Homo sapiens cD | 3.63 |
| | 429774 | AI522215 | Hs.50883 | KIAA1804 protein | 3.62 |
| | 448844 | AI581519 | Hs.177164 | ESTs | 3.61 |
| 55 | 402473 | AB033035 | Hs.51965 | KIAA1209 protein | 3.61 |
| | 441085 | AW136551 | Hs.181245 | Homo sapiens cDNA FLJ12532 fis, clone NT | 3.61 |
| | 429534 | AW976987 | Hs.163327 | ESTs, Weakly similar to 2109260A B cell | 3.60 |
| | 414706 | AW340125 | Hs.76989 | KIAA0097 gene product | 3.60 |
| | 436211 | AK001581 | Hs.334828 | hypothetical protein FLJ10719; KIAA1794 | 3.59 |
| 60 | 422938 | NM_001809 | Hs.1594 | centromere protein A (17kD) | 3.59 |
| | 451381 | BE241831 | Hs.172330 | hypothetical protein MGC2705 | 3.58 |
| | 428664 | AK001666 | Hs.189095 | similar to SALL1 (sal (Drosophila)-like | 3.58 |
| | 424345 | AK001380 | Hs.145479 | Homo sapiens cDNA FLJ10518 fis, clone NT | 3.58 |
| | 440717 | AA904527 | Hs.42207 | ESTs | 3.58 |
| 65 | 450698 | W31489 | Hs.95044 | ESTs, Weakly similar to I38022 hypotheti | 3.58 |
| | 423675 | AI990509 | Hs.131342 | small inducible cytokine subfamily A (Cy | 3.58 |
| | 424882 | AI379461 | Hs.153636 | far upstream element (FUSE) binding prot | 3.57 |
| | 410784 | AW803201 | | gb:IL2-UM0077-070500-080-E06 UM0077 Homo | 3.55 |
| | 411096 | U80034 | Hs.68583 | mitochondrial intermediate peptidase | 3.55 |
| 70 | 430294 | AI538226 | Hs.32976 | guanine nucleotide binding protein 4 | 3.54 |
| | 439225 | AA192669 | Hs.45032 | ESTs | 3.54 |
| | 429183 | AB014604 | Hs.197955 | KIAA0704 protein | 3.54 |
| | 419948 | AB041035 | Hs.93847 | NADPH oxidase 4 | 3.53 |
| | 443426 | AF098158 | Hs.9329 | chromosome 20 open reading frame 1 | 3.52 |
| 75 | 408556 | U49516 | Hs.46362 | 5-hydroxytryptamine (serotonin) receptor | 3.52 |
| | 417048 | AI088775 | Hs.55498 | geranylgeranyl diphosphate synthase 1 | 3.52 |
| | 432101 | AI918950 | Hs.123642 | EphA3 | 3.52 |
| | 419216 | AU076718 | Hs.164021 | small inducible cytokine subfamily B (Cy | 3.51 |
| | 444754 | T83911 | Hs.11881 | transmembrane 4 superfamily member 4 | 3.51 |
| 80 | 422093 | AF151852 | Hs.111449 | CGI-94 protein | 3.50 |
| | 404766 | NA | | NA | 3.50 |
| | 441513 | AW014557 | Hs.112420 | ESTs | 3.50 |
| | 444301 | AK000136 | Hs.10760 | asporin (LRR class 1) | 3.50 |
| | 417315 | AI080042 | Hs.336901 | ribosomal protein S24 | 3.50 |

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|----|--------|-----------|-----------|--|------|
| 5 | 407182 | AA312551 | Hs.230157 | ESTs | 3.49 |
| | 443204 | AW205878 | Hs.29643 | Homo sapiens cDNA FLJ13103 fis, clone NT | 3.49 |
| | 432289 | AI860145 | Hs.55118 | ESTs | 3.49 |
| | 453644 | AI813444 | Hs.42197 | ESTs | 3.48 |
| | 427986 | NA5214 | Hs.282387 | Homo sapiens cDNA: FLJ21837 fis, clone H | 3.48 |
| 10 | 405466 | | | NA | 3.48 |
| | 410804 | U64820 | Hs.66521 | Machado-Joseph disease (spinocerebellar | 3.48 |
| | 430357 | AW976789 | Hs.165607 | ESTs | 3.46 |
| | 418428 | Y12490 | Hs.85092 | thyroid hormone receptor interactor 11 | 3.46 |
| | 422260 | AA315993 | Hs.105484 | regenerating gene type IV | 3.46 |
| 15 | 421928 | AF013758 | Hs.109643 | polyadenylate binding protein-interactin | 3.46 |
| | 451403 | AA855569 | Hs.40919 | Homo sapiens cDNA FLJ14511 fis, clone NT | 3.46 |
| | 406117 | | | NA | 3.46 |
| | 458242 | BE299588 | Hs.28465 | Homo sapiens cDNA: FLJ21869 fis, clone H | 3.46 |
| | 408562 | AI436323 | Hs.31141 | Homo sapiens mRNA for KIAA1568 protein, | 3.45 |
| 20 | 440105 | AA694010 | Hs.6932 | Homo sapiens clone Z3809 mRNA sequence | 3.45 |
| | 443767 | BE562136 | Hs.9736 | proteasome (prosome, macropain) 26S subu | 3.45 |
| | 426320 | W47595 | Hs.169300 | transforming growth factor, beta 2 | 3.45 |
| | 444478 | W07318 | Hs.240 | M-phase phosphoprotein 1 | 3.45 |
| | 425904 | AI805990 | Hs.82238 | POP4 (processing of precursor, S. cerev | 3.44 |
| 25 | 416702 | AA186428 | Hs.85591 | ESTs | 3.44 |
| | 448668 | AI560305 | Hs.199852 | ESTs | 3.42 |
| | 410004 | AI298027 | Hs.5057 | carboxypeptidase D | 3.42 |
| | 428771 | AB028992 | Hs.193143 | KIAA1069 protein | 3.42 |
| | 446619 | AU076643 | Hs.313 | secreted phosphoprotein 1 (osteopontin, | 3.42 |
| 30 | 429628 | H09604 | Hs.13268 | ESTs | 3.40 |
| | 448816 | AB033052 | Hs.22151 | KIAA1226 protein | 3.40 |
| | 456032 | AW957446 | Hs.301711 | ESTs | 3.39 |
| | 439635 | AA477288 | Hs.94891 | hypothetical protein FLJ22729 | 3.39 |
| | 414275 | AW970254 | Hs.889 | Charol-Leyden crystal protein | 3.38 |
| 35 | 447207 | AA442233 | Hs.17731 | hypothetical protein FLJ12892 | 3.38 |
| | 416057 | AI927382 | Hs.29857 | ESTs | 3.38 |
| | 430704 | AW813091 | Hs.335799 | ESTs | 3.38 |
| | 423600 | AI633559 | Hs.310359 | ESTs | 3.38 |
| | 453891 | AB037751 | Hs.36353 | Homo sapiens mRNA full length insert cDN | 3.38 |
| 40 | 430178 | AW449612 | Hs.152475 | ESTs | 3.37 |
| | 417791 | AW965339 | Hs.111471 | ESTs | 3.37 |
| | 408867 | AA437199 | Hs.656 | cell division cycle 25C | 3.37 |
| | 449802 | AW901804 | Hs.23984 | hypothetical protein FLJ20147 | 3.37 |
| | 457003 | S78234 | Hs.172405 | cell division cycle 27 | 3.36 |
| 45 | 458076 | R80061 | Hs.164478 | hypothetical protein FLJ21939 similar to | 3.36 |
| | 435203 | BE384982 | Hs.5076 | Homo sapiens cDNA: FLJ22128 fis, clone H | 3.36 |
| | 418782 | AI792648 | Hs.14665 | ESTs | 3.34 |
| | 449722 | BE280074 | Hs.23960 | cyclin B1 | 3.34 |
| | 447984 | AI457263 | Hs.37244 | ESTs | 3.34 |
| 50 | 451103 | R52804 | Hs.25956 | DKFZP564D206 protein | 3.34 |
| | 408812 | BE397160 | Hs.254763 | ESTs, Weakly similar to A42442 integrin | 3.34 |
| | 448305 | AA625207 | Hs.264915 | Homo sapiens cDNA FLJ12908 fis, clone NT | 3.34 |
| | 418849 | AW474547 | Hs.53565 | Homo sapiens PIG-M mRNA for mannosyltran | 3.33 |
| | 450531 | AW301032 | Hs.203800 | ESTs | 3.32 |
| 55 | 411263 | BE297802 | Hs.69360 | kinesin-like 6 (mitotic centromere-assoc | 3.32 |
| | 416530 | U62801 | Hs.79361 | kalikrein 6 (neurosin, zyme) | 3.31 |
| | 425746 | NM_001701 | Hs.159440 | bile acid Coenzyme A: amino acid N-acylt | 3.30 |
| | 421037 | AI684808 | Hs.197653 | ESTs | 3.30 |
| | 430388 | AA356923 | Hs.240770 | nuclear cap binding protein subunit 2, 2 | 3.30 |
| 60 | 433132 | AB026264 | Hs.284245 | hypothetical protein IMPACT | 3.30 |
| | 447078 | AW885727 | Hs.301570 | ESTs | 3.30 |
| | 402408 | NA | | NA | 3.29 |
| | 437044 | AL035864 | Hs.69517 | cDNA for differentially expressed CO16 g | 3.29 |
| | 423126 | AA322245 | Hs.290165 | ESTs | 3.28 |
| 65 | 446223 | BE300091 | Hs.119699 | hypothetical protein FLJ12969 | 3.27 |
| | 451917 | AW391351 | Hs.50820 | Homo sapiens unknown mRNA | 3.27 |
| | 419335 | AW960146 | Hs.284137 | hypothetical protein FLJ12888 | 3.26 |
| | 411078 | AI222020 | Hs.182364 | CocoaCrisp | 3.26 |
| | 419790 | U79250 | Hs.93201 | glycerol-3-phosphate dehydrogenase 2 (mi | 3.26 |
| 70 | 427119 | AW880562 | Hs.114574 | ESTs | 3.26 |
| | 400250 | NA | | NA | 3.26 |
| | 429044 | AI261490 | Hs.145527 | ESTs | 3.25 |
| | 451050 | AW937420 | Hs.69662 | ESTs | 3.24 |
| | 447425 | AI963747 | Hs.18573 | acylphosphatase 1, erythrocyte (common) | 3.24 |
| 75 | 410389 | AW954049 | Hs.8177 | ESTs, Weakly similar to PIHUB5 salivary | 3.23 |
| | 416565 | AW000960 | Hs.44970 | endoplasmic reticulum resident protein 5 | 3.22 |
| | 442028 | AI239437 | Hs.48945 | ESTs | 3.22 |
| | 409110 | AA191493 | Hs.48778 | niban protein | 3.22 |
| | 418926 | AA232658 | Hs.105794 | UDP-glucose:glycoprotein glucosyltransfe | 3.22 |
| 80 | 408353 | BE439838 | Hs.44298 | mitochondrial ribosomal protein S17 | 3.21 |
| | 445417 | AK001058 | Hs.12680 | Homo sapiens cDNA FLJ10196 fis, clone HE | 3.20 |
| | 442979 | AW440782 | Hs.174743 | ESTs | 3.20 |
| | 439292 | AA090421 | Hs.5355 | hypothetical protein MGCS347 | 3.20 |
| | 440953 | AI683036 | Hs.124135 | Homo sapiens cDNA FLJ13051 fis, clone NT | 3.20 |
| | 447020 | T27308 | Hs.16986 | hypothetical protein FLJ11046 | 3.20 |
| | 451181 | AI796330 | Hs.207461 | ESTs | 3.19 |
| | 422809 | AK001379 | Hs.121028 | hypothetical protein FLJ10549 | 3.19 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| 5 | 411573 | AB029000 | Hs.70823 | KIAA1077 protein | 3.19 |
| | 424539 | L02911 | Hs.150402 | activin A receptor, type I | 3.18 |
| | 443179 | A928402 | Hs.6933 | hypothetical protein FLJ12684 | 3.18 |
| | 452545 | N31940 | Hs.14434 | ESTs, Weakly similar to I38022 hypotheti | 3.18 |
| | 433024 | AA573847 | Hs.26549 | KIAA1708 protein | 3.18 |
| | 414737 | A1160386 | Hs.125087 | ESTs | 3.18 |
| | 444230 | H95537 | Hs.146067 | ESTs | 3.18 |
| | 419741 | NM_007019 | Hs.93002 | ubiquitin carrier protein E2-C | 3.17 |
| 10 | 428945 | AW192803 | Hs.98974 | ESTs, Weakly similar to S65824 reverse t | 3.17 |
| | 424085 | NM_002914 | Hs.139226 | replication factor C (activator 1) 2 (40 | 3.17 |
| | 418661 | NM_001949 | Hs.1189 | E2F transcription factor 3 | 3.17 |
| | 443598 | AW499970 | Hs.14822 | ESTs, Weakly similar to I78885 serine/th | 3.16 |
| | 413516 | BE145907 | | gb:MR0-HT0208-221299-204-e12 HT0208 Homo | 3.16 |
| | 434389 | AA971233 | Hs.128098 | ESTs | 3.16 |
| 15 | 431322 | AW970622 | | gb:EST382704 MAGE resequences, MAGK Homo | 3.15 |
| | 432158 | W33165 | Hs.22983 | UDP-glucose:glycoprotein glucosyltransfe | 3.15 |
| | 453331 | A1240665 | Hs.8895 | ESTs | 3.15 |
| | 410286 | A1739159 | Hs.61898 | DKFZP586N2124 protein | 3.14 |
| 20 | 408687 | AL110280 | Hs.301152 | Homo sapiens mRNA; cDNA DKFZp434F053 (tr | 3.14 |
| | 422789 | AK001113 | Hs.120842 | hypothetical protein FLJ10251 | 3.14 |
| | 419078 | M93119 | Hs.89584 | insulinoma-associated 1 | 3.14 |
| | 414080 | AA135257 | Hs.47783 | B aggressive lymphoma gene | 3.14 |
| | 451525 | AW001757 | Hs.14005 | ESTs | 3.13 |
| 25 | 453775 | NM_002916 | Hs.35120 | replication factor C (activator 1) 4 (37 | 3.13 |
| | 433183 | AF231338 | Hs.222024 | transcription factor BMAL2 | 3.12 |
| | 424783 | AA913909 | Hs.153088 | TATA box binding protein (TBP)-associate | 3.12 |
| | 413170 | BE068819 | | gb:MR0-BT0374-220300-001-b03 BT0374 Homo | 3.12 |
| | 437181 | A1306615 | Hs.125343 | ESTs, Weakly similar to KIAA0758 protein | 3.12 |
| 30 | 442991 | BE281238 | Hs.8886 | hypothetical protein FLJ20424 | 3.11 |
| | 453867 | A1929383 | Hs.33032 | hypothetical protein DKFZp434N185 | 3.11 |
| | 437641 | AA811452 | Hs.291911 | ESTs | 3.10 |
| | 428651 | AF196478 | Hs.188401 | annexin A10 | 3.09 |
| | 427927 | A1879165 | Hs.2227 | CCAAT/enhancer binding protein (C/EBP). | 3.09 |
| 35 | 419196 | AF110908 | Hs.297660 | TNF receptor-associated factor 3 | 3.09 |
| | 414569 | AF109298 | Hs.118258 | prostate cancer associated protein 1 | 3.09 |
| | 408633 | AW963372 | Hs.46677 | PRO2000 protein | 3.09 |
| | 403381 | | | NA | 3.08 |
| | 444619 | BE538082 | Hs.8172 | ESTs, Moderately similar to A46010 X-link | 3.08 |
| 40 | 422363 | T55979 | Hs.115474 | replication factor C (activator 1) 3 (38 | 3.08 |
| | 434138 | AA625804 | | gb:zu86h01.s1 Soares_testis_NHT Homo sap | 3.07 |
| | 425322 | U63630 | Hs.155637 | protein kinase, DNA-activated, catalytic | 3.07 |
| | 436556 | A1364997 | Hs.7572 | ESTs | 3.07 |
| | 427043 | AA397679 | Hs.3991 | ESTs | 3.06 |
| 45 | 443055 | AV653742 | Hs.15536 | hypothetical protein DKFZp761J139 | 3.06 |
| | 419229 | A827237 | Hs.282884 | ESTs | 3.05 |
| | 414718 | H95348 | Hs.107987 | ESTs | 3.05 |
| | 439737 | A1751438 | Hs.41271 | Homo sapiens mRNA full length insert cDN | 3.05 |
| | 448587 | A1539652 | Hs.28338 | KIAA1546 protein | 3.04 |
| 50 | 448595 | AB014544 | Hs.21572 | KIAA0644 gene product | 3.04 |
| | 407201 | N31998 | Hs.164256 | hypothetical protein FLJ20657 | 3.04 |
| | 423065 | R96158 | Hs.267130 | Homo sapiens, clone MGC:5406, mRNA, comp | 3.04 |
| | 431980 | AA523696 | Hs.324507 | hypothetical protein FLJ20986 | 3.04 |
| | 416198 | H27332 | Hs.99598 | hypothetical protein MGC5338 | 3.04 |
| 55 | 429410 | X98494 | Hs.201676 | M-phase phosphoprotein 10 (U3 small nucl | 3.04 |
| | 432140 | AK000404 | Hs.272688 | hypothetical protein FLJ20397 | 3.03 |
| | 441031 | A110584 | Hs.7645 | fibrinogen, B beta polypeptide | 3.03 |
| | 446142 | A1754693 | Hs.145968 | ESTs | 3.02 |
| | 402167 | | | NA | 3.02 |
| 60 | 402299 | | | NA | 3.02 |
| | 417830 | AW504786 | Hs.122579 | hypothetical protein FLJ10461 | 3.02 |
| | 419910 | AA662913 | Hs.190173 | ESTs, Weakly similar to A46010 X-linked | 3.02 |
| | 424001 | W67883 | Hs.137476 | paternally expressed 10 | 3.01 |
| | 413930 | M86153 | Hs.75618 | RAB11A, member RAS oncogene family | 3.01 |
| 65 | 439924 | A1985897 | Hs.125293 | ESTs | 3.01 |
| | 414343 | AL036166 | Hs.323378 | coated vesicle membrane protein | 3.01 |
| | 432201 | A1538613 | Hs.298241 | Transmembrane protease, serine 3 | 3.00 |
| | 445845 | A1261870 | Hs.145555 | ESTs | 3.00 |
| | 420727 | H75701 | Hs.99886 | complement component 4-binding protein, | 3.00 |
| 70 | 427510 | Z47542 | Hs.179312 | small nuclear RNA activating complex, po | 3.00 |
| | 403637 | NA | | NA | 3.00 |
| | 410947 | AK000305 | Hs.67055 | hypothetical protein FLJ20298 | 3.00 |
| | 413430 | R22479 | Hs.167073 | Homo sapiens cDNA FLJ13047 fis, clone NT | 3.00 |
| | 423575 | C18863 | Hs.163443 | Homo sapiens cDNA FLJ11576 fis, clone HE | 2.99 |
| 75 | 426711 | AA383471 | Hs.180669 | conserved gene amplified in osteosarcoma | 2.99 |
| | 442204 | A1635450 | Hs.21914 | ESTs | 2.98 |
| | 429682 | NM_006306 | Hs.211602 | SMC1 (structural maintenance of chromoso | 2.98 |
| | 419227 | BE537383 | Hs.89739 | cholinergic receptor, nicotinic, beta po | 2.97 |
| | 447233 | AW246333 | Hs.17901 | Homo sapiens, clone IMAGE:3937015, mRNA, | 2.97 |
| | 441826 | AW503803 | Hs.129915 | phosphotriesterase related | 2.97 |
| 80 | 433404 | T32982 | Hs.102720 | ESTs | 2.96 |
| | 450506 | NM_004460 | Hs.418 | fibroblast activation protein, alpha | 2.96 |
| | 423880 | BE278111 | Hs.134200 | DKFZP564C186 protein | 2.96 |
| | 411750 | BE562298 | Hs.71827 | KIAA0112 protein; homolog of yeast ribos | 2.96 |

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|----|--------|-----------|-----------|--|------|
| | 408155 | AB014528 | Hs.43133 | KIAA0628 gene product | 2.96 |
| | 424131 | AA335714 | Hs.199665 | ESTs | 2.96 |
| | 451250 | AA491275 | Hs.236940 | hypothetical protein FLJ12542 | 2.96 |
| 5 | 425154 | NM_001851 | Hs.154850 | collagen, type IX, alpha 1 | 2.96 |
| | 447829 | AI433029 | Hs.164104 | ESTs | 2.95 |
| | 410561 | BE540255 | Hs.6994 | Homo sapiens cDNA: FLJ22044 fis, clone H | 2.95 |
| | 417873 | BE266659 | Hs.293659 | Homo sapiens, Similar to RIKEN cDNA A430 | 2.95 |
| | 452693 | T79153 | Hs.48589 | zinc finger protein 228 | 2.95 |
| 10 | 407742 | AF186252 | Hs.38084 | sulfotransferase family, cytosolic, 1C, | 2.94 |
| | 421430 | AW207555 | Hs.97093 | Homo sapiens cDNA: FLJ23004 fis, clone L | 2.94 |
| | 407995 | AI094748 | Hs.100134 | hypothetical protein FLJ12787 | 2.94 |
| | 413281 | AA861271 | Hs.222024 | transcription factor BMAL2 | 2.94 |
| | 452381 | H23329 | Hs.290880 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.94 |
| 15 | 441020 | W79283 | Hs.35962 | ESTs | 2.94 |
| | 425397 | J04088 | Hs.156346 | topoisomerase (DNA) II alpha (170kD) | 2.94 |
| | 420005 | AW271106 | Hs.133294 | ESTs | 2.93 |
| | 412530 | AA766268 | Hs.266273 | hypothetical protein FLJ13346 | 2.93 |
| | 435602 | AF217515 | Hs.283532 | uncharacterized bone marrow protein BM03 | 2.93 |
| 20 | 447247 | AW369351 | Hs.287955 | Homo sapiens cDNA FLJ13090 fis, clone NT | 2.93 |
| | 443341 | AW631480 | Hs.8688 | ESTs | 2.92 |
| | 436481 | AA379597 | Hs.5199 | HSPC150 protein similar to ubiquitin-con | 2.92 |
| | 410144 | W07189 | Hs.68185 | ESTs, Weakly similar to ARL3_HUMAN ADP-R | 2.92 |
| | 434450 | S78664 | Hs.87 | retinoblastoma-like 1 (p107) | 2.92 |
| 25 | 450402 | BE218027 | Hs.89969 | ESTs | 2.92 |
| | 422026 | U80736 | Hs.110826 | trinucleotide repeat containing 9 | 2.92 |
| | 421562 | AA530994 | Hs.334471 | ghrelin precursor | 2.92 |
| | 410434 | AF051152 | Hs.63668 | toll-like receptor 2 | 2.92 |
| | 422665 | AJ011812 | Hs.119018 | transcription factor NRF | 2.91 |
| 30 | 428966 | AF059214 | Hs.194687 | cholesterol 25-hydroxylase | 2.90 |
| | 412416 | AI628253 | Hs.22580 | alkylglycerone phosphate synthase | 2.90 |
| | 446232 | AI281848 | Hs.194691 | retinoic acid induced 3 | 2.90 |
| | 454600 | AW810001 | | gb:MR4-ST0124-270300-005-b11 ST0124 Homo | 2.90 |
| 35 | 438018 | AK001160 | Hs.5999 | hypothetical protein FLJ10298 | 2.90 |
| | 433252 | AB040957 | Hs.151343 | KIAA1524 protein | 2.90 |
| | 444355 | BE383686 | Hs.191621 | ESTs, Moderately similar to ALU6_HUMAN A | 2.90 |
| | 443054 | AI745185 | Hs.8939 | yes-associated protein 65 kDa | 2.89 |
| | 421308 | AA687322 | Hs.192843 | leucine zipper protein FKSG14 | 2.89 |
| | 411643 | AI924519 | Hs.192570 | hypothetical protein FLJ22028 | 2.89 |
| 40 | 419559 | Y07828 | Hs.91096 | ring finger protein | 2.89 |
| | 433527 | AW235613 | Hs.133020 | ESTs | 2.88 |
| | 426274 | D38122 | Hs.2007 | tumor necrosis factor (ligand) superfamily | 2.88 |
| | 406182 | NA | | NA | 2.88 |
| | 432731 | R31178 | Hs.287820 | fibronectin 1 | 2.88 |
| 45 | 429274 | AI379772 | Hs.99206 | ESTs | 2.87 |
| | 418216 | AA662240 | Hs.283099 | AF15q14 protein | 2.87 |
| | 410166 | AK001376 | Hs.59346 | hypothetical protein FLJ10514 | 2.86 |
| | 452665 | AW839326 | Hs.330414 | ESTs, Moderately similar to S65657 alpha | 2.86 |
| | 424696 | BE439547 | Hs.151903 | GrpE-like protein cochaperone | 2.86 |
| 50 | 410174 | AA306007 | Hs.59461 | DKFZP434C245 protein | 2.85 |
| | 443640 | AI872643 | Hs.134218 | ESTs | 2.85 |
| | 432912 | BE007371 | Hs.200313 | ESTs | 2.85 |
| | 431611 | U58766 | Hs.264428 | tissue specific transplantation antigen | 2.85 |
| | 446565 | D13757 | Hs.311 | phosphoribosyl pyrophosphate amidotransf | 2.85 |
| 55 | 424770 | AA425562 | Hs.11065 | Homo sapiens HDCME13P mRNA, partial cds | 2.84 |
| | 418845 | AA852985 | Hs.89232 | chromobox homolog 5 (Drosophila HP1 alph | 2.84 |
| | 403639 | NA | | NA | 2.84 |
| | 451110 | AI955040 | Hs.265398 | ESTs, Weakly similar to transformation-r | 2.84 |
| | 416185 | AW975861 | Hs.47367 | KIAA1785 protein | 2.84 |
| 60 | 444665 | BE613126 | Hs.47783 | B aggressive lymphoma gene | 2.83 |
| | 423441 | R68649 | Hs.278359 | absent in melanoma 1 like | 2.83 |
| | 450584 | AA040403 | Hs.60371 | ESTs | 2.83 |
| | 420191 | AW003565 | Hs.192323 | Homo sapiens mRNA for FLJ00057 protein, | 2.83 |
| | 425599 | AW366745 | Hs.214140 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.83 |
| 65 | 424408 | AI754813 | Hs.146428 | collagen, type V, alpha 1 | 2.83 |
| | 448769 | N66037 | Hs.38173 | ESTs | 2.82 |
| | 444946 | AW139205 | Hs.156457 | hypothetical protein FLJ22408 | 2.82 |
| | 435347 | AW014873 | Hs.116963 | ESTs | 2.82 |
| | 438435 | AA807142 | Hs.42194 | hypothetical protein FLJ22649 similar to | 2.82 |
| 70 | 427687 | AW003867 | Hs.1570 | histamine receptor H1 | 2.82 |
| | 426951 | AA393636 | Hs.97454 | ESTs | 2.82 |
| | 427970 | AA418187 | Hs.330515 | ESTs | 2.82 |
| | 442577 | AA292998 | Hs.163900 | ESTs | 2.82 |
| | 441016 | AW138653 | Hs.25845 | ESTs | 2.81 |
| 75 | 414774 | X02419 | Hs.77274 | plasminogen activator, urokinase | 2.81 |
| | 417160 | N76497 | Hs.1787 | proteolipid protein 1 (Pelizaeus-Merzbac | 2.81 |
| | 409346 | AL162066 | Hs.54320 | hypothetical protein DKFZp762D096 | 2.81 |
| | 410407 | X66839 | Hs.63287 | carbonic anhydrase IX | 2.81 |
| | 407137 | T97307 | | gb:ye53h05.s1 Soares fetal liver spleen | 2.81 |
| 80 | 435849 | BE305242 | Hs.16098 | claudin 2 | 2.80 |
| | 426695 | AW118191 | Hs.112729 | ESTs | 2.80 |
| | 428301 | AW628666 | Hs.98440 | ESTs, Weakly similar to I38022 hypotheti | 2.80 |
| | 420759 | T11832 | Hs.127797 | Homo sapiens cDNA FLJ11381 fis, clone HE | 2.80 |
| | 421341 | AJ243212 | Hs.279611 | deleted in malignant brain tumors 1 | 2.80 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 419423 | D26488 | Hs.90315 | KIAA0007 protein | 2.79 |
| | 452355 | N54926 | Hs.29202 | G protein-coupled receptor 34 | 2.79 |
| | 425826 | U97698 | Hs.159593 | mucin 6, gastric | 2.79 |
| 5 | 457465 | AW301344 | Hs.122908 | DNA replication factor | 2.79 |
| | 426472 | BE246138 | Hs.30853 | ESTs | 2.79 |
| | 424081 | NM_006413 | Hs.139120 | ribonuclease P (30kD) | 2.78 |
| | 425851 | NM_001490 | Hs.159642 | glucosaminyl (N-acetyl) transferase 1, c | 2.78 |
| | 419236 | AA330447 | Hs.135159 | Homo sapiens cDNA FLJ11481 fis, clone HE | 2.78 |
| 10 | 423430 | AF112481 | Hs.128501 | RAD54, S. cerevisiae, homolog of, B | 2.78 |
| | 410011 | AB020641 | Hs.57856 | PFTAIR protein kinase 1 | 2.78 |
| | 453700 | AB009426 | Hs.560 | apolipoprotein B mRNA editing enzyme, ca | 2.78 |
| | 431250 | BE264649 | Hs.251377 | taxol resistance associated gene 3 | 2.77 |
| | 414043 | AI521210 | Hs.97977 | ESTs | 2.77 |
| | 418054 | NM_002318 | Hs.83354 | lysyl oxidase-like 2 | 2.77 |
| 15 | 439223 | AW238299 | Hs.250618 | UL16 binding protein 2 | 2.76 |
| | 425956 | M50828 | Hs.164568 | fibroblast growth factor 7 (keratinocyte | 2.76 |
| | 437612 | AA827715 | Hs.105153 | Homo sapiens, clone IMAGE:3461987, mRNA, | 2.76 |
| | 426119 | W94997 | Hs.189917 | ESTs | 2.76 |
| 20 | 459574 | AI741122 | Hs.101810 | Homo sapiens cDNA FLJ14232 fis, clone NT | 2.76 |
| | 442339 | BE299668 | Hs.227591 | ESTs, Weakly similar to 1901303A Leu zip | 2.76 |
| | 414334 | AA824298 | Hs.21331 | hypothetical protein FLJ10036 | 2.76 |
| | 418217 | AI910647 | Hs.13442 | ESTs | 2.76 |
| | 420022 | AA256253 | Hs.120817 | ESTs | 2.76 |
| 25 | 408243 | Y00787 | Hs.624 | interleukin 8 | 2.75 |
| | 421346 | Z34277 | Hs.103707 | apomucin | 2.75 |
| | 421379 | Y15221 | Hs.103982 | small inducible cytokine subfamily B (Cy | 2.75 |
| | 425773 | N21279 | Hs.237749 | ESTs | 2.75 |
| | 449611 | AI970394 | Hs.197075 | ESTs | 2.74 |
| 30 | 424827 | AI057094 | Hs.96867 | Homo sapiens cDNA: FLJ23155 fis, clone L | 2.74 |
| | 448621 | AI097144 | Hs.5250 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.74 |
| | 428523 | AW974540 | Hs.98626 | ESTs | 2.73 |
| | 410839 | NM_006849 | Hs.66581 | protein disulfide isomerase | 2.73 |
| | 437380 | AL359577 | Hs.112198 | Homo sapiens mRNA; cDNA DKFZp547M073 (fr | 2.73 |
| 35 | 424641 | AB001106 | Hs.151413 | glia maturation factor, beta | 2.73 |
| | 431708 | AI698136 | Hs.108873 | ESTs | 2.73 |
| | 436209 | AW850417 | Hs.254020 | ESTs, Moderately similar to unnamed prot | 2.73 |
| | 441790 | AW294909 | Hs.132208 | ESTs | 2.73 |
| 40 | 428862 | NM_000346 | Hs.2316 | SRY (sex determining region Y)-box 9 (ca | 2.73 |
| | 409506 | NM_006153 | Hs.54589 | NCK adaptor protein 1 | 2.73 |
| | 423482 | BE280172 | Hs.129228 | galactokinase 2 | 2.73 |
| | 417015 | M83772 | Hs.80876 | flavin containing monooxygenase 3 | 2.72 |
| | 448165 | NM_005591 | Hs.202379 | meiotic recombination (S. cerevisiae) 11 | 2.72 |
| | 448826 | AI580252 | Hs.293246 | ESTs, Weakly similar to putative p150 [H | 2.72 |
| 45 | 447803 | BE620578 | Hs.30858 | ESTs, Weakly similar to S65657 alpha-1C- | 2.72 |
| | 429703 | T93154 | Hs.28705 | ESTs | 2.72 |
| | 448796 | AA147829 | Hs.301431 | endothelial zinc finger protein induced | 2.72 |
| | 410902 | AW809665 | | gb:MR4-ST0124-261099-015-g07 ST0124 Homo | 2.72 |
| 50 | 424745 | AA214618 | Hs.152759 | activator of S phase kinase | 2.72 |
| | 454469 | AW792775 | | gb:CM0-UM0001-010300-258-g10 UM0001 Homo | 2.72 |
| | 458632 | AI744445 | Hs.167073 | Homo sapiens cDNA FLJ13047 fis, clone NT | 2.72 |
| | 452012 | AA307703 | Hs.279766 | kinesin family member 4A | 2.72 |
| | 422109 | S73265 | Hs.1473 | gastrin-releasing peptide | 2.72 |
| | 438008 | AA775026 | Hs.203802 | ESTs | 2.72 |
| 55 | 420552 | AK000492 | Hs.98806 | hypothetical protein | 2.71 |
| | 427038 | NM_014633 | Hs.173288 | KIAA0155 gene product | 2.71 |
| | 409239 | AA740875 | Hs.44307 | ESTs, Moderately similar to I38022 hypot | 2.71 |
| | 425371 | D49441 | Hs.155981 | mesothelin | 2.71 |
| | 439857 | AA847194 | Hs.232002 | ESTs | 2.71 |
| 60 | 455309 | AW894017 | | gb:RC4-NN0027-150400-012-g04 NN0027 Homo | 2.71 |
| | 439580 | AF086401 | Hs.293847 | ESTs, Moderately similar to S65657 alpha | 2.70 |
| | 437257 | AI283085 | Hs.290931 | ESTs, Weakly similar to YFJ7_YEAST HYPOT | 2.70 |
| | 435039 | AW043921 | Hs.130526 | ESTs | 2.70 |
| | 438796 | W67821 | Hs.109590 | genethonin 1 | 2.70 |
| 65 | 407013 | U35637 | | gb:Human nebulin mRNA, partial cds | 2.70 |
| | 445413 | AA151342 | Hs.12677 | CGI-147 protein | 2.70 |
| | 418416 | U11700 | Hs.84999 | ATPase, Cu++ transporting, beta polypept | 2.70 |
| | 441362 | BE614410 | Hs.23044 | RAD51 (S. cerevisiae) homolog (E coli Re | 2.69 |
| | 448045 | AJ297436 | Hs.20166 | prostate stem cell antigen | 2.69 |
| 70 | 441868 | AI400276 | Hs.183485 | ESTs | 2.69 |
| | 449076 | AI627826 | Hs.209109 | ESTs | 2.69 |
| | 427528 | AI077143 | Hs.179565 | minichromosome maintenance deficient (S. | 2.69 |
| | 427617 | D42063 | Hs.199179 | RAN binding protein 2 | 2.69 |
| | 414618 | AI204600 | Hs.96978 | hypothetical protein MGC10764 | 2.69 |
| | 441350 | AB020690 | Hs.7782 | paraneoplastic antigen MA2 | 2.68 |
| 75 | 419310 | AA236233 | Hs.188716 | ESTs | 2.68 |
| | 445279 | R41900 | Hs.22245 | ESTs | 2.68 |
| | 439741 | BE379646 | Hs.6904 | Homo sapiens mRNA full length insert cDN | 2.68 |
| | 446692 | Z44514 | Hs.156829 | Homo sapiens mRNA for KIAA1763 protein, | 2.68 |
| | 449300 | AI656959 | Hs.222165 | ESTs | 2.68 |
| 80 | 444585 | AW170015 | Hs.6594 | ESTs | 2.68 |
| | 444384 | BE174527 | Hs.11065 | Homo sapiens HDOME13P mRNA, partial cds | 2.68 |
| | 448104 | AI674818 | Hs.316433 | Homo sapiens cDNA FLJ11375 fis, clone HE | 2.67 |
| | 446839 | BE091926 | Hs.16244 | mitotic spindle coiled-coil related prot | 2.67 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 428361 | NM_015905 | Hs.183858 | transcriptional intermediary factor 1 | 2.67 |
| | 418971 | AA360392 | Hs.87113 | ESTs | 2.66 |
| | 446152 | AI292036 | Hs.150028 | ESTs | 2.66 |
| 5 | 441553 | AA281219 | Hs.121296 | ESTs | 2.66 |
| | 403548 | | | NA | 2.66 |
| | 452699 | AW295390 | Hs.213062 | ESTs | 2.66 |
| | 449532 | W74653 | Hs.271593 | ESTs, Moderately similar to A47582 B-cel | 2.66 |
| | 453985 | N44545 | Hs.251865 | ESTs | 2.65 |
| 10 | 409956 | AW103354 | Hs.727 | inhibin, beta A (activin A, activin AB a | 2.65 |
| | 409446 | AI561173 | Hs.67688 | ESTs | 2.65 |
| | 422094 | AF129535 | Hs.272027 | F-box only protein 5 | 2.65 |
| | 445462 | AA378776 | Hs.288649 | hypothetical protein MGC3077 | 2.64 |
| | 432670 | AA806536 | Hs.291841 | ESTs | 2.64 |
| 15 | 418634 | AK000064 | Hs.86905 | ATPase, H+ transporting, lysosomal (vacu | 2.64 |
| | 453628 | AW243307 | Hs.83937 | hypothetical protein | 2.64 |
| | 442117 | AW664964 | Hs.128899 | ESTs | 2.64 |
| | 416248 | H99169 | Hs.23450 | mitochondrial ribosomal protein S25 | 2.64 |
| | 414631 | AW970130 | Hs.65406 | ESTs | 2.64 |
| 20 | 423268 | BE386898 | Hs.131162 | ESTs, Weakly similar to ALU5_HUMAN ALU S | 2.64 |
| | 413597 | AW302885 | Hs.117183 | ESTs | 2.63 |
| | 446031 | AI271704 | Hs.18987 | Homo sapiens BAC clone RP11-505D17 from | 2.63 |
| | 450142 | AW207469 | Hs.24485 | chondroitin sulfate proteoglycan 6 (bama | 2.63 |
| | 436304 | AA339622 | Hs.108887 | ESTs | 2.63 |
| 25 | 439832 | T81829 | Hs.14870 | Homo sapiens, Similar to hect domain and | 2.62 |
| | 449207 | AL044222 | Hs.23255 | nucleoporin 153kD | 2.62 |
| | 416111 | AA033813 | Hs.79018 | chromatin assembly factor 1, subunit A (| 2.62 |
| | 414747 | U30872 | Hs.77204 | centromere protein F (350/400kD, mitosis | 2.62 |
| | 423811 | AW299598 | Hs.50895 | homeo box C4 | 2.62 |
| 30 | 439474 | AI824060 | Hs.211501 | ESTs | 2.62 |
| | 417218 | AA005247 | Hs.285754 | met proto-oncogene (hepatocyte growth fa | 2.62 |
| | 408031 | AA081395 | Hs.42173 | Homo sapiens cDNA FLJ10366 fis, clone NT | 2.62 |
| | 442821 | BE391929 | Hs.8752 | transmembrane protein 4 | 2.62 |
| | 418245 | AA088767 | Hs.83883 | transmembrane, prostate androgen induced | 2.62 |
| 35 | 447917 | AL048037 | Hs.164588 | ESTs, Moderately similar to neuronal thr | 2.61 |
| | 424840 | D79987 | Hs.153479 | extra spindle poles, S. cerevisiae, homo | 2.61 |
| | 443268 | AI800271 | Hs.129445 | hypothetical protein FLJ12496 | 2.61 |
| | 403056 | RS8624 | Hs.2186 | eukaryotic translation elongation factor | 2.61 |
| | 433037 | NM_014158 | Hs.279938 | HSPC067 protein | 2.61 |
| 40 | 410358 | AW975168 | Hs.13337 | ESTs, Weakly similar to unnamed protein | 2.60 |
| | 426181 | AA371422 | Hs.334371 | hypothetical protein MGC13096 | 2.60 |
| | 414853 | U31116 | Hs.77501 | sarcoglycan, beta (43kD dystrophin-assoc | 2.60 |
| | 457233 | AI355009 | Hs.221698 | ESTs | 2.60 |
| 45 | 416049 | AI970536 | Hs.16603 | hypothetical protein FLJ13163 | 2.60 |
| | 418946 | AI798841 | Hs.164526 | ESTs | 2.60 |
| | 441891 | AW129145 | Hs.128076 | ESTs | 2.60 |
| | 443742 | AW627805 | Hs.145421 | ESTs | 2.60 |
| | 433868 | AA612960 | Hs.337300 | ESTs | 2.60 |
| | 442717 | R88362 | Hs.180591 | ESTs, Weakly similar to T23976 hypotheti | 2.59 |
| 50 | 444542 | AI161293 | Hs.280380 | aminopeptidase | 2.59 |
| | 452940 | AA029722 | Hs.2173 | fucosyltransferase 4 (alpha (1,3) fucosy | 2.59 |
| | 429170 | NM_001394 | Hs.2359 | dual specificity phosphatase 4 | 2.59 |
| | 417531 | NM_003157 | Hs.1087 | serine/threonine kinase 2 | 2.59 |
| | 401458 | | | NA | 2.58 |
| 55 | 436016 | AA806465 | Hs.121536 | Human DNA sequence from clone RP11-472E5 | 2.58 |
| | 430980 | AW971904 | Hs.122164 | diaphanous (Drosophila, homolog) 3 | 2.58 |
| | 441581 | BE551408 | Hs.127196 | ESTs | 2.58 |
| | 435693 | AI033134 | Hs.119887 | ESTs | 2.58 |
| | 431814 | BE256242 | Hs.270847 | delta-tubulin | 2.58 |
| 60 | 448269 | AW263155 | Hs.14559 | hypothetical protein FLJ10540 | 2.58 |
| | 422765 | AW409701 | Hs.1578 | baculoviral IAP repeat-containing 5 (sur | 2.58 |
| | 456999 | AA319798 | Hs.298581 | eukaryotic translation elongation factor | 2.58 |
| | 425234 | AW152225 | Hs.165909 | ESTs, Weakly similar to I38022 hypotheti | 2.58 |
| | 434423 | NM_006769 | Hs.3844 | LIM domain only 4 | 2.57 |
| 65 | 425782 | U66468 | Hs.159525 | cell growth regulatory with EF-hand doma | 2.57 |
| | 433929 | AI375499 | Hs.27379 | ESTs | 2.57 |
| | 414907 | X90725 | Hs.77597 | polo (Drosophila)-like kinase | 2.57 |
| | 411789 | AF245505 | Hs.72157 | DKFZP564I1922 protein | 2.57 |
| | 435627 | W88774 | Hs.118370 | ESTs | 2.57 |
| 70 | 432168 | AK000563 | Hs.272805 | hypothetical protein FLJ20556 | 2.57 |
| | 432375 | BE536069 | Hs.2962 | S100 calcium-binding protein P | 2.57 |
| | 424057 | AI339874 | Hs.126593 | ESTs | 2.57 |
| | 424315 | AW614850 | Hs.193384 | putative 28 kDa protein | 2.57 |
| | 435663 | AI023707 | Hs.134273 | ESTs | 2.56 |
| 75 | 439277 | R80061 | Hs.164478 | hypothetical protein FLJ21939 similar to | 2.56 |
| | 427747 | AW411425 | Hs.180655 | serine/threonine kinase 12 | 2.56 |
| | 438182 | AW342140 | Hs.182545 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.56 |
| | 421102 | AI470093 | Hs.283085 | protocadherin beta 6 | 2.56 |
| | 445725 | AK000956 | Hs.13209 | hypothetical protein FLJ10094 | 2.56 |
| 80 | 448243 | AW369771 | Hs.52620 | integrin, beta 8 | 2.56 |
| | 442881 | AI023175 | Hs.167022 | ESTs | 2.56 |
| | 422165 | AL041199 | Hs.1481 | histidine decarboxylase | 2.56 |
| | 425843 | BE313280 | Hs.159627 | death associated protein 3 | 2.56 |
| | 448569 | BE382657 | Hs.21486 | signal transducer and activator of trans | 2.55 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| 5 | 416806 | NM_000288 | Hs.79993 | peroxisomal biogenesis factor 7 | 2.55 |
| | 438113 | AI467908 | Hs.8882 | ESTs | 2.55 |
| | 413374 | NM_001034 | Hs.75319 | ribonucleotide reductase M2 polypeptide | 2.55 |
| | 448275 | BE514434 | Hs.20830 | kinesin-like 2 | 2.55 |
| | 419987 | NM_005014 | Hs.94070 | osteomodulin | 2.55 |
| | 439929 | S73205 | | gb:insulin activator factor (human, panc | 2.55 |
| | 452240 | AI591147 | Hs.61232 | ESTs | 2.55 |
| | 417806 | AI867277 | Hs.183733 | ESTs | 2.55 |
| 10 | 421482 | AL135462 | Hs.104715 | inversin | 2.55 |
| | 456884 | AA054679 | Hs.155150 | ribonuclease P (14kD) | 2.55 |
| | 442961 | BE614474 | Hs.289074 | F-box only protein 22 | 2.55 |
| | 411274 | NM_002776 | Hs.69423 | kallikrein 10 | 2.55 |
| | 419359 | AL043202 | Hs.90073 | chromosome segregation 1 (yeast homolog) | 2.54 |
| 15 | 448666 | NM_014953 | Hs.323346 | KIAA1008 protein | 2.54 |
| | 428911 | Z43846 | Hs.194478 | Homo sapiens mRNA; cDNA DKFZp43401572 (f | 2.54 |
| | 452778 | R71338 | Hs.5921 | Homo sapiens cDNA: FLJ21592 fs, clone C | 2.54 |
| | 430733 | AW975920 | Hs.283361 | ESTs | 2.54 |
| | 421184 | NM_003616 | Hs.102456 | survival of motor neuron protein interac | 2.54 |
| 20 | 435361 | AI168596 | Hs.117117 | ESTs | 2.54 |
| | 452833 | BE559681 | Hs.30736 | KIAA0124 protein | 2.54 |
| | 422330 | D30783 | Hs.115263 | epiregulin | 2.54 |
| | 424962 | NM_012288 | Hs.153954 | TRAM-like protein | 2.54 |
| | 430264 | AA470519 | | gb:nc71110.s1 NCI_CGAP_Pr1 Homo sapiens | 2.53 |
| 25 | 447178 | AW594641 | Hs.192417 | ESTs | 2.53 |
| | 411773 | NM_006799 | Hs.72026 | protease, serine, 21 (testisin) | 2.53 |
| | 433571 | AA765256 | Hs.135191 | ESTs, Weakly similar to unnamed protein | 2.53 |
| | 419449 | HI8417 | Hs.57483 | Homo sapiens cDNA FLJ14294 fs, clone PL | 2.53 |
| | 448019 | AW947164 | Hs.195641 | ESTs, Moderately similar to I38022 hypot | 2.53 |
| 30 | 409435 | AI810721 | Hs.95424 | ESTs | 2.52 |
| | 417900 | BE250127 | Hs.82906 | CDC20 (cell division cycle 20, S. cerevi | 2.52 |
| | 431385 | BE178536 | Hs.11090 | membrane-spanning 4-domains, subfamily A | 2.52 |
| | 422314 | K01900 | Hs.73890 | interferon, alpha 8 | 2.52 |
| | 441343 | AI970348 | Hs.132230 | ESTs | 2.52 |
| 35 | 417185 | NM_002484 | Hs.81469 | nucleotide binding protein 1 (E.coli Min | 2.52 |
| | 401747 | | | NA | 2.52 |
| | 448526 | AB028946 | Hs.21361 | KIAA1023 protein | 2.52 |
| | 419488 | AA316241 | Hs.90691 | nucleophosmin/nucleoplasmin 3 | 2.52 |
| | 413627 | BE182082 | Hs.246973 | ESTs | 2.51 |
| 40 | 441285 | NM_002374 | Hs.167 | microtubule-associated protein 2 | 2.51 |
| | 446921 | AB012113 | Hs.16530 | small inducible cytokine subfamily A (Cy | 2.51 |
| | 429357 | AA779725 | Hs.164589 | ESTs | 2.51 |
| | 443171 | BE281128 | Hs.9030 | TONDU | 2.50 |
| | 446636 | AC002563 | Hs.15767 | citron (rho-interacting, serine/threonin | 2.50 |
| 45 | 420795 | AA323037 | Hs.128645 | sorting nexin 16 | 2.50 |
| | 448582 | AI538880 | Hs.94812 | ESTs | 2.50 |
| | 445459 | AI478629 | Hs.158465 | likely ortholog of mouse putative IKK re | 2.50 |
| | 423909 | AI223183 | Hs.135194 | immunoglobulin superfamily, member 6 | 2.50 |
| | 414315 | Z24878 | | gb:HSB65D052 STRATAGENE Human skeletal m | 2.50 |
| 50 | 407568 | AA740964 | Hs.62699 | ESTs | 2.50 |
| | 453911 | AW503857 | Hs.4007 | Sarcolemmal-associated protein | 2.50 |
| | 431571 | AW500486 | Hs.180610 | splicing factor proline/glutamine rich (| 2.50 |
| | 433843 | AW021423 | Hs.112819 | ESTs | 2.50 |
| | 456254 | T19844 | | gb:B711F Heart Homo sapiens cDNA clone B | 2.50 |
| 55 | 403137 | | | NA | 2.50 |
| | 425895 | AI269484 | Hs.161427 | zinc finger protein 215 | 2.50 |
| | 418612 | AB037788 | Hs.224961 | cleavage and polyadenylation specific fa | 2.50 |

TABLE 45B:

| | | |
|----|-------------|---------------------------------------|
| 60 | Pkey: | Unique Eos probaset identifier number |
| | CAT number: | Gene cluster number |
| | Accession: | Genbank accession numbers |

| | | | |
|----|--------|------------|--|
| 65 | Pkey | CAT Number | Accessions |
| | 410784 | 1221005_1 | AW803201 BE079700 BE062940 |
| | 410902 | 1226078_1 | AW809665 AW810108 AW809781 AW809844 |
| | 411765 | 125700_1 | H43346 AA248302 AA095182 |
| | 413170 | 1351880_1 | BE068819 BE068821 BE068825 |
| | 413516 | 1374595_1 | BE145907 BE145796 BE145803 BE145851 BE145923 BE145812 BE145809 BE145852 BE145856 |
| | 414315 | 143512_1 | Z24878 AA494098 F13654 AA494040 AA143127 |
| 70 | 428858 | 296453_1 | AA436760 AW237453 BE327496 N47347 N56967 |
| | 430264 | 315008_1 | AA470519 BE303010 BE302954 BE384120 |
| | 431322 | 331543_1 | AW970622 AA503009 AA502998 AA502989 AA502805 T92188 |
| | 434138 | 380572_1 | AA625804 AW418787 AW074833 AI675642 AI933368 |
| | 436411 | 419334_1 | AW674352 AA715374 Z25205 |
| 75 | 438159 | 45106_-2 | Z83947 |
| | 439929 | 48059_-1 | S73205 |
| | 451105 | 859083_1 | AI761324 AW880941 AW880937 |
| | 452453 | 918300_1 | AI902519 AI902518 AI902516 |
| | 454469 | 1213727_1 | AW792775 BE072509 AW792958 |
| 80 | 454600 | 1226077_1 | AW810001 AW810092 AW810170 AW809884 AW809664 AW810353 AW810428 AW810209 AW810429 AW810154 AW810168 AW809786 AW810006 |
| | 454821 | 1236365_1 | AW809672 AW809694 AW810552 AW810345 AW810432 AW809950 |
| | 455309 | 1278153_1 | AW833504 AW833751 AW833493 AW833341 |
| | | | AW894017 AW893956 AW894032 |

456254 1699246_1 T19844 T11755 T11830 T20136 T11957 R45834 R45828 R15595

TABLE 45C:

5 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA
 Strand: sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 NL_position: Indicates DNA strand from which exons were predicted.
 Indicates nucleotide positions of predicted exons.

| | | | | |
|----|--------|---------|--------|---|
| 10 | Pkey | Ref | Strand | NL_position |
| | 401458 | 9187886 | Plus | 76485-77597 |
| | 401644 | 8576138 | Plus | 82655-83959 |
| | 401747 | 9789672 | Minus | 118596-118816,119119-119244,119609-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011 |
| 15 | 402167 | 8571795 | Plus | 109122-110357 |
| | 402299 | 6693370 | Plus | 23367-25175 |
| | 402408 | 9796239 | Minus | 110326-110491 |
| | 403137 | 9211494 | Minus | 92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337 |
| 20 | 403381 | 9438267 | Minus | 26009-26178 |
| | 403422 | 9665041 | Minus | 151169-151561 |
| | 403548 | 8081591 | Minus | 38760-39352 |
| | 403637 | 8671936 | Minus | 142647-142771,145531-145762 |
| | 403639 | 8671948 | Plus | 113234-113326,115186-115287,119649-119786 |
| 25 | 403776 | 7770611 | Minus | 1414-1513,1624-1756 |
| | 404253 | 9367202 | Minus | 55675-56055 |
| | 404440 | 7528051 | Plus | 80430-81581 |
| | 404766 | 7882612 | Minus | 158681-158882,160838-160973 |
| | 404996 | 6007890 | Plus | 37999-38145,38652-38998,39727-39872,40557-40674,42351-42450 |
| 30 | 405466 | 7767904 | Minus | 64498-64675 |
| | 405770 | 2735037 | Plus | 61057-62075 |
| | 405817 | 4071056 | Plus | 19914-20112,25655-25810 |
| | 406117 | 9142932 | Plus | 54304-54584 |
| | 406182 | 5923650 | Minus | 28256-28935 |

TABLE 46A: ABOUT 1303 GENES UP-REGULATED IN STOMACH CANCER COMPARED TO NORMAL STOMACH

Table 46A lists about 1303 genes up-regulated in stomach cancer compared to normal stomach. These were selected as for Table 45A except using non-malignant stomach specimens in determining the denominator value and the ratio was equal to or greater than 5.0.

40 Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal body tissue

| | | | | | |
|----|--------|-----------|-----------|---|-------|
| 45 | Pkey | ExAccn | UnigenelD | Unigene Title | R1 |
| | 446619 | AU076643 | Hs.313 | secreted phosphoprotein 1 (osteopontin, | 80.50 |
| | 414152 | NM_003248 | Hs.75774 | thrombospondin 4 | 70.52 |
| | 421552 | AF026692 | Hs.105700 | secreted frizzled-related protein 4 | 65.30 |
| 50 | 428698 | AA852773 | Hs.334838 | KIAA1866 protein | 61.90 |
| | 428368 | BE440042 | Hs.83326 | matrix metalloproteinase 3 (stromelysin | 50.60 |
| | 409041 | AB033025 | Hs.50081 | KIAA1199 protein | 44.50 |
| | 452281 | T93500 | Hs.28792 | Homo sapiens cDNA FLJ11041 fis, clone PL | 41.10 |
| | 452862 | AW378065 | Hs.8687 | ESTs | 33.50 |
| 55 | 427585 | D31152 | Hs.179729 | collagen, type X, alpha 1 (Schmid metaph | 32.10 |
| | 424834 | AK001432 | Hs.153408 | Homo sapiens cDNA FLJ10570 fis, clone NT | 26.90 |
| | 428398 | AI249368 | Hs.98558 | ESTs | 26.40 |
| | 409757 | NM_001898 | Hs.123114 | cystatin SN | 25.48 |
| | 403776 | | | NA | 24.90 |
| 60 | 427674 | NM_003528 | Hs.2178 | H2B histone family, member Q | 23.80 |
| | 419968 | X04430 | Hs.93913 | interleukin 6 (interferon, beta 2) | 23.10 |
| | 427108 | AB028976 | Hs.173571 | KIAA1053 protein | 21.76 |
| | 452401 | NM_007115 | Hs.29352 | tumor necrosis factor, alpha-induced pro | 20.70 |
| | 400419 | AF084545 | | NA | 20.40 |
| 65 | 415989 | AI267700 | Hs.317584 | ESTs | 19.80 |
| | 432101 | AI918950 | Hs.123642 | EphA3 | 19.70 |
| | 418994 | AA296520 | Hs.89546 | selectin E (endothelial adhesion molecucl | 19.00 |
| | 452110 | T47667 | Hs.28005 | Homo sapiens cDNA FLJ11309 fis, clone PL | 18.40 |
| | 412652 | AI801777 | Hs.6774 | ESTs | 18.20 |
| 70 | 414430 | AI346201 | Hs.76118 | ubiquitin carboxyl-terminal esterase L1 | 17.71 |
| | 422168 | AA586894 | Hs.112408 | S100 calcium-binding protein A7 (psorias | 17.38 |
| | 448988 | Y09763 | Hs.22785 | gamma-aminobutyric acid (GABA) A recepto | 17.36 |
| | 437446 | AA788946 | Hs.16869 | ESTs, Moderately similar to CA1C RAT COL | 17.00 |
| | 440594 | AW445167 | Hs.126036 | ESTs | 17.00 |
| 75 | 430044 | AA464510 | Hs.152812 | ESTs | 17.00 |
| | 426647 | AA243464 | Hs.294101 | pre-B-cell leukemia transcription factor | 16.90 |
| | 414737 | AI160386 | Hs.125087 | ESTs | 16.50 |
| | 427335 | AA448542 | Hs.251677 | G antigen 7B | 16.30 |
| | 423453 | AW450737 | Hs.128791 | CGI-09 protein | 15.50 |
| 80 | 414569 | AF109298 | Hs.118258 | prostate cancer associated protein 1 | 15.40 |
| | 401961 | NA | | NA | 15.40 |
| | 434551 | BE387162 | Hs.280858 | ESTs, Highly similar to A35661 DNA excis | 15.40 |
| | 432069 | AW975868 | Hs.294100 | ESTs | 15.30 |
| | 434699 | AA643687 | Hs.149425 | Homo sapiens cDNA FLJ11980 fis, clone HE | 15.30 |

| | | | | | |
|----|--------|-----------|-----------|--|-------|
| | 409062 | AL157488 | Hs.50150 | Homo sapiens mRNA: cDNA DKFZp564B182 (lr | 15.30 |
| | 400289 | X07820 | Hs.2258 | matrix metalloproteinase 10 (stromelysin | 15.20 |
| | 415138 | C18356 | Hs.295944 | tissue factor pathway inhibitor 2 | 15.20 |
| 5 | 428820 | AA436187 | Hs.172631 | integrin, alpha M (complement component | 15.19 |
| | 410763 | AF279145 | Hs.8966 | hypothetical protein FLJ21776 | 15.10 |
| | 438639 | AI276360 | Hs.31409 | ESTs | 15.10 |
| | 458997 | AW937420 | Hs.69662 | ESTs | 15.00 |
| | 432731 | R31178 | Hs.287820 | fibronectin 1 | 14.90 |
| 10 | 459247 | N46243 | Hs.110373 | ESTs, Highly similar to T42626 secreted | 14.70 |
| | 451099 | R52795 | Hs.25954 | interleukin 13 receptor, alpha 2 | 14.70 |
| | 452242 | R50956 | Hs.159993 | glycosyltransferase | 14.70 |
| | 426427 | M86699 | Hs.169840 | TTK protein kinase | 14.50 |
| | 439924 | AI985897 | Hs.125293 | ESTs | 14.45 |
| 15 | 414869 | AA157291 | Hs.21479 | ubiquitin 1 | 14.40 |
| | 411573 | AB029000 | Hs.70823 | KIAA1077 protein | 14.40 |
| | 418693 | AI750878 | Hs.87409 | thrombospondin 1 | 14.37 |
| | 421823 | N40850 | Hs.28625 | ESTs | 14.30 |
| | 423903 | M57765 | Hs.1721 | interleukin 11 | 14.20 |
| 20 | 419227 | BES37383 | Hs.89739 | cholinergic receptor, nicotinic, beta po | 14.10 |
| | 447417 | AW732858 | Hs.143067 | KIAA1602 protein | 13.96 |
| | 416406 | D86961 | Hs.79299 | lipoma HMGIC fusion partner-like 2 | 13.90 |
| | 446392 | AF142419 | Hs.15020 | homolog of mouse quaking QKI (KH domain | 13.90 |
| | 412863 | AA121673 | Hs.59757 | zinc finger protein 281 | 13.90 |
| 25 | 449509 | AA001615 | Hs.84561 | ESTs | 13.80 |
| | 440953 | AI683036 | Hs.124135 | Homo sapiens cDNA FLJ13051 fs, clone NT | 13.80 |
| | 432415 | T16971 | Hs.289014 | ESTs, Weakly similar to A43932 mucin 2 p | 13.60 |
| | 428769 | AW207175 | Hs.106771 | ESTs | 13.60 |
| | 416292 | AA179233 | Hs.42390 | nasopharyngeal carcinoma susceptibility | 13.41 |
| 30 | 424580 | AA446539 | Hs.339024 | ESTs, Weakly similar to A46010 X-linked | 13.40 |
| | 438459 | T49300 | Hs.35304 | Homo sapiens cDNA FLJ13655 fs, clone PL | 13.30 |
| | 431958 | X63629 | Hs.2877 | cadherin 3, type 1, P-cadherin (placenta | 13.26 |
| | 406972 | M32053 | | gb:Human H19 RNA gene, complete cds. | 13.19 |
| | 432368 | AW970244 | Hs.162188 | ESTs | 13.16 |
| 35 | 424806 | AA382523 | Hs.105689 | MSTP031 protein | 13.08 |
| | 440351 | AF030933 | Hs.7179 | RAD1 (S. pombe) homolog | 12.98 |
| | 437789 | AI581344 | Hs.127812 | ESTs, Weakly similar to T17330 hypotheti | 12.90 |
| | 447164 | AF026941 | Hs.17518 | Homo sapiens cig5 mRNA, partial sequence | 12.80 |
| | 417412 | X16896 | Hs.82112 | interleukin 1 receptor, type I | 12.80 |
| 40 | 402363 | NA | | NA | 12.78 |
| | 444301 | AK000136 | Hs.10760 | asporin (LRR class 1) | 12.76 |
| | 416783 | AA206186 | Hs.79889 | monocyte to macrophage differentiation-a | 12.60 |
| | 435706 | W31254 | Hs.7045 | GL004 protein | 12.50 |
| | 414618 | AI204600 | Hs.96978 | hypothetical protein MGC10764 | 12.50 |
| 45 | 439737 | AI751438 | Hs.41271 | Homo sapiens mRNA full length insert cDN | 12.49 |
| | 405770 | | | NA | 12.46 |
| | 418678 | NM_001327 | Hs.167379 | cancer/testis antigen | 12.45 |
| | 414132 | AI801235 | Hs.48480 | ESTs | 12.40 |
| | 410434 | AF051152 | Hs.63668 | loli-like receptor 2 | 12.30 |
| 50 | 451092 | AI207256 | Hs.13766 | Homo sapiens mRNA for FLJ00074 protein, | 12.26 |
| | 407891 | AA486620 | Hs.41135 | endomucin-2 | 12.20 |
| | 450506 | NM_004460 | Hs.418 | fibroblast activation protein, alpha | 12.01 |
| | 411213 | AA676939 | Hs.69285 | neuropilin 1 | 12.00 |
| | 436476 | AA326108 | Hs.33829 | bHLH protein DEC2 | 12.00 |
| 55 | 413582 | AW295647 | Hs.71331 | hypothetical protein MGC5350 | 11.90 |
| | 449318 | AW236021 | Hs.78531 | Homo sapiens, Similar to RIKEN cDNA 5730 | 11.90 |
| | 401747 | | | NA | 11.88 |
| | 409619 | AK001015 | Hs.55220 | BCL2-associated athanogene 2 | 11.84 |
| | 432596 | AJ224741 | Hs.278461 | matrilin 3 | 11.80 |
| 60 | 400298 | AA032279 | Hs.61635 | six transmembrane epithelial antigen of | 11.73 |
| | 425688 | U48361 | Hs.159223 | NGF-A binding protein 2 (ERG1 binding p | 11.72 |
| | 407938 | AA905097 | Hs.85050 | phospholamban | 11.70 |
| | 419948 | AB041035 | Hs.93847 | NADPH oxidase 4 | 11.70 |
| | 459645 | AA074346 | Hs.250715 | ESTs | 11.51 |
| 65 | 438462 | AI624122 | Hs.89578 | general transcription factor IIH, polype | 11.50 |
| | 434851 | AA806164 | Hs.116502 | ESTs | 11.50 |
| | 418699 | BES39639 | Hs.173030 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 11.47 |
| | 413453 | AA129640 | Hs.128065 | ESTs | 11.40 |
| | 442028 | AI239437 | Hs.48945 | ESTs | 11.40 |
| 70 | 428479 | Y00272 | Hs.184572 | cell division cycle 2, G1 to S and G2 to | 11.39 |
| | 453313 | BE005771 | Hs.153746 | hypothetical protein FLJ22490 | 11.20 |
| | 421633 | AF121860 | Hs.106260 | sorting nexin 10 | 11.20 |
| | 410339 | AI916499 | Hs.298258 | ESTs | 11.20 |
| | 448111 | AA053486 | Hs.20315 | interferon-induced protein with tetratri | 11.15 |
| 75 | 453857 | AL080235 | Hs.35861 | DKFZP586E1621 protein | 11.15 |
| | 430217 | N47863 | Hs.336901 | ribosomal protein S24 | 11.10 |
| | 452823 | AB012124 | Hs.30696 | transcription factor-like 5 (basic helix | 11.10 |
| | 416530 | U62801 | Hs.79361 | kalikrein 6 (neurosin, zyme) | 11.06 |
| | 416854 | H40164 | Hs.80296 | Purkinje cell protein 4 | 10.90 |
| 80 | 447072 | D61594 | Hs.17279 | tyrosylprotein sulfotransferase 1 | 10.90 |
| | 424882 | AJ379461 | Hs.153636 | far upstream element (FUSE) binding prot | 10.80 |
| | 448593 | AW004854 | Hs.228320 | hypothetical protein FLJ23537 | 10.80 |
| | 408750 | BE294069 | Hs.93581 | hypothetical protein FLJ10512 | 10.80 |
| | 450221 | AA328102 | Hs.24641 | cytoskeleton associated protein 2 | 10.80 |

| | | | | | |
|----|--------|-----------|-----------|--|-------|
| | 436411 | AW674352 | | gb:ba63c07.y1 NIH_MGC_12 Homo sapiens cD | |
| | 441693 | AA384673 | Hs.7943 | RPB5-mediated protein | 10.80 |
| | 414922 | 000723 | Hs.77631 | glycine cleavage system protein H (amino | 10.80 |
| 5 | 441801 | AW242799 | Hs.86366 | ESTs | 10.80 |
| | 417173 | U61397 | Hs.81424 | ubiquitin-like 1 (sentrin) | 10.80 |
| | 415727 | BE501389 | Hs.20848 | ESTs, Weakly similar to APAF_HUMAN APOPT | 10.80 |
| | 414142 | AW368397 | Hs.150042 | Homo sapiens cDNA FLJ14438 fs, clone HE | 10.80 |
| | 421650 | AA781795 | Hs.122587 | ESTs | 10.80 |
| 10 | 439999 | AA115811 | Hs.6838 | ras homolog gene family, member E | 10.80 |
| | 421814 | L12350 | Hs.108623 | thrombospondin 2 | 10.70 |
| | 415060 | AJ223810 | Hs.43213 | ESTs, Weakly similar to IEFS_HUMAN TRANS | 10.69 |
| | 421462 | AF016495 | Hs.104624 | aquaporin 9 | 10.67 |
| | 410444 | W73484 | | gb:zd54e04.s1 Soares_fetal_heart_NbHH19W | 10.66 |
| 15 | 409743 | N48721 | Hs.183506 | hypothetical protein FLJ14213 | 10.61 |
| | 446142 | AJ754693 | Hs.145968 | ESTs | 10.60 |
| | 444114 | T58003 | Hs.10323 | Homo sapiens mRNA from chromosome 5q31-3 | 10.60 |
| | 423020 | AA383092 | Hs.1608 | replication protein A3 (14kD) | 10.60 |
| | 453891 | AB037751 | Hs.36353 | Homo sapiens mRNA full length insert cDN | 10.55 |
| 20 | 417352 | AA195919 | | gb:zp95h09.r1 Stratagene muscle 937209 H | 10.50 |
| | 417866 | AW067903 | Hs.82772 | collagen, type XI, alpha 1 | 10.46 |
| | 427718 | AJ798680 | Hs.25933 | ESTs | 10.42 |
| | 412589 | R28660 | Hs.24305 | ESTs | 10.40 |
| | 433332 | AI367347 | Hs.44898 | Homo sapiens clone TCCCTA00151 mRNA sequ | 10.40 |
| 25 | 424717 | H03754 | Hs.152213 | wingless-type MMTV integration site fami | 10.40 |
| | 450434 | AA166950 | Hs.195870 | hypothetical protein FLJ14991 | 10.30 |
| | 409044 | AI129586 | Hs.33033 | hypothetical protein FLJ14623 | 10.30 |
| | 423600 | AI633559 | Hs.310359 | ESTs | 10.30 |
| | 433819 | AW511097 | Hs.112765 | ESTs | 10.30 |
| 30 | 415076 | NM_000857 | Hs.77890 | guanylate cyclase 1, soluble, beta 3 | 10.18 |
| | 410503 | AW975746 | Hs.188662 | KIAA1702 protein | 10.10 |
| | 433800 | AI034361 | Hs.135150 | lung type-I cell membrane-associated gly | 10.10 |
| | 429357 | AA779725 | Hs.164589 | ESTs | 10.10 |
| | 452838 | U65011 | Hs.30743 | preferentially expressed antigen in meta | 10.00 |
| 35 | 414117 | W88559 | Hs.1787 | proteolipid protein 1 (Pelizaeus-Merzbac | 10.00 |
| | 416198 | H27332 | Hs.99598 | hypothetical protein MGCS338 | 10.00 |
| | 413918 | AW015898 | Hs.71245 | ESTs | 10.00 |
| | 400570 | NA | | NA | 10.00 |
| | 439333 | AW384710 | Hs.125258 | Homo sapiens cDNA FLJ13795 fs, clone TH | 10.00 |
| 40 | 444863 | AW384082 | Hs.104879 | serine (or cysteine) proteinase inhibito | 9.97 |
| | 450101 | AV649989 | Hs.24385 | Human hbc647 mRNA sequence | 9.93 |
| | 434352 | AF129505 | Hs.86492 | small muscle protein, X-linked | 9.90 |
| | 453160 | AI263307 | Hs.239884 | H2B histone family, member L | 9.90 |
| | 433929 | AJ375499 | Hs.27379 | ESTs | 9.90 |
| 45 | 413273 | U75679 | Hs.75257 | stem-loop (histone) binding protein | 9.89 |
| | 437536 | X91221 | Hs.144465 | ESTs | 9.81 |
| | 441350 | AB020690 | Hs.7782 | paraneoplastic antigen MA2 | 9.80 |
| | 452291 | AF015592 | Hs.28853 | CDC7 (cell division cycle 7, S. cerevisi | 9.80 |
| 50 | 438913 | AI380429 | Hs.172445 | ESTs | 9.80 |
| | 417849 | AW291587 | Hs.82733 | nidogen 2 | 9.80 |
| | 424086 | AI351010 | Hs.102267 | lysyl oxidase | 9.78 |
| | 428186 | AW504300 | Hs.295605 | mannosidase, alpha, class 2A, member 2 | 9.72 |
| | 414422 | AA147224 | Hs.337232 | ESTs | 9.70 |
| | 419197 | N48921 | Hs.27441 | KIAA1615 protein | 9.70 |
| 55 | 427660 | AI741320 | Hs.114121 | Homo sapiens cDNA: FLJ23228 fs, clone C | 9.70 |
| | 449347 | AV649748 | Hs.295901 | KIAA0493 protein | 9.70 |
| | 409643 | AW450866 | Hs.257359 | ESTs | 9.70 |
| | 436209 | AW850417 | Hs.254020 | ESTs, Moderately similar to unnamed prot | 9.70 |
| | 439608 | AW864696 | Hs.301732 | hypothetical protein MGCS306 | 9.70 |
| 60 | 430290 | AI734110 | Hs.136355 | ESTs | 9.60 |
| | 447124 | AW976438 | Hs.17428 | RBP1-like protein | 9.60 |
| | 413879 | AA132961 | Hs.212533 | Homo sapiens cDNA: FLJ22572 fs, clone H | 9.60 |
| | 408101 | AW968504 | Hs.123073 | CDC2-related protein kinase 7 | 9.60 |
| | 418067 | AI127958 | Hs.83393 | cystatin E/M | 9.58 |
| 65 | 424001 | W67883 | Hs.137476 | paternally expressed 10 | 9.54 |
| | 443037 | AW500305 | Hs.299166 | syntaxin 7 | 9.50 |
| | 428493 | AK001745 | Hs.184628 | hypothetical protein FLJ10883 | 9.50 |
| | 420170 | U43374 | Hs.95631 | Human normal keratinocyte mRNA | 9.50 |
| | 409269 | AA576953 | Hs.22972 | hypothetical protein FLJ13352 | 9.50 |
| 70 | 443162 | T49951 | Hs.9029 | DKFZP434G032 protein | 9.50 |
| | 444381 | BE387335 | Hs.283713 | ESTs, Weakly similar to S64054 hypotheti | 9.45 |
| | 424026 | AI798295 | Hs.137576 | ribosomal protein L34 pseudogene 1 | 9.43 |
| | 440052 | AI633744 | Hs.195648 | ESTs, Weakly similar to I38022 hypotheti | 9.40 |
| | 403137 | | | NA | 9.40 |
| 75 | 418051 | AW192535 | Hs.19479 | ESTs | 9.37 |
| | 418701 | AA814948 | Hs.96343 | ESTs, Weakly similar to ALUC_HUMAN !!!! | 9.35 |
| | 430291 | AV660345 | Hs.238126 | CGI-49 protein | 9.30 |
| | 426137 | AL040683 | Hs.167031 | DKFZP566D133 protein | 9.30 |
| | 400195 | NA | | NA | 9.30 |
| 80 | 411529 | AA430348 | Hs.317596 | Homo sapiens cDNA FLJ12927 fs, clone NT | 9.30 |
| | 423936 | U77629 | Hs.135639 | achaele-scutle complex (Drosophila) horn | 9.20 |
| | 414259 | W44633 | Hs.301296 | Homo sapiens cDNA: FLJ23131 fs, clone L | 9.20 |
| | 416661 | AA634543 | Hs.79440 | IGF-II mRNA-binding protein 3 | 9.20 |
| | 405543 | NA | | NA | 9.20 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 420900 | AL045633 | Hs.44269 | ESTs | 9.11 |
| | 450757 | BE081050 | Hs.31570 | ESTs, Weakly similar to KIAA1324 protein | 9.10 |
| | 410929 | H47233 | Hs.30643 | ESTs | 9.10 |
| 5 | 427319 | AW631495 | Hs.27135 | B-cell receptor-associated protein BAP29 | 9.10 |
| | 443745 | AB039670 | Hs.9728 | ALEX1 protein | 9.10 |
| | 436574 | AW293527 | Hs.126465 | ESTs | 9.10 |
| | 407192 | AA609200 | | gb:af12e02.s1 Soares_testis_NHT Homo sap | 9.08 |
| | 426075 | AW513691 | Hs.270149 | ESTs, Weakly similar to 2109260A B cell | 9.07 |
| 10 | 408778 | AI500519 | Hs.63382 | hypothetical protein PRO2714 | 9.03 |
| | 434542 | AA769310 | Hs.61260 | hypothetical protein FLJ13164 | 9.00 |
| | 404440 | | | NA | 9.00 |
| | 407168 | R45175 | Hs.117183 | ESTs | 9.00 |
| | 451678 | AA374181 | Hs.26799 | DKFZP564D0764 protein | 9.00 |
| | 431946 | AJ018336 | Hs.131730 | ESTs | 8.92 |
| 15 | 408875 | NM_015434 | Hs.48604 | DKFZP434B168 protein | 8.90 |
| | 409928 | AL137163 | Hs.57549 | hypothetical protein dJ47384 | 8.90 |
| | 430294 | AI538226 | Hs.32976 | guanine nucleotide binding protein 4 | 8.89 |
| | 445029 | AF196481 | Hs.12256 | mdline 2 | 8.86 |
| | 442717 | R88362 | Hs.180591 | ESTs, Weakly similar to T23976 hypotheti | 8.80 |
| 20 | 409089 | NM_014781 | Hs.50421 | KIAA0203 gene product | 8.80 |
| | 419261 | X07876 | Hs.89791 | wingless-type MMTV integration site fami | 8.80 |
| | 416190 | N54000 | | gb:yy99d02.r1 Soares_multiple_sclerosis_ | 8.80 |
| | 444783 | AK001468 | Hs.62180 | anillin (Drosophila Scraps homolog), act | 8.77 |
| | 416440 | AI823912 | Hs.79335 | Homo sapiens, Similar to SVW/SNF related | 8.76 |
| 25 | 421262 | AA286746 | Hs.9343 | Homo sapiens cDNA FLJ14265 fis, clone PL | 8.70 |
| | 441031 | AI110684 | Hs.7645 | fibrinogen, B beta polypeptide | 8.70 |
| | 452234 | AW084176 | Hs.223296 | ESTs, Weakly similar to I38022 hypotheti | 8.70 |
| | 452822 | X85689 | Hs.288617 | hypothetical protein FLJ22621 | 8.70 |
| | 430462 | AI584156 | Hs.105640 | Homo sapiens, clone IMAGE:4139775, mRNA, | 8.65 |
| 30 | 426457 | AW894667 | Hs.169965 | chimerin (chimaerin) 1 | 8.65 |
| | 412054 | W87482 | Hs.302209 | ESTs | 8.64 |
| | 450236 | AW162998 | Hs.24684 | KIAA1376 protein | 8.63 |
| | 418782 | AJ792648 | Hs.14665 | ESTs | 8.60 |
| | 452631 | AI188658 | Hs.87496 | ESTs | 8.60 |
| 35 | 425268 | AI807883 | Hs.180059 | Homo sapiens cDNA FLJ20653 fis, clone KA | 8.60 |
| | 432014 | H66741 | Hs.38540 | ESTs, Weakly similar to ALU4_HUMAN ALU S | 8.60 |
| | 440270 | NM_015986 | Hs.7120 | cytokine receptor-like molecule 9 | 8.60 |
| | 414784 | NM_000344 | Hs.288986 | survival of motor neuron 1, telomeric | 8.60 |
| 40 | 426809 | BE313114 | Hs.29706 | ESTs | 8.60 |
| | 419704 | AA429104 | Hs.45057 | ESTs | 8.60 |
| | 452909 | NM_015368 | Hs.30985 | pannexin 1 | 8.60 |
| | 432639 | AW973785 | | gb:EST385886 MAGE resequences, MAGM Homo | 8.60 |
| | 430418 | R98852 | Hs.35029 | heart and neural crest derivatives expre | 8.58 |
| 45 | 450480 | X82125 | Hs.25040 | zinc finger protein 239 | 8.58 |
| | 444984 | H15474 | Hs.132898 | fatty acid desaturase 1 | 8.58 |
| | 419086 | NM_000216 | Hs.89591 | Kallmann syndrome 1 sequence | 8.57 |
| | 430518 | AW363687 | Hs.82916 | chaperonin containing TCP1, subunit 6A (| 8.50 |
| | 424735 | U31875 | Hs.272499 | short-chain alcohol dehydrogenase family | 8.50 |
| 50 | 414061 | NM_000699 | Hs.300280 | amylase, alpha 2A; pancreatic | 8.50 |
| | 407894 | AJ278313 | Hs.41143 | phosphoinositide-specific phospholipase | 8.50 |
| | 441079 | AW150697 | Hs.107418 | ESTs | 8.50 |
| | 419354 | M62839 | Hs.1252 | apolipoprotein H (beta-2-glycoprotein I) | 8.50 |
| | 418618 | U66097 | Hs.86724 | GTP cyclohydrolase 1 (dopa-responsive dy | 8.50 |
| 55 | 416565 | AW000960 | Hs.44970 | endoplasmic reticulum resident protein 5 | 8.50 |
| | 441540 | C01367 | Hs.127128 | ESTs | 8.50 |
| | 416434 | AW163045 | Hs.79334 | nuclear factor, interleukin 3 regulated | 8.50 |
| | 417801 | AA417383 | Hs.82582 | integrin, beta-like 1 (with EGF-like rep | 8.50 |
| | 426855 | AL117427 | Hs.172778 | Homo sapiens mRNA: cDNA DKFZp566P013 (tr | 8.48 |
| 60 | 436515 | AJ278111 | Hs.195292 | putative tumor antigen | 8.43 |
| | 416315 | AA179483 | Hs.73605 | ESTs | 8.42 |
| | 408432 | AW195262 | | gb:xn67b05.x1 NCL_CGAP_CML1 Homo sapiens | 8.40 |
| | 410094 | BE147897 | Hs.58593 | general transcription factor IIF, polype | 8.40 |
| | 419198 | AA234938 | Hs.87384 | ESTs | 8.36 |
| 65 | 448920 | AW408009 | Hs.22580 | adlyglycerone phosphate synthase | 8.36 |
| | 410305 | AF030409 | Hs.62185 | solute carrier family 9 (sodium/hydrogen | 8.31 |
| | 408687 | AL110280 | Hs.301152 | Homo sapiens mRNA: cDNA DKFZp434F053 (tr | 8.30 |
| | 427707 | NM_005578 | Hs.180398 | LIM domain-containing preferred transloc | 8.30 |
| | 459060 | H89244 | Hs.303627 | heterogeneous nuclear ribonucleoprotein | 8.30 |
| | 451957 | AI796320 | Hs.10299 | Homo sapiens cDNA FLJ13545 fis, clone PL | 8.30 |
| 70 | 443977 | AL120986 | Hs.150627 | ESTs, Weakly similar to I38022 hypotheti | 8.30 |
| | 457997 | AA806616 | Hs.209523 | ESTs | 8.30 |
| | 451934 | AI540842 | Hs.61082 | ESTs | 8.30 |
| | 404335 | | | NA | 8.30 |
| 75 | 445073 | AW291389 | Hs.13056 | hypothetical protein FLJ13920 | 8.30 |
| | 431566 | AF176012 | Hs.260720 | J domain containing protein 1 | 8.29 |
| | 446307 | TS0083 | Hs.9094 | ESTs | 8.28 |
| | 423928 | AA332680 | | gb:EST36768 Embryo, 8 week I Homo sapien | 8.26 |
| | 436420 | AA443966 | Hs.31595 | ESTs | 8.25 |
| | 426110 | NM_002913 | Hs.166563 | replication factor C (activator 1) 1 (14 | 8.25 |
| 80 | 442988 | AI026130 | Hs.131683 | ESTs | 8.25 |
| | 402408 | NA | | NA | 8.24 |
| | 438707 | L08239 | Hs.5326 | amino acid system N transporter 2; porcu | 8.23 |
| | 425770 | NM_014363 | Hs.159492 | spastic ataxia of Charlevoix-Saguenay (s | 8.22 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 448704 | AW080932 | Hs.249247 | heterogeneous nuclear protein similar to | 8.21 |
| | 452682 | AA456193 | Hs.9071 | progesterone membrane binding protein | 8.20 |
| | 411984 | NM_005419 | Hs.72988 | signal transducer and activator of trans | 8.20 |
| 5 | 420018 | U56387 | Hs.94376 | proprotein convertase subtilisin/kexin I | 8.20 |
| | 437048 | AA743240 | Hs.91582 | ESTs | 8.20 |
| | 424653 | AW977534 | Hs.151469 | calcium/calmodulin-dependent serine prot | 8.20 |
| | 447066 | BE167667 | Hs.32163 | ESTs | 8.20 |
| | 425932 | M81650 | Hs.19668 | semenogelin I | 8.20 |
| 10 | 431819 | AA515995 | Hs.152334 | ESTs | 8.20 |
| | 431810 | X67155 | Hs.270845 | kinesin-like 5 (mitotic kinesin-like pro | 8.20 |
| | 459702 | AI204995 | | gb:an03c03.x1 Stratagene schizo brain S1 | 8.20 |
| | 406687 | M31126 | Hs.272620 | pregnancy specific beta-1-glycoprotein 9 | 8.18 |
| | 413109 | AW389845 | Hs.110855 | ESTs | 8.17 |
| | 424720 | M89907 | Hs.152292 | SWI/SNF related, matrix associated, acti | 8.16 |
| 15 | 424335 | AW021508 | Hs.28170 | ESTs | 8.10 |
| | 453096 | AW294631 | Hs.11325 | ESTs | 8.10 |
| | 427738 | NM_000318 | Hs.180612 | peroxisomal membrane protein 3 (35kD, Ze | 8.10 |
| | 457796 | AA913389 | Hs.126691 | ESTs | 8.10 |
| 20 | 429340 | N35938 | Hs.199429 | Homo sapiens mRNA; cDNA DKFZp434M2216 (f | 8.10 |
| | 445165 | AV652831 | | gb:AV652831 GLC Homo sapiens cDNA clone | 8.08 |
| | 418046 | W49670 | Hs.56044 | ESTs | 8.06 |
| | 426269 | H15302 | Hs.168950 | Homo sapiens mRNA; cDNA DKFZp566A1046 (f | 8.04 |
| | 439451 | AF086270 | Hs.278554 | heterochromatin-like protein 1 | 8.02 |
| 25 | 419559 | Y07828 | Hs.91096 | ring finger protein | 8.02 |
| | 409268 | AA625304 | Hs.188554 | ESTs | 8.00 |
| | 447207 | AA442233 | Hs.17731 | hypothetical protein FLJ12892 | 8.00 |
| | 446977 | AW863613 | Hs.156798 | ESTs | 8.00 |
| | 424565 | AW102723 | Hs.75295 | guanylate cyclase 1, soluble, alpha 3 | 8.00 |
| 30 | 407013 | U35637 | | gb:Human nebulin mRNA, partial cds | 7.99 |
| | 414523 | AU076633 | Hs.76353 | serine (or cysteine) proteinase inhibito | 7.98 |
| | 440637 | AW900115 | Hs.7309 | Homo sapiens clone 23741 mRNA sequence | 7.96 |
| | 417076 | AW973454 | Hs.238442 | ESTs, Moderately similar to ALU7_HUMAN A | 7.95 |
| | 425921 | NM_007231 | Hs.162211 | solute carrier family 6 (neurotransmitte | 7.94 |
| 35 | 415585 | R59946 | Hs.184852 | KIAA1553 protein | 7.92 |
| | 453331 | AI240665 | Hs.8895 | ESTs | 7.92 |
| | 445527 | W39694 | Hs.83286 | ESTs, Weakly similar to S14747 sphingomy | 7.90 |
| | 417318 | AW953937 | Hs.12891 | ESTs | 7.90 |
| | 429393 | AA383024 | Hs.201603 | Homo sapiens mRNA; cDNA DKFZp434D0917 (f | 7.90 |
| 40 | 444769 | AI191650 | Hs.221436 | ESTs | 7.90 |
| | 444272 | AI138596 | Hs.154619 | ESTs | 7.90 |
| | 425264 | AA353953 | Hs.20369 | ESTs, Weakly similar to gonadotropin ind | 7.90 |
| | 412642 | BE244598 | Hs.809 | hepatocyte growth factor (hepatopoietin A; | 7.90 |
| | 453765 | BE279901 | Hs.35091 | hypothetical protein FLJ10775 | 7.90 |
| 45 | 421558 | AB011125 | Hs.105749 | KIAA0553 protein | 7.90 |
| | 446444 | AI743737 | Hs.24370 | ESTs | 7.90 |
| | 420000 | AB036063 | Hs.94262 | p53-inducible ribonucleotide reductase s | 7.86 |
| | 437237 | BE513073 | | gb:601171435F1 NIH_MGC_15 Homo sapiens c | 7.86 |
| | 409582 | R27430 | Hs.271565 | ESTs | 7.84 |
| 50 | 419235 | AW470411 | Hs.288433 | neurotrimin | 7.83 |
| | 439620 | AA838727 | Hs.124405 | ESTs, Weakly similar to A46010 X-linked | 7.82 |
| | 441690 | R81733 | Hs.33106 | ESTs | 7.80 |
| | 417735 | AA188175 | Hs.82506 | KIAA1254 protein | 7.80 |
| | 441795 | N58115 | Hs.21137 | AD024 protein | 7.80 |
| 55 | 442992 | AI914699 | Hs.13297 | ESTs | 7.80 |
| | 422554 | AA312219 | Hs.296338 | ESTs | 7.80 |
| | 423123 | NM_012247 | Hs.124027 | SELENOPHOSPHATE SYNTHETASE ; Human selen | 7.80 |
| | 428627 | BE002993 | Hs.187660 | putative Rab5 GDP/GTP exchange factor ho | 7.80 |
| | 429228 | AI553633 | Hs.337139 | ESTs | 7.80 |
| 60 | 429399 | AA452244 | Hs.16727 | ESTs | 7.80 |
| | 436396 | AI683487 | Hs.152213 | wingless-type MMTV integration site fami | 7.77 |
| | 455510 | AA422029 | Hs.143640 | ESTs, Weakly similar to hyperpolarizatio | 7.76 |
| | 429396 | AW954598 | Hs.201626 | Homo sapiens clone 25015 mRNA sequence | 7.75 |
| | 453439 | AI572438 | Hs.32976 | guanine nucleotide binding protein 4 | 7.75 |
| 65 | 410561 | BE540255 | Hs.6994 | Homo sapiens cDNA: FLJ22044 fis, clone H | 7.71 |
| | 442875 | BE623003 | Hs.23625 | Homo sapiens clone TCCCTA00142 mRNA sequ | 7.71 |
| | 428655 | H05769 | Hs.188757 | Homo sapiens, clone MGC:5564, mRNA, comp | 7.70 |
| | 413374 | NM_001034 | Hs.75319 | ribonucleotide reductase M2 polypeptide | 7.70 |
| | 404996 | | | NA | 7.70 |
| 70 | 418947 | W52990 | Hs.22860 | ESTs | 7.70 |
| | 427401 | U20582 | Hs.2149 | actin like protein | 7.70 |
| | 410748 | BE383816 | Hs.12532 | chromosome 1 open reading frame 21 | 7.70 |
| | 426262 | AI792141 | Hs.196270 | folate transporter/carrier | 7.70 |
| | 446955 | AW613138 | Hs.156747 | ESTs | 7.70 |
| 75 | 449199 | AI990122 | Hs.196988 | ESTs | 7.70 |
| | 443212 | AW269515 | Hs.102500 | hypothetical protein FLJ20481 | 7.70 |
| | 446155 | AI553695 | Hs.159422 | Homo sapiens cDNA FLJ13997 fis, clone Y7 | 7.70 |
| | 427164 | AB037721 | Hs.173871 | KIAA1300 protein | 7.70 |
| | 452627 | AI122843 | Hs.184319 | ESTs, Weakly similar to KIAA1005 protein | 7.70 |
| 80 | 452588 | AA889120 | Hs.110637 | homeo box A10 | 7.70 |
| | 451838 | AW005866 | Hs.193969 | ESTs | 7.67 |
| | 422956 | BE545072 | Hs.122579 | hypothetical protein FLJ10461 | 7.66 |
| | 451227 | R84429 | Hs.151944 | ESTs, Weakly similar to high-risk human | 7.66 |
| | 450701 | H39960 | Hs.288467 | Homo sapiens cDNA FLJ12280 fis, clone MA | 7.65 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 432695 | D63480 | Hs.278634 | KIAA0146 protein | 7.63 |
| | 447476 | BE293466 | Hs.20880 | ESTs, Weakly similar to I38022 hypotheti | 7.60 |
| | 447289 | AW247017 | Hs.36978 | melanoma antigen, family A, 3 | 7.60 |
| 5 | 447505 | AL049266 | Hs.18724 | Homo sapiens mRNA: cDNA DKFZp564F093 (fr | 7.60 |
| | 423065 | R96158 | Hs.267130 | Homo sapiens, clone MGC:5406, mRNA, comp | 7.60 |
| | 437396 | BE140396 | Hs.21621 | hypothetical protein DKFZp7620076 | 7.60 |
| | 450628 | AW382884 | Hs.204715 | ESTs | 7.60 |
| | 418995 | H39599 | Hs.294008 | ESTs | 7.60 |
| 10 | 416402 | NM_000715 | Hs.1012 | complement component 4-binding protein, NA | 7.60 |
| | 405545 | | | hypothetical protein MGC16275 | 7.60 |
| | 440866 | AJ703103 | Hs.271360 | ESTs | 7.60 |
| | 421281 | AI299139 | Hs.17517 | cartilage intermediate layer protein, nu | 7.60 |
| | 424634 | NM_003613 | Hs.151407 | ESTs, Moderately similar to I38022 hypot | 7.60 |
| 15 | 421041 | N36914 | Hs.14691 | hypothetical protein FLJ11457 | 7.54 |
| | 453311 | AW104911 | Hs.126707 | hypothetical protein MGC15754 | 7.50 |
| | 453060 | AW294092 | Hs.21594 | hypothetical protein FLJ14813 | 7.50 |
| | 417655 | AA780791 | Hs.14014 | serine/threonine kinase 2 | 7.50 |
| | 417531 | NM_003157 | Hs.1087 | solute carrier family 7 (cationic amino | 7.50 |
| 20 | 444099 | D87432 | Hs.10315 | dickkopf (Xenopus laevis) homolog 1 | 7.50 |
| | 407853 | AA336797 | Hs.40499 | fibronectin leucine rich transmembrane p | 7.50 |
| | 408920 | AL120071 | Hs.48998 | ESTs, Weakly similar to I38022 hypotheti | 7.48 |
| | 447806 | W03616 | Hs.10432 | ESTs | 7.48 |
| | 424748 | AA346257 | Hs.134933 | ESTs | 7.46 |
| 25 | 421089 | AB037771 | Hs.101799 | KIAA1350 protein | 7.42 |
| | 444856 | AI888057 | Hs.12097 | acylphosphatase 1, erythrocyte (common) | 7.41 |
| | 447425 | AI963747 | Hs.18573 | ESTs, Weakly similar to alternatively sp | 7.40 |
| | 418450 | R84397 | Hs.193651 | ESTs, Weakly similar to MUC2_HUMAN MUCIN | 7.40 |
| | 434539 | AW748078 | Hs.214410 | ESTs | 7.40 |
| 30 | 437036 | AI571514 | Hs.133022 | hemoglobin, alpha 2 | 7.40 |
| | 414680 | AA743331 | Hs.272572 | Homo sapiens cDNA: FLJ21880 fis, clone H | 7.40 |
| | 451815 | AW974911 | Hs.184793 | ESTs | 7.40 |
| | 433577 | AW007080 | Hs.8817 | ESTs, Moderately similar to S65657 alpha | 7.40 |
| | 453652 | AW009640 | Hs.28368 | transcription factor NRF | 7.40 |
| 35 | 422655 | AJ011812 | Hs.119018 | zinc finger protein | 7.40 |
| | 424188 | AW954552 | Hs.142634 | gb:zn43e07.s1 Stratagene HeLa cell s3 93 | 7.40 |
| | 407300 | AA102616 | | hypothetical protein DKFZp434A1315 | 7.40 |
| | 431494 | AA991355 | Hs.298312 | ESTs | 7.40 |
| | 452958 | AA883929 | Hs.40527 | hypothetical protein FLJ20212 | 7.40 |
| 40 | 418763 | AK000219 | Hs.88367 | ESTs, Weakly similar to A47582 B-cell gr | 7.40 |
| | 428279 | AA425310 | Hs.155766 | Homo sapiens mRNA: cDNA DKFZp434K2172 (f | 7.40 |
| | 449570 | F07693 | Hs.23869 | ESTs, Weakly similar to putative p150 [H | 7.40 |
| | 449601 | AA461509 | Hs.293565 | ESTs | 7.40 |
| | 438490 | AW593272 | Hs.301299 | highly expressed in cancer, rich in leuc | 7.40 |
| 45 | 410044 | BE566742 | Hs.58169 | ras homolog gene family, member B | 7.38 |
| | 429509 | AW614420 | Hs.204354 | itchy (mouse homolog) E3 ubiquitin prote | 7.38 |
| | 433393 | AF038564 | Hs.98074 | pleiomorphic adenoma gene-like 1 | 7.37 |
| | 434096 | AW662958 | Hs.75825 | ESTs | 7.36 |
| | 425773 | N21279 | Hs.237749 | RAN binding protein 8 | 7.36 |
| 50 | 422755 | T25365 | Hs.119587 | Homo sapiens cDNA FLJ13585 fis, clone PL | 7.35 |
| | 410566 | AA373210 | Hs.43047 | ESTs | 7.35 |
| | 412851 | AI826502 | Hs.106149 | E2F transcription factor 3 | 7.35 |
| | 418661 | NM_001949 | Hs.1189 | ESTs | 7.34 |
| | 436246 | AW450963 | Hs.119991 | kinesin-like protein 2 | 7.33 |
| 55 | 433159 | AB035898 | Hs.150587 | GPI-anchored metastasis-associated prote | 7.32 |
| | 444781 | NM_014400 | Hs.11950 | DC32 | 7.31 |
| | 453878 | AW964440 | Hs.19025 | Niemann-Pick disease, type C1 | 7.31 |
| | 414696 | AF002020 | Hs.76918 | novel Ras family protein | 7.30 |
| 60 | 402250 | AV655272 | Hs.20252 | ESTs | 7.30 |
| | 439039 | AI656707 | Hs.48713 | interleukin 18 (interferon-gamma-inducin | 7.30 |
| | 417976 | BE565892 | Hs.83077 | hypothetical protein DKFZp434K1421 | 7.30 |
| | 419436 | AA991639 | Hs.242413 | aspartyl-tRNA synthetase | 7.30 |
| | 417006 | AW673606 | Hs.80758 | hypothetical protein NUF2R | 7.30 |
| | 425420 | BE536911 | Hs.234545 | tachykinin receptor 2 | 7.29 |
| 65 | 425889 | M57414 | Hs.161305 | ESTs | 7.26 |
| | 442969 | AI025499 | Hs.132238 | homolog of mouse transient receptor pote | 7.25 |
| | 446360 | N42553 | Hs.267914 | NOD2 protein | 7.25 |
| | 438022 | AW517524 | Hs.135201 | gb:EST66864 Fetal lung III Homo sapiens | 7.24 |
| 70 | 407183 | AA358015 | | hypothetical protein similar to small G | 7.24 |
| | 429882 | AA278898 | Hs.225979 | transcription elongation factor A (SII)- | 7.22 |
| | 420120 | AL049610 | Hs.95243 | NA | 7.20 |
| | 400212 | | | ESTs | 7.20 |
| | 431812 | AA515902 | Hs.130650 | 15 kDa selenoprotein | 7.20 |
| | 419481 | AI879195 | Hs.90606 | ESTs | 7.20 |
| 75 | 447078 | AW885727 | Hs.301570 | ESTs | 7.20 |
| | 413200 | AA127395 | Hs.222414 | ESTs | 7.20 |
| | 411750 | BE562298 | Hs.71827 | KIAA0112 protein; homolog of yeast ribos | 7.20 |
| | 439901 | N73885 | Hs.124169 | ESTs | 7.20 |
| | 411815 | AA156679 | Hs.125790 | leucine-rich repeat-containing 2 | 7.20 |
| 80 | 459279 | AW814996 | | gb:MR1-ST0206-170400-024-h09 ST0206 Homo | 7.20 |
| | 445263 | H57646 | Hs.42586 | KIAA1560 protein | 7.20 |
| | 413801 | M62246 | Hs.35406 | ESTs, Highly similar to unnamed protein | 7.20 |
| | 418407 | AL044818 | Hs.84928 | nuclear transcription factor Y, beta | 7.20 |
| | 452221 | C21322 | Hs.288057 | hypothetical protein FLJ22242 | 7.20 |

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|----|--------|-----------|-----------|--|------|
| | 425202 | AW962282 | Hs.152049 | ESTs, Weakly similar to I38022 hypothe | 7.20 |
| | 403764 | | | NA | 7.20 |
| | 416896 | A1752862 | Hs.5638 | KIAA1572 protein | 7.20 |
| 5 | 416636 | N32536 | Hs.42645 | ESTs | 7.20 |
| | 428071 | AF212848 | Hs.182339 | ets homologous factor | 7.20 |
| | 450142 | AW207469 | Hs.24485 | chondroitin sulfate proteoglycan 6 (barn | 7.18 |
| | 451017 | BE391847 | Hs.181173 | hypothetical protein MGC10771 | 7.17 |
| | 409759 | N40285 | Hs.81182 | histamine N-methyltransferase | 7.16 |
| 10 | 452448 | AW182440 | Hs.61389 | ESTs, Weakly similar to unnamed protein | 7.16 |
| | 427951 | A1826125 | Hs.43546 | ESTs | 7.16 |
| | 407939 | W05608 | Hs.312679 | ESTs, Weakly similar to A49019 dynein he | 7.15 |
| | 419457 | AA243146 | Hs.209334 | ESTs, Moderately similar to S23A_HUMAN P | 7.12 |
| | 411769 | A1694575 | Hs.27207 | KIAA0982 protein | 7.11 |
| 15 | 430355 | NM_006219 | Hs.239818 | phosphoinositide-3-kinase, catalytic, be | 7.10 |
| | 419511 | AA429750 | Hs.75113 | general transcription factor IIIA | 7.10 |
| | 409032 | AW301807 | Hs.297260 | ESTs | 7.10 |
| | 424539 | L02911 | Hs.150402 | actin A receptor, type I | 7.10 |
| | 439221 | AA737106 | Hs.32250 | ESTs, Moderately similar to I78885 serin | 7.10 |
| 20 | 430719 | AA488988 | Hs.293796 | ESTs | 7.10 |
| | 408020 | AA127940 | Hs.62781 | ESTs | 7.10 |
| | 420218 | AW958037 | Hs.286 | ribosomal protein L4 | 7.10 |
| | 443487 | A1073491 | Hs.269887 | ESTs, Highly similar to KPBB_HUMAN PHOSP | 7.10 |
| | 414865 | AA157155 | Hs.274414 | hypothetical protein FLJ14457 | 7.10 |
| 25 | 428724 | AL390128 | Hs.191268 | KIAA1530 protein | 7.10 |
| | 413293 | AL047483 | Hs.302498 | GTP-binding protein homologous to Saccha | 7.10 |
| | 419126 | A1810144 | Hs.135276 | ESTs | 7.09 |
| | 437044 | AL035864 | Hs.69517 | cDNA for differentially expressed CO16 g | 7.09 |
| | 433730 | AK002135 | Hs.3542 | hypothetical protein FLJ11273 | 7.07 |
| 30 | 417381 | AF164142 | Hs.82042 | solute carrier family 23 (nucleobase tra | 7.07 |
| | 457019 | AA421844 | Hs.12830 | hypothetical protein | 7.07 |
| | 409697 | AB018348 | Hs.55947 | KIAA0805 protein | 7.06 |
| | 400977 | NA | | NA | 7.06 |
| | 436668 | AA831857 | Hs.209071 | ESTs | 7.03 |
| 35 | 451684 | AF216751 | Hs.26813 | COA14 | 7.03 |
| | 404029 | | | NA | 7.02 |
| | 448719 | AA033627 | Hs.21858 | trinucleotide repeat containing 3 | 7.02 |
| | 445577 | N40696 | Hs.137064 | cytoplasmic polyadenylation element bind | 7.00 |
| | 419647 | AA348947 | Hs.91816 | hypothetical protein | 7.00 |
| 40 | 442075 | AW136928 | | gb:U1-H-B11-adp-d-08-0-U1.s1 NCI_CGAP_Su | 7.00 |
| | 429598 | AA811257 | Hs.269710 | ESTs | 7.00 |
| | 450832 | AW970602 | Hs.105421 | ESTs | 7.00 |
| | 421389 | AA531291 | Hs.101064 | Homo sapiens cDNA FLJ12777 fis, clone NT | 7.00 |
| | 453931 | AL121278 | Hs.25144 | ESTs | 7.00 |
| 45 | 432343 | NM_002960 | Hs.2961 | S100 calcium-binding protein A3 | 7.00 |
| | 452979 | AW167599 | Hs.232282 | ESTs | 7.00 |
| | 431696 | AA259068 | Hs.267819 | protein phosphatase 1, regulatory (inhib | 7.00 |
| | 413583 | AL120806 | Hs.5888 | ESTs | 7.00 |
| | 436758 | AW977167 | Hs.155272 | ESTs | 7.00 |
| 50 | 455944 | BE160643 | | gb:PM1-HT0422-291299-002-f03 HT0422 Homo | 6.98 |
| | 430302 | AL137502 | Hs.238679 | Rag D protein | 6.96 |
| | 437613 | R19892 | Hs.10267 | MIL1 protein | 6.96 |
| | 440524 | R71264 | Hs.16798 | ESTs | 6.95 |
| | 451047 | AB022317 | Hs.25887 | sema domain, immunoglobulin domain (Ig). | 6.93 |
| 55 | 450377 | AB033091 | Hs.74313 | KIAA1265 protein | 6.93 |
| | 457396 | Z20964 | Hs.323817 | DKFZP547E1010 protein | 6.93 |
| | 417393 | R10484 | Hs.82071 | Cbp/p300-interacting transactivator, wit | 6.92 |
| | 414417 | BE299433 | Hs.68533 | KIAA1679 protein | 6.92 |
| | 412246 | A1160873 | Hs.69233 | zinc finger protein | 6.90 |
| 60 | 411003 | AA181018 | Hs.13056 | hypothetical protein FLJ13920 | 6.90 |
| | 413833 | Z15005 | Hs.75573 | centromere protein E (312kD) | 6.90 |
| | 405696 | NA | | NA | 6.90 |
| | 431689 | AA305688 | Hs.267695 | UDP-Gal:betaGlcNAc beta 1,3-galactosyltr | 6.90 |
| | 414429 | R51494 | Hs.71818 | ESTs | 6.90 |
| 65 | 424641 | AB001106 | Hs.151413 | gla maturation factor, beta | 6.90 |
| | 418895 | AA894638 | Hs.14600 | ESTs | 6.90 |
| | 445900 | AF070526 | Hs.13429 | Homo sapiens clone 24787 mRNA sequence | 6.90 |
| | 446006 | NM_004403 | Hs.13530 | deafness, autosomal dominant 5 | 6.90 |
| | 432038 | AA524746 | Hs.162110 | ESTs | 6.87 |
| | 446610 | AV659433 | Hs.282984 | ESTs, Weakly similar to I38022 hypothe | 6.86 |
| 70 | 451286 | AW139789 | Hs.16370 | Homo sapiens cDNA FLJ11652 fis, clone HE | 6.86 |
| | 408915 | NM_016651 | Hs.48950 | heptacellular carcinoma novel gene-3 pro | 6.85 |
| | 418934 | T83845 | Hs.191116 | ESTs | 6.82 |
| | 435143 | R12375 | Hs.194600 | ESTs | 6.82 |
| | 442660 | AW138174 | Hs.130651 | ESTs | 6.82 |
| 75 | 432729 | AK000292 | Hs.278732 | hypothetical protein FLJ20285 | 6.81 |
| | 435990 | A1015862 | Hs.131793 | ESTs | 6.80 |
| | 449062 | AJ272268 | Hs.22958 | calcium channel, voltage-dependent, alph | 6.80 |
| | 453688 | AW381270 | Hs.194110 | hypothetical protein PRO2730 | 6.80 |
| 80 | 421476 | AW953805 | Hs.21887 | ESTs | 6.80 |
| | 430510 | AW162916 | Hs.241576 | hypothetical protein PRO2577 | 6.80 |
| | 409045 | AA635062 | Hs.50094 | Homo sapiens mRNA; cDNA DKFZp434O0515 (f | 6.80 |
| | 410298 | A1693821 | Hs.182185 | ESTs | 6.80 |
| | 420560 | AW207748 | Hs.59115 | ESTs | 6.80 |

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|----|--------|-----------|-----------|--|------|
| | 427752 | AA470687 | Hs.104772 | ESTs | 6.80 |
| | 414080 | AA135257 | Hs.47783 | B aggressive lymphoma gene | 6.80 |
| | 422420 | U03398 | Hs.1524 | tumor necrosis factor (ligand) superfamily | 6.80 |
| 5 | 416913 | AW934714 | | gb:RC1-DT0001-031299-011-a11 DT0001 Homo | 6.80 |
| | 426890 | AA393167 | Hs.41294 | ESTs | 6.80 |
| | 411773 | NM_006799 | Hs.72026 | protease, serine, 21 (testisin) | 6.80 |
| | 413328 | Y15723 | Hs.75295 | guanylate cyclase 1, soluble, alpha 3 | 6.79 |
| | 437619 | AW351491 | Hs.334853 | hypothetical protein FLJ23544 | 6.79 |
| 10 | 434267 | AI206589 | Hs.116243 | ESTs | 6.79 |
| | 419358 | T78763 | Hs.90063 | neurocalcin delta | 6.79 |
| | 435854 | AJ278120 | Hs.4996 | putative ankyrin-repeat containing prote | 6.78 |
| | 424925 | NM_002432 | Hs.153837 | myeloid cell nuclear differentiation ant | 6.77 |
| | 443184 | AI638728 | Hs.131973 | ESTs | 6.77 |
| | 444484 | AK002126 | Hs.11260 | hypothetical protein FLJ11264 | 6.77 |
| 15 | 429483 | AA974832 | Hs.128708 | ESTs | 6.76 |
| | 425605 | BE544300 | Hs.7076 | KIAA1705 protein | 6.76 |
| | 425045 | AW953186 | Hs.92400 | ESTs | 6.76 |
| | 438776 | AW245243 | Hs.334368 | hypothetical protein MGC11257 | 6.75 |
| 20 | 458174 | AA781530 | Hs.127236 | hypothetical protein FLJ12879 | 6.74 |
| | 445129 | R39878 | Hs.21394 | ESTs | 6.74 |
| | 435532 | AW291488 | Hs.117305 | Homo sapiens, clone IMAGE:3682908, mRNA | 6.73 |
| | 444442 | AI149234 | Hs.298423 | ESTs, Moderately similar to I54374 gene | 6.73 |
| | 431240 | AA496790 | Hs.179481 | ESTs | 6.72 |
| 25 | 422109 | S73265 | Hs.1473 | gastrin-releasing peptide | 6.70 |
| | 416655 | AW968613 | Hs.79428 | BCL2/adenovirus E1B 19kD-interacting pro | 6.70 |
| | 423811 | AW299598 | Hs.50895 | homeo box C4 | 6.70 |
| | 443695 | AW204099 | Hs.337720 | ESTs, Weakly similar to AF126780 1 retin | 6.70 |
| | 420686 | AI950339 | Hs.40782 | ESTs | 6.70 |
| 30 | 419574 | AK001989 | Hs.91165 | hypothetical protein | 6.70 |
| | 418269 | AA806113 | Hs.189025 | ESTs | 6.70 |
| | 434164 | AW207019 | Hs.148135 | serine/threonine kinase 33 | 6.70 |
| | 408660 | AA525775 | Hs.292523 | ESTs, Moderately similar to PC4259 ferri | 6.70 |
| | 453370 | AI470523 | Hs.139336 | ATP-binding cassette, sub-family C (CFTR | 6.70 |
| 35 | 409506 | NM_006153 | Hs.54589 | NCK adaptor protein 1 | 6.70 |
| | 454029 | W05150 | Hs.37034 | homeo box A5 | 6.70 |
| | 413365 | AW205188 | Hs.124304 | Homo sapiens cDNA FLJ14635 fis, clone NT | 6.70 |
| | 447247 | AW369351 | Hs.287955 | Homo sapiens cDNA FLJ13090 fis, clone NT | 6.70 |
| | 426566 | AF131836 | Hs.170453 | tropomodulin | 6.70 |
| 40 | 446261 | AA313893 | Hs.306219 | hypothetical protein FLJ12615 similar to | 6.70 |
| | 408547 | AA574291 | Hs.57837 | ESTs | 6.70 |
| | 430458 | AA479300 | Hs.225706 | ESTs, Weakly similar to I38022 hypotheti | 6.70 |
| | 413627 | BE182082 | Hs.246973 | ESTs | 6.70 |
| | 410498 | AA355749 | | gb:EST64459 Jurkat T-cells VI Homo sapie | 6.70 |
| 45 | 434015 | AA844518 | Hs.300876 | hypothetical protein FLJ13386 | 6.70 |
| | 453691 | H12235 | Hs.226505 | ESTs | 6.68 |
| | 415068 | Z19448 | Hs.131887 | ESTs, Weakly similar to T24396 hypotheti | 6.68 |
| | 415885 | D79983 | Hs.78894 | KIAA0161 gene product | 6.68 |
| | 405529 | AW410458 | Hs.5258 | chromosome 11 open reading frame2 | 6.68 |
| 50 | 438242 | AW241910 | Hs.122254 | ESTs, Weakly similar to JX0369 collagen | 6.68 |
| | 442643 | U82756 | Hs.8551 | PRP4/STK/WD splicing factor | 6.67 |
| | 424802 | X79201 | Hs.153221 | synovial sarcoma, translocated to X chro | 6.67 |
| | 415007 | BE244332 | Hs.77770 | adaptor-related protein complex 3, mu 2 | 6.67 |
| | 458714 | R20916 | Hs.202501 | ESTs | 6.66 |
| 55 | 414591 | AI888490 | Hs.55902 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 6.65 |
| | 433260 | AB040966 | Hs.83575 | KIAA1533 protein | 6.65 |
| | 400268 | NA | | NA | 6.63 |
| | 453180 | N46243 | Hs.110373 | ESTs, Highly similar to T42626 secreted | 6.62 |
| | 403973 | NA | | NA | 6.60 |
| 60 | 436862 | AI821940 | Hs.264622 | ESTs, Moderately similar to ALU8_HUMAN A | 6.60 |
| | 428046 | AW812795 | Hs.155381 | ESTs, Moderately similar to I38022 hypot | 6.60 |
| | 453387 | AI990741 | Hs.252809 | ESTs | 6.60 |
| | 424084 | AI940675 | Hs.20914 | hypothetical protein FLJ23056 | 6.60 |
| | 418444 | AI902899 | Hs.85155 | butyrate response factor 1 (EGF-response | 6.60 |
| 65 | 448172 | N75276 | Hs.135904 | ESTs | 6.60 |
| | 409571 | AA504249 | Hs.187585 | ESTs | 6.60 |
| | 423025 | AA831267 | Hs.12244 | hypothetical protein FLJ20097 | 6.60 |
| | 430701 | AI760833 | Hs.293971 | ESTs | 6.60 |
| | 450373 | AI915790 | Hs.337282 | ESTs | 6.60 |
| 70 | 419384 | AA490866 | Hs.39429 | ESTs | 6.60 |
| | 429828 | AB019494 | Hs.225767 | IDN3 protein | 6.60 |
| | 441761 | AI222880 | | gb:qp40c06.x1 NCI_CGAP_Co8 Homo sapiens | 6.60 |
| | 411048 | AK001742 | Hs.67991 | hypothetical protein DKFZp434G0522 | 6.60 |
| | 421111 | BE299047 | Hs.43532 | ESTs, Weakly similar to T20177 hypotheti | 6.60 |
| 75 | 407424 | AF120493 | | gb:Homo sapiens elastase 1 precursor (EL | 6.59 |
| | 412396 | AW947895 | | gb:PM1-MT0010-200300-001-110 MT0010 Homo | 6.57 |
| | 416209 | AA236776 | Hs.79078 | MAD2 [mitotic arrest deficient, yeast, h | 6.57 |
| | 406674 | AA332152 | Hs.288036 | tRNA isopentenylpyrophosphate transferas | 6.57 |
| | 400860 | | | NA | 6.56 |
| 80 | 457893 | AA744292 | | gb:ny51d05.s1 NCI_CGAP_Pr18 Homo sapiens | 6.55 |
| | 426108 | AA622037 | Hs.166468 | programmed cell death 5 | 6.54 |
| | 422133 | AW612779 | Hs.333159 | Homo sapiens laryngeal carcinoma related | 6.54 |
| | 421044 | AF061871 | Hs.311736 | Human DNA sequence from clone RP1-238D15 | 6.54 |
| | 414136 | AA812434 | Hs.119023 | SMC2 (structural maintenance of chromoso | 6.53 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 400351 | AF060169 | Hs.272369 | Homo sapiens AS11 protein mRNA, partial | 6.52 |
| | 413670 | AB000115 | Hs.75470 | hypothetical protein, expressed in osteo | 6.52 |
| | 410416 | BE410072 | Hs.63304 | protein phosphatase methyltransferase-1 | 6.50 |
| 5 | 419852 | AW503756 | Hs.286184 | hypothetical protein dJ551D2.5 | 6.50 |
| | 419677 | N77342 | Hs.21851 | Homo sapiens cDNA FLJ12900 fis, clone NT | 6.50 |
| | 431806 | AF186114 | Hs.270737 | tumor necrosis factor (ligand) superfamily | 6.50 |
| | 429774 | AI522215 | Hs.50883 | KIAA1804 protein | 6.50 |
| | 428228 | AA424352 | Hs.210586 | ESTs | 6.50 |
| 10 | 418134 | AA397769 | Hs.86617 | ESTs | 6.50 |
| | 403859 | NA | | NA | 6.50 |
| | 422704 | AA972147 | Hs.132275 | ESTs | 6.50 |
| | 416737 | AF154335 | Hs.79691 | LIM domain protein | 6.50 |
| | 429854 | R55508 | Hs.99472 | ESTs | 6.50 |
| 15 | 422672 | X12784 | Hs.119129 | collagen, type IV, alpha 1 | 6.50 |
| | 453600 | BE246211 | Hs.119120 | E3 ubiquitin ligase SMURF1 | 6.49 |
| | 454835 | AW833763 | | gb:QV4-TT0008-130100-077-d10 TT0008 Homo | 6.48 |
| | 434603 | AF147384 | | gb:Homo sapiens full length insert cDNA | 6.48 |
| | 408243 | Y00787 | Hs.624 | interleukin 8 | 6.48 |
| 20 | 429317 | AA831552 | Hs.268016 | Homo sapiens cDNA: FLJ21243 fis, clone C | 6.48 |
| | 451316 | AI770011 | Hs.208310 | ESTs | 6.47 |
| | 448339 | AL035920 | Hs.20938 | RNA binding motif, single stranded inter | 6.46 |
| | 433423 | BE407127 | Hs.8997 | heat shock 70kD protein 1A | 6.46 |
| | 410358 | AW975168 | Hs.13337 | ESTs, Weakly similar to unnamed protein | 6.44 |
| 25 | 434025 | AF114264 | Hs.216381 | Homo sapiens clone HH409 unknown mRNA | 6.44 |
| | 440526 | AI832243 | Hs.211471 | ESTs | 6.42 |
| | 432727 | AA305233 | Hs.278712 | eukaryotic translation initiation factor | 6.42 |
| | 433009 | AA761668 | | gb:nz24c08.s1 NCL_CGAP_GCB1 Homo sapiens | 6.41 |
| | 435782 | N49433 | Hs.285737 | Homo sapiens cDNA: FLJ20895 fis, clone A | 6.40 |
| 30 | 415071 | AK002197 | Hs.284270 | Homo sapiens cDNA FLJ11335 fis, clone PL | 6.40 |
| | 407162 | N63855 | Hs.142634 | zinc finger protein | 6.40 |
| | 446152 | AI292036 | Hs.150028 | ESTs | 6.40 |
| | 422828 | AL133396 | Hs.121281 | prion protein 2 (dublet) | 6.40 |
| 35 | 418866 | T65754 | | gb:yc11c07.s1 Stratagene lung (937210) H | 6.40 |
| | 411411 | AA345241 | Hs.55950 | ESTs, Weakly similar to KIAA1330 protein | 6.40 |
| | 429039 | AI524793 | Hs.301897 | ESTs | 6.40 |
| | 447254 | NM_004153 | Hs.17908 | origin recognition complex, subunit 1 (y | 6.40 |
| | 435159 | AA668879 | Hs.116649 | ESTs | 6.40 |
| 40 | 429625 | AA455568 | Hs.193814 | ESTs | 6.40 |
| | 430180 | AA331406 | Hs.75456 | A kinase (PRKA) anchor protein 10 | 6.40 |
| | 408420 | NM_006915 | Hs.44766 | retinitis pigmentosa 2 (X-linked recessi | 6.40 |
| | 426572 | AB037783 | Hs.170623 | hypothetical protein FLJ11183 | 6.40 |
| | 449911 | AI262106 | Hs.12653 | ESTs | 6.40 |
| | 440105 | AA694010 | Hs.6932 | Homo sapiens clone 23809 mRNA sequence | 6.40 |
| 45 | 440395 | AA884412 | Hs.216342 | ESTs | 6.40 |
| | 429500 | X78565 | Hs.289114 | hexabrachion (lenscrin C, cytotoxin) | 6.37 |
| | 417771 | AA804698 | Hs.82547 | retinoic acid receptor responder (tazaro | 6.36 |
| | 417092 | H97508 | Hs.181165 | eukaryotic translation elongation factor | 6.36 |
| | 412227 | AW902282 | | gb:QV3-NN1023-260400-169-g10 NN1023 Homo | 6.36 |
| 50 | 400845 | | | NA | 6.36 |
| | 403546 | NA | | NA | 6.36 |
| | 412345 | AW938386 | | gb:PM4-DT0057-201299-002-G10 DT0057 Homo | 6.35 |
| | 422186 | AW962364 | Hs.129051 | ESTs | 6.34 |
| 55 | 426990 | AL044315 | Hs.173094 | Homo sapiens mRNA for KIAA1750 protein, | 6.34 |
| | 417687 | AI828596 | Hs.250691 | ESTs | 6.33 |
| | 426223 | AW977812 | Hs.130391 | ESTs | 6.32 |
| | 417588 | Z44510 | | gb:HSC22D091 normalized infant brain cDN | 6.32 |
| | 432629 | AW860548 | Hs.280658 | ESTs | 6.31 |
| 60 | 440495 | AA887212 | Hs.14161 | hypothetical protein DKFZp434i1930 | 6.31 |
| | 407771 | AL138272 | Hs.62713 | ESTs | 6.31 |
| | 417517 | AF001176 | Hs.82238 | POP4 (processing of precursor, S. cerev | 6.30 |
| | 431041 | AA490967 | Hs.197955 | KIAA0704 protein | 6.30 |
| | 445571 | AI378000 | Hs.158489 | ESTs, Weakly similar to Z184_HUMAN ZINC | 6.30 |
| | 433309 | AA807060 | Hs.126558 | ESTs | 6.30 |
| 65 | 415659 | W27214 | Hs.78547 | zinc finger protein (clone 647) | 6.30 |
| | 420271 | AI954365 | Hs.42892 | ESTs | 6.30 |
| | 426921 | AA037145 | Hs.172865 | cleavage stimulation factor, 3' pre-RNA, | 6.30 |
| | 400950 | NA | | NA | 6.30 |
| | 429692 | N48422 | Hs.9977 | ESTs, Weakly similar to B34087 hypotheti | 6.30 |
| 70 | 439813 | AA846321 | Hs.124501 | ESTs | 6.30 |
| | 449444 | AW818436 | Hs.23590 | solute carrier family 16 (monocarboxylic | 6.30 |
| | 453596 | AA441838 | Hs.62905 | hypothetical protein FLJ14834 | 6.30 |
| | 446847 | TS1454 | Hs.82845 | Homo sapiens cDNA: FLJ21930 fis, clone H | 6.30 |
| | 435820 | AA700580 | Hs.189000 | ESTs | 6.30 |
| 75 | 452576 | AB023177 | Hs.29900 | KIAA0960 protein | 6.30 |
| | 448924 | AW450569 | Hs.188399 | ESTs | 6.30 |
| | 424343 | AW956360 | Hs.4748 | adenylate cyclase activating polypeptide | 6.30 |
| | 412591 | BE217736 | Hs.292653 | ESTs, Weakly similar to T26845 hypotheti | 6.30 |
| 80 | 426642 | AW068223 | Hs.171581 | ubiquitin C-terminal hydrolase UCH37 | 6.30 |
| | 419088 | AI538323 | Hs.52620 | integrin, beta 8 | 6.30 |
| | 401424 | | | NA | 6.30 |
| | 412189 | R60982 | Hs.22581 | ESTs | 6.30 |
| | 435501 | AW051819 | Hs.129908 | KIAA0591 protein | 6.30 |
| | 408221 | AA912183 | Hs.47447 | ESTs | 6.28 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 413943 | AW294416 | Hs.144687 | Homo sapiens cDNA FLJ12981 fis, clone NT | 6.28 |
| | 416845 | H95279 | | gb:yu20h02.s1 Soares fetal liver spleen | 6.27 |
| | 402732 | NA | | NA | 6.26 |
| 5 | 413224 | AI732470 | Hs.191157 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 6.24 |
| | 415642 | U19878 | Hs.336224 | transmembrane protein with EGF-like and | 6.24 |
| | 449284 | BE502240 | Hs.38592 | hypothetical protein FLJ23342 | 6.24 |
| | 419548 | AW978142 | Hs.326248 | Homo sapiens cDNA: FLJ22071 fis, clone H | 6.23 |
| | 453880 | AI803166 | Hs.28462 | ESTs, Weakly similar to I38022 hypotheti | 6.22 |
| 10 | 422675 | BE018517 | Hs.119140 | eukaryotic translation initiation factor | 6.22 |
| | 413384 | NM_000401 | Hs.75334 | exosomoses (multiple) 2 | 6.21 |
| | 445584 | AF217518 | Hs.8360 | PTD012 protein | 6.21 |
| | 451065 | AW295132 | Hs.222231 | ESTs, Weakly similar to granule cell mar | 6.21 |
| | 420807 | AA280627 | Hs.57846 | ESTs | 6.20 |
| 15 | 421155 | H87879 | Hs.102267 | lysyl oxidase | 6.20 |
| | 441421 | AA356792 | Hs.334824 | hypothetical protein FLJ14825 | 6.20 |
| | 440209 | H05049 | Hs.22269 | neurexin 3 | 6.20 |
| | 408170 | AW204516 | Hs.31835 | ESTs | 6.20 |
| | 433590 | N98410 | Hs.48364 | Homo sapiens regulator of G-protein sign | 6.20 |
| 20 | 442008 | AI457814 | Hs.270272 | ESTs | 6.20 |
| | 420617 | AK001652 | Hs.99423 | ATP-dependent RNA helicase | 6.20 |
| | 402343 | | | NA | 6.20 |
| | 432682 | AI376400 | Hs.159588 | ESTs | 6.20 |
| | 452109 | AI525873 | Hs.61164 | hypothetical protein FLJ14909 | 6.20 |
| 25 | 429954 | AI918130 | Hs.21374 | ESTs | 6.20 |
| | 417256 | U94332 | Hs.81791 | tumor necrosis factor receptor superfam | 6.20 |
| | 435525 | AI831297 | Hs.123310 | ESTs | 6.20 |
| | 413604 | R51767 | | gb:yg73g11.r1 Soares infant brain 1N1B H | 6.20 |
| | 425305 | AA363025 | Hs.155572 | Human clone 23801 mRNA sequence | 6.20 |
| 30 | 443285 | AI301918 | Hs.334264 | ESTs | 6.20 |
| | 446565 | D13757 | Hs.311 | phosphoribosyl pyrophosphate amidotransf | 6.20 |
| | 451027 | AW519204 | Hs.40808 | ESTs | 6.20 |
| | 452243 | AL355715 | Hs.28555 | programmed cell death 9 | 6.19 |
| | 429782 | NM_005754 | Hs.220689 | Ras-GTPase-activating protein SH3-domain | 6.17 |
| 35 | 424060 | X92108 | Hs.138629 | H.sapiens mRNA for subtelomeric repeat s | 6.17 |
| | 432494 | AA551060 | | gb:bnk74f02.s1 NCI_CGAP_Sch1 Homo sapiens | 6.16 |
| | 448186 | AA262105 | Hs.4094 | Homo sapiens cDNA FLJ14208 fis, clone NT | 6.14 |
| | 419638 | N46504 | Hs.91747 | profilin 2 | 6.13 |
| | 445595 | W25950 | Hs.14512 | DIPB protein | 6.13 |
| 40 | 433036 | AA574091 | Hs.105964 | ESTs | 6.13 |
| | 457155 | AL110243 | Hs.187991 | DKFZP564A122 protein | 6.13 |
| | 443715 | AI583187 | Hs.9700 | cyclin E1 | 6.13 |
| | 422867 | L32137 | Hs.1584 | cartilage oligomeric matrix protein (pse | 6.12 |
| | 453286 | AA034319 | Hs.29041 | Homo sapiens cDNA FLJ14177 fis, clone NT | 6.11 |
| 45 | 424897 | D63216 | Hs.153684 | frizzled-related protein | 6.11 |
| | 429188 | AB011171 | Hs.198037 | KIAA0599 protein | 6.11 |
| | 434894 | AW977850 | Hs.23856 | hypothetical protein MGC5297 | 6.10 |
| | 413339 | AI818080 | Hs.194290 | ESTs | 6.10 |
| | 453685 | AL110309 | | gb:DKFZp564L0278_r1 564 (synonym: hbr2) | 6.10 |
| 50 | 421195 | BE464560 | Hs.133017 | ESTs | 6.10 |
| | 453296 | AA034413 | Hs.62560 | ESTs | 6.10 |
| | 444985 | AI677737 | Hs.28329 | hypothetical protein FLJ14005 | 6.10 |
| | 423492 | AF020761 | Hs.129683 | ubiquitin-conjugating enzyme E2D 1 (homo | 6.10 |
| | 419841 | BE005848 | Hs.7326 | ESTs | 6.10 |
| 55 | 429190 | H18650 | Hs.92602 | ESTs | 6.10 |
| | 426116 | AA868729 | Hs.144694 | ESTs | 6.10 |
| | 451441 | AA017601 | Hs.84529 | ESTs, Weakly similar to Z202_HUMAN ZINC | 6.10 |
| | 401740 | | | NA | 6.10 |
| | 441953 | H11695 | Hs.322901 | disrupter of silencing 10 | 6.10 |
| 60 | 401464 | AF039241 | Hs.9028 | histone deacetylase 5 | 6.10 |
| | 405033 | | | NA | 6.10 |
| | 410743 | AA089474 | Hs.272153 | ESTs | 6.10 |
| | 454758 | AW845266 | | gb:IL2-CT0031-160999-003-808 CT0031 Homo | 6.10 |
| | 417728 | AW138437 | Hs.24790 | KIAA1573 protein | 6.10 |
| 65 | 418553 | T88964 | | gb:yd97a07.r1 Soares fetal liver spleen | 6.09 |
| | 431617 | AK000738 | Hs.264636 | hypothetical protein FLJ20731 | 6.08 |
| | 455608 | BE011437 | | gb:CM4-BN0220-080500-170-03 BN0220 Homo | 6.08 |
| | 450755 | AA010984 | Hs.159464 | ESTs | 6.07 |
| | 455217 | AW867534 | | gb:MR0-SN0037-160400-004-e05 SN0037 Homo | 6.07 |
| 70 | 437179 | AA393508 | Hs.300642 | serologically defined colon cancer anti | 6.06 |
| | 408622 | AA056060 | Hs.202577 | Homo sapiens cDNA FLJ12166 fis, clone MA | 6.06 |
| | 415308 | F05251 | | gb:HSC04H101 normalized infant brain cDN | 6.06 |
| | 428417 | AK001699 | Hs.184227 | F-box only protein 21 | 6.05 |
| | 426501 | AW043782 | Hs.293616 | ESTs | 6.03 |
| 75 | 431077 | AI659133 | Hs.115660 | hypothetical protein FLJ12810 | 6.03 |
| | 403040 | | | NA | 6.02 |
| | 445704 | AI493742 | Hs.165210 | ESTs, Moderately similar to I38022 hypot | 6.02 |
| | 415637 | R25517 | | gb:yg44f01.r1 Soares infant brain 1N1B H | 6.02 |
| | 427925 | N51323 | Hs.255935 | Homo sapiens, clone IMAGE:3448993, mRNA | 6.02 |
| | 404702 | NA | | NA | 6.02 |
| 80 | 433183 | AF231338 | Hs.222024 | transcription factor BMAL2 | 6.01 |
| | 437762 | T78028 | Hs.154679 | synaptotagmin I | 6.01 |
| | 443833 | AI654108 | Hs.135125 | ESTs | 6.01 |
| | 422263 | AA307639 | Hs.129908 | KIAA0591 protein | 6.00 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 420909 | AI640551 | Hs.88878 | Homo sapiens cDNA: FLJ23536 fis. clone L | 6.00 |
| | 407612 | U26403 | Hs.37142 | ephrin-A5 | 6.00 |
| | 450715 | AI266484 | Hs.31570 | ESTs, Weakly similar to KIAA1324 protein | 6.00 |
| 5 | 453853 | AL040600 | Hs.188083 | ESTs | 6.00 |
| | 444188 | AI393165 | Hs.699 | peptidylprolyl isomerase B (cyclophilin | 6.00 |
| | 451813 | NM_016117 | Hs.27182 | phospholipase A2-activating protein | 6.00 |
| | 422505 | AL120862 | Hs.124165 | ESTs | 6.00 |
| | 420734 | AW972872 | Hs.293736 | ESTs | 6.00 |
| 10 | 455082 | BE148180 | | gb:RC0-HT0232-211099-011-e04 HT0232 Homo | 6.00 |
| | 444200 | AA327113 | Hs.149057 | ESTs | 6.00 |
| | 447432 | AW958473 | Hs.301957 | nudix (nucleoside diphosphate linked moi | 6.00 |
| | 419752 | AA249573 | Hs.152618 | ESTs, Moderately similar to ZN91_HUMAN Z | 6.00 |
| | 428412 | AA428240 | Hs.126083 | ESTs | 6.00 |
| 15 | 407790 | AI027274 | Hs.288941 | Homo sapiens cDNA FLJ14866 fis. clone PL | 6.00 |
| | 428945 | AW192803 | Hs.58974 | ESTs, Weakly similar to S65824 reverse t | 6.00 |
| | 431878 | AA521207 | Hs.270202 | ESTs, Weakly similar to ALU4_HUMAN ALU S | 6.00 |
| | 425282 | AW163518 | Hs.155485 | huntingtin interacting protein 2 | 6.00 |
| | 401093 | | | NA | 6.00 |
| 20 | 411861 | AW867875 | | gb:MR0-SN0040-050500-003-f11 SN0040 Homo | 6.00 |
| | 411800 | N39342 | Hs.103042 | microtubule-associated protein 1B | 5.99 |
| | 446925 | AW974605 | Hs.176669 | ESTs | 5.98 |
| | 401708 | NA | | NA | 5.98 |
| | 449894 | AK001578 | Hs.24129 | CLLL7 protein | 5.97 |
| 25 | 403278 | NA | | NA | 5.96 |
| | 455212 | AW866330 | | gb:QV4-SN0024-080400-167-e01 SN0024 Homo | 5.96 |
| | 410116 | AW630671 | Hs.58636 | squamous cell carcinoma antigen recogniz | 5.96 |
| | 441271 | AA927290 | Hs.130462 | ESTs | 5.95 |
| | 404072 | | | NA | 5.95 |
| 30 | 431596 | T34708 | Hs.272927 | Sec23 (S. cerevisiae) homolog A | 5.94 |
| | 421622 | AB037748 | Hs.106204 | KIAA1327 protein | 5.93 |
| | 441300 | R35063 | Hs.181536 | ESTs | 5.92 |
| | 445517 | AF208855 | Hs.12830 | hypothetical protein | 5.91 |
| | 429559 | AI985345 | Hs.26425 | ESTs | 5.91 |
| 35 | 443767 | BE562136 | Hs.9736 | proteasome (prosome, macropain) 26S subu | 5.91 |
| | 440510 | H08427 | Hs.309165 | ESTs, Weakly similar to ISHUS protein d | 5.90 |
| | 414727 | BE466904 | | gb:h22803.x1 NCI_CGAP_GC6 Homo sapiens | 5.90 |
| | 451686 | AA059246 | Hs.110293 | ESTs | 5.90 |
| | 438032 | BE045624 | Hs.152992 | ESTs | 5.90 |
| 40 | 450470 | Z75330 | Hs.286148 | stromal antigen 1 | 5.90 |
| | 430533 | AA480895 | Hs.201552 | ESTs, Weakly similar to T17288 hypotheti | 5.90 |
| | 432662 | AL049314 | Hs.280700 | ESTs | 5.90 |
| | 451742 | T77609 | Hs.117970 | ankyrin 2, neuronal | 5.90 |
| | 431217 | NM_013427 | Hs.250830 | Rho GTPase activating protein 6 | 5.90 |
| 45 | 412537 | AL031778 | Hs.797 | nuclear transcription factor Y, alpha | 5.90 |
| | 447233 | AW246333 | Hs.17901 | Homo sapiens, clone IMAGE:3937015, mRNA, | 5.90 |
| | 410804 | U64820 | Hs.66521 | Machado-Joseph disease (spinocerebellar | 5.90 |
| | 452619 | AW298597 | Hs.61884 | Homo sapiens, clone IMAGE:4298026, mRNA, | 5.90 |
| | 433865 | N29862 | Hs.44104 | ESTs | 5.90 |
| 50 | 453403 | BE466639 | Hs.61779 | Homo sapiens cDNA FLJ13591 fis. clone PL | 5.90 |
| | 448743 | AB032962 | Hs.21896 | KIAA1136 protein | 5.90 |
| | 447153 | AA805202 | Hs.315562 | ESTs | 5.90 |
| | 425793 | AA363946 | Hs.20969 | ESTs | 5.90 |
| | 404632 | | | NA | 5.90 |
| 55 | 446364 | AB006624 | Hs.14912 | KIAA0286 protein | 5.90 |
| | 452240 | AI591147 | Hs.61232 | ESTs | 5.90 |
| | 410424 | AA084984 | | gb:zn11a08.r1 Stratagene hNT neuron (937 | 5.90 |
| | 404170 | | | NA | 5.89 |
| 60 | 458390 | AI792585 | Hs.133272 | ESTs, Weakly similar to ALLUC_HUMAN !!!! | 5.89 |
| | 408296 | AL117452 | Hs.44155 | DKFZP586G1517 protein | 5.88 |
| | 444406 | AI147237 | Hs.300697 | immunoglobulin heavy constant gamma 3 (G | 5.87 |
| | 413894 | BE177983 | | gb:RC3-HT0600-230300-021-g10 HT0600 Homo | 5.87 |
| | 453922 | AF053306 | Hs.36708 | budding uninhibited by benzimidazoles 1 | 5.86 |
| | 445700 | AW208257 | Hs.156326 | Human DNA sequence from clone RP11-145L2 | 5.86 |
| 65 | 443377 | AI792547 | Hs.133292 | ESTs | 5.86 |
| | 419162 | AA234591 | Hs.304123 | ESTs | 5.85 |
| | 436608 | AA628980 | Hs.192371 | down syndrome critical region protein DS | 5.84 |
| | 428650 | AI560456 | Hs.107319 | ESTs | 5.84 |
| | 437410 | AW023340 | Hs.14880 | ESTs | 5.84 |
| 70 | 428303 | AW974476 | Hs.183601 | regulator of G-protein signalling 16 | 5.84 |
| | 401004 | | | NA | 5.83 |
| | 414504 | AW069181 | Hs.115175 | sterile-alpha motif and leucine zipper c | 5.83 |
| | 410979 | BE151480 | | gb:RC0-HT0295-071199-011-e01 HT0295 Homo | 5.82 |
| | 424576 | BE154142 | Hs.96833 | ESTs | 5.82 |
| 75 | 439352 | BE614347 | Hs.169615 | hypothetical protein FLJ20989 | 5.81 |
| | 423057 | AW961597 | Hs.130816 | ESTs, Moderately similar to I38022 hypot | 5.80 |
| | 429250 | H56585 | Hs.198308 | tryptophan rich basic protein | 5.80 |
| | 413048 | M93221 | Hs.75182 | mannose receptor, C type 1 | 5.80 |
| | 451367 | AA923729 | Hs.26322 | cell cycle related kinase | 5.80 |
| 80 | 418647 | AA226198 | | gb:nc26a07.s1 NCI_CGAP_Pr1 Homo sapiens | 5.80 |
| | 421589 | AW954177 | Hs.82919 | cullin 2 | 5.80 |
| | 427969 | NM_001963 | Hs.2230 | epidermal growth factor (beta-urogastron | 5.80 |
| | 451406 | AI694320 | Hs.6295 | ESTs, Weakly similar to T17248 hypotheti | 5.80 |
| | 436096 | H55931 | Hs.269582 | ESTs | 5.80 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 443353 | AI052659 | Hs.133255 | ESTs | 5.80 |
| | 457244 | AA581385 | Hs.162473 | ESTs, Weakly similar to I38022 hypothei | 5.80 |
| | 407746 | AK001962 | Hs.38114 | hypothetical protein FLJ11100 | 5.80 |
| 5 | 440688 | AW404591 | Hs.147440 | ESTs, Weakly similar to Z192_HUMAN ZINC | 5.80 |
| | 445745 | AB007924 | Hs.13245 | KIAA0455 gene product | 5.80 |
| | 405637 | NA | | NA | 5.80 |
| | 415293 | R49462 | Hs.106541 | ESTs | 5.80 |
| | 440404 | AI015881 | Hs.324527 | mitochondrial ribosomal protein S5 | 5.80 |
| | 442227 | AW771958 | Hs.175437 | ESTs, Moderately similar to PC4259 ferri | 5.80 |
| 10 | 423395 | AA326613 | | gb:EST29922 Cerebellum II Homo sapiens c | 5.80 |
| | 410555 | U92649 | Hs.64311 | a disintegrin and metalloproteinase doma | 5.80 |
| | 416000 | R82342 | Hs.79856 | ESTs, Weakly similar to S65657 alpha-1C- | 5.80 |
| | 422108 | AA297914 | Hs.111749 | postmeiotic segregation increased (S. ce | 5.80 |
| | 430818 | AI311928 | | gb:qo89h04.x1 NCI_CGAP_Kid5 Homo sapiens | 5.80 |
| 15 | 444749 | AI190672 | Hs.65926 | ESTs | 5.80 |
| | 417515 | L24203 | Hs.82237 | ataxia-telangiectasia group D-associated | 5.79 |
| | 456192 | D84109 | Hs.80248 | RNA-binding protein gene with multiple s | 5.78 |
| | 411253 | AW833897 | | gb:QV0-TT0009-111199-055-b07 TT0009 Homo | 5.78 |
| 20 | 417219 | AW973473 | Hs.220936 | ESTs | 5.78 |
| | 409450 | AW628650 | Hs.61260 | hypothetical protein FLJ13164 | 5.76 |
| | 412013 | AA400753 | Hs.43761 | ESTs, Weakly similar to A46010 X-linked | 5.76 |
| | 425566 | AW162943 | Hs.250618 | UL16 binding protein 2 | 5.75 |
| | 417877 | AI025829 | Hs.86320 | ESTs | 5.75 |
| 25 | 437114 | AA836641 | Hs.163085 | ESTs | 5.75 |
| | 421238 | AB033101 | Hs.102796 | Homo sapiens cDNA FLJ10708 fs, clone NT | 5.74 |
| | 428959 | AF100779 | Hs.194680 | WNT1 inducible signaling pathway protein | 5.73 |
| | 415209 | F00183 | Hs.172004 | titin | 5.73 |
| | 429922 | Z97630 | Hs.226117 | H1 histone family, member 0 | 5.72 |
| 30 | 420022 | AA256253 | Hs.120817 | ESTs | 5.71 |
| | 431485 | BE621320 | Hs.257486 | hypothetical protein FLJ20062 | 5.71 |
| | 424304 | NM_001395 | Hs.144879 | dual specificity phosphatase 9 | 5.71 |
| | 434276 | AF123659 | Hs.93605 | leucine zipper, putative tumor suppresso | 5.71 |
| | 438085 | R52518 | Hs.7967 | ESTs | 5.70 |
| 35 | 444379 | N99035 | Hs.222657 | ESTs | 5.70 |
| | 401348 | NA | | NA | 5.70 |
| | 428878 | AA436884 | Hs.48926 | ESTs | 5.70 |
| | 422564 | AI148006 | Hs.222120 | ESTs | 5.70 |
| | 452560 | BE077084 | Hs.336432 | ESTs | 5.70 |
| 40 | 408384 | BE144344 | Hs.7589 | ESTs, Weakly similar to A46010 X-linked | 5.70 |
| | 409948 | AA078643 | | gb:7P08801 Chromosome 7 Placental cDNA L | 5.70 |
| | 421166 | AA305407 | Hs.102308 | potassium inwardly-rectifying channel, s | 5.70 |
| | 439231 | AW581935 | Hs.141480 | Homo sapiens mRNA; cDNA DKFZp434N079 (fr | 5.70 |
| | 439203 | AA448930 | Hs.8453 | KIAA1587 protein | 5.70 |
| 45 | 442029 | AW956698 | Hs.14456 | neural precursor cell expressed, develop | 5.70 |
| | 451922 | BE463995 | Hs.211033 | ESTs | 5.70 |
| | 407808 | AA663559 | Hs.279789 | histone deacetylase 3 | 5.70 |
| | 428161 | M96954 | Hs.182741 | TIA1 cytotoxic granule-associated RNA-bi | 5.70 |
| | 413430 | R22479 | Hs.167073 | Homo sapiens cDNA FLJ13047 fs, clone NT | 5.70 |
| 50 | 428223 | AA424313 | Hs.98402 | ESTs | 5.70 |
| | 427972 | AA864870 | Hs.181304 | putative gene product | 5.70 |
| | 416283 | NM_005429 | Hs.79141 | vascular endothelial growth factor C | 5.70 |
| | 416319 | AI815601 | Hs.79197 | CD83 antigen (activated B lymphocytes, i | 5.70 |
| | 458044 | AW979114 | Hs.326135 | ESTs | 5.70 |
| 55 | 432911 | AW807634 | Hs.279799 | putative zinc finger protein NY-REN-34 a | 5.70 |
| | 411643 | AI924519 | Hs.192570 | hypothetical protein FLJ22028 | 5.70 |
| | 408867 | AA437199 | Hs.656 | cell division cycle 25C | 5.70 |
| | 428679 | AA431765 | | gb:zw80c03.s1 Soares_testis_NHT Homo sap | 5.70 |
| | 428822 | W28418 | Hs.30715 | potassium voltage-gated channel, Isk-rel | 5.70 |
| 60 | 409570 | AW418720 | Hs.167583 | ESTs | 5.70 |
| | 457441 | BE467737 | Hs.146125 | ESTs | 5.70 |
| | 409101 | NM_004297 | Hs.50612 | guanine nucleotide binding protein (G pr | 5.70 |
| | 420192 | AA256281 | Hs.105040 | ESTs | 5.69 |
| | 423582 | BE000831 | Hs.23837 | Homo sapiens cDNA FLJ11812 fs, clone HE | 5.69 |
| 65 | 454511 | AW948146 | | gb:RC0-MT0013-280300-031-e02 MT0013 Homo | 5.68 |
| | 419586 | AI088485 | Hs.144759 | ESTs, Weakly similar to I38022 hypothei | 5.67 |
| | 416777 | AF146760 | Hs.79844 | DKFZP564M1416 protein | 5.67 |
| | 435849 | BE305242 | Hs.16098 | claudin 2 | 5.67 |
| | 457892 | AA744389 | | gb:ny51e10.s1 NCI_CGAP_Pr18 Homo sapiens | 5.66 |
| 70 | 450191 | AW137243 | Hs.222446 | ESTs | 5.66 |
| | 438653 | AW188099 | Hs.131813 | ESTs | 5.66 |
| | 422910 | AI269508 | Hs.121591 | Human DNA sequence from PAC 257A7 on chr | 5.66 |
| | 453694 | AW504918 | Hs.258208 | Homo sapiens, clone MGC.15606, mRNA, com | 5.66 |
| | 445302 | AK001537 | Hs.12488 | hypothetical protein FLJ10675 | 5.66 |
| 75 | 446080 | AI221741 | Hs.117777 | ESTs | 5.65 |
| | 425474 | Z48054 | Hs.158084 | peroxisome receptor 1 | 5.65 |
| | 432542 | AW083920 | Hs.16098 | claudin 2 | 5.65 |
| | 446983 | AA157484 | Hs.97199 | complement component C1q receptor | 5.65 |
| | 420898 | AB002379 | Hs.100113 | KIAA0381 protein | 5.65 |
| 80 | 401372 | | | NA | 5.64 |
| | 428541 | AI862570 | Hs.299214 | Homo sapiens, clone IMAGE:2822295, mRNA, | 5.63 |
| | 426249 | F05422 | Hs.168352 | nucleoporin-like protein 1 | 5.63 |
| | 459705 | BE082764 | Hs.270252 | ESTs, Weakly similar to androgen recepto | 5.63 |
| | 451863 | AL120634 | Hs.305923 | ATPase, Ca ⁺⁺ transporting, plasma membra | 5.62 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 426316 | NM_002430 | Hs.268515 | meningioma (disrupted in balanced translocation) | 5.62 |
| | 401183 | | | NA | 5.62 |
| | 426029 | AW294138 | Hs.255277 | ESTs | 5.61 |
| 5 | 443462 | AI064690 | Hs.171176 | ESTs | 5.61 |
| | 447102 | BE167434 | Hs.98471 | ESTs, Weakly similar to T18712 hypothetical protein | 5.60 |
| | 419150 | T29618 | Hs.89640 | TEK tyrosine kinase, endothelial (venous) | 5.60 |
| | 444577 | AI207721 | Hs.11393 | RAD51 (S. cerevisiae) homolog C | 5.60 |
| | 423605 | AF047826 | Hs.129887 | cadherin 19, type 2 | 5.60 |
| 10 | 413447 | AW969388 | Hs.10450 | Homo sapiens cDNA: FLJ22063 fis, clone H | 5.60 |
| | 442957 | AI949952 | Hs.49397 | ESTs | 5.60 |
| | 424296 | AI631874 | Hs.155140 | casein kinase 2, alpha 1 polypeptide | 5.60 |
| | 430679 | R44428 | Hs.22801 | ESTs | 5.60 |
| | 449358 | AA001229 | Hs.131436 | ESTs | 5.60 |
| | 418348 | AI537167 | Hs.96322 | hypothetical protein FLJ23560 | 5.60 |
| 15 | 433133 | AB027249 | Hs.104741 | PDZ-binding kinase; T-cell originated protein | 5.60 |
| | 444059 | R69743 | Hs.116774 | integrin, alpha 1 | 5.60 |
| | 438157 | AW137011 | Hs.49576 | ESTs | 5.60 |
| | 428233 | AI358831 | Hs.20578 | ESTs | 5.60 |
| 20 | 434265 | AA846811 | Hs.130554 | Homo sapiens cDNA: FLJ23089 fis, clone L | 5.60 |
| | 451652 | AA018968 | Hs.133536 | ESTs | 5.59 |
| | 422762 | AI031320 | Hs.119976 | Human DNA sequence from clone RP1-20N2 o | 5.59 |
| | 447591 | AI675417 | Hs.282855 | ESTs | 5.58 |
| | 417958 | AA767382 | Hs.193417 | ESTs | 5.57 |
| 25 | 438146 | Z36842 | Hs.57548 | ESTs | 5.57 |
| | 413595 | AW235215 | Hs.16145 | ESTs | 5.57 |
| | 422406 | AF025441 | Hs.116206 | Opa-interacting protein 5 | 5.56 |
| | 420529 | D25259 | Hs.319844 | ESTs, Moderately similar to I54374 gene | 5.56 |
| | 439582 | W79161 | Hs.118327 | Homo sapiens cDNA FLJ11522 fis, clone HE | 5.56 |
| 30 | 408744 | AW806177 | | gb:MR1-UM0108-130400-003-d04 UM0108 Homo | 5.56 |
| | 447230 | AW972147 | Hs.101395 | hypothetical protein MGC11352 | 5.54 |
| | 428856 | AA436735 | Hs.183171 | hypothetical protein FLJ22002 | 5.54 |
| | 446813 | AA971436 | Hs.16218 | KIAA0903 protein | 5.53 |
| | 451424 | AI862026 | Hs.302810 | Novel human gene mapping to chromosome 20 | 5.53 |
| 35 | 410516 | BE537917 | Hs.90034 | hypothetical protein FLJ21916 | 5.53 |
| | 453994 | BE180964 | Hs.165590 | ribosomal protein S13 | 5.53 |
| | 435583 | AA767714 | Hs.291627 | ESTs | 5.52 |
| | 431585 | BE242803 | Hs.262823 | hypothetical protein FLJ10326 | 5.51 |
| | 408912 | AB011084 | Hs.48924 | KIAA0512 gene product; ALEX2 | 5.51 |
| 40 | 427965 | R97130 | Hs.189699 | ESTs | 5.51 |
| | 433611 | AW327692 | Hs.3446 | mitogen-activated protein kinase kinase | 5.51 |
| | 401244 | | | NA | 5.50 |
| | 410784 | AW803201 | | gb:IL2-UM0077-070500-080-E06 UM0077 Homo | 5.50 |
| | 434006 | AF113688 | | gb:Homo sapiens clone FLB4630 | 5.50 |
| 45 | 425650 | NM_001944 | Hs.1925 | desmoglein 3 (permpig vulgaris antigen) | 5.50 |
| | 427507 | AF240467 | Hs.179152 | tol-like receptor 7 | 5.50 |
| | 423268 | BE386898 | Hs.131162 | ESTs, Weakly similar to ALU5_HUMAN ALU S | 5.50 |
| | 405065 | NA | | NA | 5.50 |
| | 444302 | AI140115 | Hs.225130 | ESTs | 5.50 |
| 50 | 418183 | NM_001772 | Hs.83731 | CD33 antigen (gp67) | 5.50 |
| | 435586 | AI279137 | Hs.151498 | ESTs | 5.50 |
| | 438279 | AA805166 | Hs.154762 | HIV-1 rev binding protein 2 | 5.50 |
| | 427189 | H82453 | Hs.5635 | ESTs | 5.50 |
| | 415263 | AA948033 | Hs.130853 | ESTs | 5.50 |
| 55 | 441818 | AI530451 | Hs.7976 | KIAA0332 protein | 5.50 |
| | 407834 | AW084991 | Hs.26100 | ESTs | 5.50 |
| | 404012 | NA | | NA | 5.50 |
| | 449932 | AI675444 | Hs.263024 | ESTs | 5.50 |
| | 423760 | AA775891 | Hs.191980 | ESTs | 5.50 |
| 60 | 431576 | M76665 | Hs.275215 | hydroxysteroid (11-beta) dehydrogenase 1 | 5.50 |
| | 423172 | R15652 | | gb:HH503-F Adult heart, Clontech Homo sa | 5.50 |
| | 422295 | AF051151 | Hs.114408 | tol-like receptor 5 | 5.50 |
| | 429044 | AI261490 | Hs.145527 | ESTs | 5.50 |
| | 433280 | AA581404 | Hs.289037 | Homo sapiens cDNA FLJ14135 fis, clone MA | 5.50 |
| 65 | 414323 | NM_014759 | Hs.334688 | KIAA0273 gene product | 5.50 |
| | 405511 | NA | | NA | 5.49 |
| | 444665 | BE613126 | Hs.47783 | B aggressive lymphoma gene | 5.49 |
| | 434434 | AA633516 | Hs.157201 | ESTs | 5.48 |
| | 421997 | R66740 | Hs.110613 | KIAA0220 protein | 5.47 |
| 70 | 410276 | AI554545 | Hs.68301 | ESTs | 5.47 |
| | 435867 | AA954229 | Hs.114052 | ESTs | 5.47 |
| | 453837 | AL138387 | Hs.256126 | baculoviral IAP repeat-containing 7 (liv | 5.47 |
| | 409617 | BE003760 | Hs.55209 | Homo sapiens mRNA; cDNA DKFZp434K0514 (f | 5.47 |
| | 430387 | AW372884 | Hs.240770 | nuclear cap binding protein subunit 2, 2 | 5.47 |
| 75 | 401629 | NA | | NA | 5.46 |
| | 433071 | BE150229 | Hs.281564 | retinal outer segment membrane protein 1 | 5.46 |
| | 458247 | R14439 | Hs.209194 | ESTs | 5.46 |
| | 418049 | AA211467 | Hs.190488 | Homo sapiens, Similar to nuclear localiz | 5.45 |
| | 418247 | R55174 | | gb:yg87h04.r1 Soares infant brain 1N1B H | 5.45 |
| 80 | 453716 | AA037675 | Hs.152675 | ESTs | 5.44 |
| | 431157 | AI823969 | Hs.132678 | ESTs | 5.44 |
| | 426873 | AI190540 | Hs.131092 | ESTs | 5.43 |
| | 437092 | AA744292 | | gb:ny51d05.s1 NCL_CGAP_Pr18 Homo sapiens | 5.42 |
| | 445782 | AW407672 | Hs.315367 | Homo sapiens, Similar to hypothetical pr | 5.42 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 447393 | AI377458 | Hs.158831 | EST | 5.42 |
| | 425283 | AA354338 | Hs.131100 | ESTs | 5.42 |
| | 401208 | NA | | NA | 5.42 |
| 5 | 430536 | AI809163 | Hs.9908 | nitrogen fixation cluster-like | 5.42 |
| | 405523 | | | NA | 5.42 |
| | 409012 | AL117435 | Hs.49725 | DKFZP434I216 protein | 5.41 |
| | 429803 | W81489 | Hs.223025 | RAB31, member RAS oncogene family | 5.41 |
| | 436982 | AB018305 | Hs.5378 | spodoin 1, (f-spondin) extracellular mat | 5.40 |
| 10 | 422892 | AA988176 | Hs.121553 | hypothetical protein FLJ20641 | 5.40 |
| | 456027 | BE327387 | Hs.13913 | KIAA1577 protein | 5.40 |
| | 411897 | AW875066 | Hs.326876 | Homo sapiens SOX6 mRNA, complete cds | 5.40 |
| | 449689 | AF228421 | Hs.23889 | DKFZP564A032 protein | 5.40 |
| | 432865 | AI753709 | Hs.152484 | ESTs, Weakly similar to I38022 hypothe | 5.40 |
| | 408248 | AW854832 | | gb:QV2-CT0261-201099-011-405 CT0261 Homo | 5.40 |
| 15 | 418516 | NM_006218 | Hs.85701 | phosphoinositide-3-kinase, catalytic, al | 5.40 |
| | 423289 | N77774 | | gb:yz83e01.r1 Soares_multiple_sclerosis_ | 5.40 |
| | 453365 | AA035211 | Hs.17404 | ESTs | 5.40 |
| | 406465 | | | NA | 5.40 |
| 20 | 441858 | AW173339 | Hs.135665 | ESTs | 5.40 |
| | 432507 | BE391093 | Hs.324667 | ESTs | 5.40 |
| | 440570 | AI205712 | Hs.125998 | ESTs | 5.40 |
| | 445062 | AI339915 | Hs.44324 | ESTs | 5.40 |
| | 421639 | NM_012082 | Hs.106309 | Friend of GATA2 | 5.40 |
| 25 | 410406 | AI969703 | Hs.1466 | glycerol kinase | 5.40 |
| | 418939 | AW630803 | Hs.89497 | lamin B1 | 5.40 |
| | 426010 | AA136563 | Hs.1975 | hypothetical protein FLJ21007 | 5.40 |
| | 400250 | NA | | NA | 5.40 |
| | 424650 | AW576156 | Hs.250824 | Homo sapiens cDNA: FLJ23435 fis, clone H | 5.40 |
| 30 | 414998 | NM_002543 | Hs.77729 | oxidised low density lipoprotein (lectin | 5.39 |
| | 433384 | AI021992 | Hs.124244 | ESTs | 5.38 |
| | 428781 | AF164799 | Hs.193384 | putative 28 kDa protein | 5.38 |
| | 438150 | AA037534 | Hs.79059 | transforming growth factor, beta recepto | 5.38 |
| | 400639 | | | NA | 5.38 |
| 35 | 426485 | NM_006207 | Hs.170040 | platelet-derived growth factor receptor- | 5.37 |
| | 424205 | AA336825 | | gb:EST41732 Endometrial tumor Homo sapie | 5.36 |
| | 459596 | H29554 | Hs.113871 | ESTs | 5.36 |
| | 408234 | AW993356 | Hs.285814 | sprouty (Drosophila) homolog 4 | 5.36 |
| | 414547 | T47770 | Hs.191463 | ESTs | 5.35 |
| 40 | 419851 | AA287987 | Hs.13477 | ESTs, Weakly similar to 1207289A reverse | 5.35 |
| | 411945 | AL033527 | Hs.92137 | v-myc avian myelocytomatosis viral oncog | 5.34 |
| | 425764 | AW996009 | Hs.112572 | Homo sapiens cDNA FLJ14130 fis, clone MA | 5.34 |
| | 405352 | | | NA | 5.33 |
| | 448030 | N30714 | Hs.325960 | membrane-spanning 4-domains, subfamily A | 5.32 |
| 45 | 424284 | BE541008 | Hs.6193 | hypothetical protein FLJ14590 | 5.32 |
| | 427741 | AW753185 | Hs.180628 | dynamitin 1-like | 5.31 |
| | 426021 | AW770897 | Hs.34392 | ESTs, Weakly similar to I38022 hypothe | 5.31 |
| | 442186 | AA984083 | Hs.269746 | ESTs, Weakly similar to T03306 PSD-95/SA | 5.30 |
| | 437319 | BE410958 | Hs.56406 | Homo sapiens cDNA FLJ13549 fis, clone PL | 5.30 |
| | 405287 | NA | | NA | 5.30 |
| 50 | 427032 | AF012023 | Hs.173274 | integrin cytoplasmic domain-associated p | 5.30 |
| | 415371 | R15239 | | gb:yf89b02.r1 Soares infant brain 1N1B H | 5.30 |
| | 420024 | AA252905 | Hs.194477 | E3 ubiquitin ligase SMURF2 | 5.30 |
| | 434408 | AI031771 | Hs.132586 | ESTs | 5.30 |
| 55 | 434739 | AA804487 | Hs.144130 | ESTs | 5.30 |
| | 421327 | AA837295 | Hs.188802 | ESTs | 5.30 |
| | 453058 | AW612293 | Hs.288684 | Homo sapiens cDNA FLJ11750 fis, clone HE | 5.30 |
| | 448776 | BE302464 | Hs.30057 | MRS2 (S. cerevisiae)-like, magnesium hom | 5.30 |
| | 417845 | AL117461 | Hs.82719 | Homo sapiens mRNA; cDNA DKFZp586F1822 (f | 5.30 |
| 60 | 430264 | AA470519 | | gb:nc71110.s1 NCI_CGAP_P1 Homo sapiens | 5.30 |
| | 411402 | BE297855 | Hs.69855 | NRAS-related gene | 5.30 |
| | 419220 | AA811938 | Hs.291759 | ESTs | 5.30 |
| | 407995 | AI094748 | Hs.100134 | hypothetical protein FLJ12787 | 5.30 |
| | 459256 | AW967468 | Hs.99821 | hypothetical protein FLJ14547 | 5.30 |
| 65 | 452449 | AW068658 | Hs.20943 | ESTs | 5.30 |
| | 430366 | AI057368 | Hs.105575 | ESTs | 5.30 |
| | 434360 | AW015415 | Hs.127780 | ESTs | 5.30 |
| | 422560 | F11469 | Hs.118281 | zinc finger protein 266 | 5.29 |
| | 441704 | AI458766 | Hs.201988 | ESTs | 5.29 |
| 70 | 443635 | AI080230 | Hs.134214 | ESTs | 5.29 |
| | 434342 | AI791138 | Hs.116768 | ESTs | 5.29 |
| | 423409 | NM_006466 | Hs.128207 | polymerase (RNA) III (DNA directed)-{39x | 5.29 |
| | 449000 | U69560 | Hs.3826 | ketch-like protein C3IP1 | 5.29 |
| | 452381 | H23329 | Hs.290880 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 5.29 |
| 75 | 409068 | AW236991 | Hs.102495 | ESTs, Moderately similar to I38022 hypot | 5.29 |
| | 434860 | AA932386 | Hs.292667 | ESTs | 5.28 |
| | 408096 | BE250162 | Hs.83765 | dihydrofolate reductase | 5.28 |
| | 418036 | Z37976 | Hs.83337 | latent transforming growth factor beta b | 5.28 |
| | 435443 | AI248674 | Hs.14295 | ESTs | 5.26 |
| 80 | 414269 | AA298489 | Hs.303171 | olfactory receptor, family 51, subfamily | 5.26 |
| | 408371 | AF161545 | Hs.279883 | hypothetical protein | 5.26 |
| | 401205 | NA | | NA | 5.26 |
| | 450904 | R07118 | Hs.189924 | ESTs | 5.26 |
| | 416351 | H49704 | Hs.173522 | ESTs | 5.26 |

| | | | | | |
|----|--------|----------|-----------|--|------|
| | 426524 | AA380611 | Hs.163841 | ESTs | 5.25 |
| | 412901 | A1127359 | Hs.289088 | heat shock 90kD protein 1, alpha | 5.25 |
| | 452487 | AW207659 | Hs.6630 | Homo sapiens cDNA FLJ13329 fis, clone OV | 5.24 |
| 5 | 444825 | AW167613 | Hs.248 | mitogen-activated protein kinase kinase | 5.24 |
| | 412953 | Z45794 | Hs.238809 | ESTs | 5.24 |
| | 404117 | NA | | NA | 5.22 |
| | 427956 | AL046175 | Hs.108169 | Homo sapiens mRNA; cDNA DKFZp586C1619 ff | 5.22 |
| | 421787 | AA227068 | Hs.108301 | nuclear receptor subfamily 2, group C, m | 5.22 |
| 10 | 437255 | R58970 | Hs.9887 | ESTs | 5.22 |
| | 424897 | AL136169 | Hs.250708 | CAAX box 1 | 5.22 |
| | 449771 | AUG68702 | Hs.54976 | ESTs | 5.20 |
| | 432193 | AA372264 | Hs.273193 | hypothetical protein FLJ10706 | 5.20 |
| | 438885 | AI886558 | Hs.184987 | ESTs | 5.20 |
| 15 | 407182 | AA312551 | Hs.230157 | ESTs | 5.20 |
| | 452150 | W42490 | Hs.260844 | ESTs | 5.20 |
| | 419680 | AA249720 | Hs.59335 | ESTs | 5.20 |
| | 438940 | AF075045 | Hs.271609 | ESTs | 5.20 |
| | 405362 | NA | | NA | 5.20 |
| 20 | 449370 | AK002114 | Hs.23495 | hypothetical protein FLJ11252 | 5.20 |
| | 442353 | BE379594 | Hs.49136 | ESTs, Moderately similar to ALU7_HUMAN A | 5.20 |
| | 409331 | M36634 | Hs.53973 | vasoactive intestinal peptide | 5.20 |
| | 415397 | H10818 | | gb:ym04f10.r1 Soares infant brain 1N1B H | 5.20 |
| | 406735 | AA603092 | | gb:np37a01.s1 NCI_CGAP_Lu1 Homo sapiens | 5.20 |
| 25 | 418489 | U76421 | Hs.85302 | adenosine deaminase, RNA-specific, B1 (h | 5.20 |
| | 431480 | AA837274 | Hs.257005 | hypothetical protein FLJ20837 | 5.20 |
| | 425523 | AB007948 | Hs.158244 | KIAA0479 protein | 5.20 |
| | 425673 | R70318 | Hs.339730 | ESTs | 5.20 |
| | 439267 | AA287747 | Hs.173012 | ESTs, Weakly similar to A46010 X-linked | 5.20 |
| 30 | 457030 | AI301740 | Hs.173381 | dihydropyrimidinase-like 2 | 5.20 |
| | 424638 | AI472106 | Hs.49303 | Homo sapiens cDNA FLJ11663 fis, clone HE | 5.20 |
| | 454434 | AA083558 | Hs.261286 | ESTs | 5.20 |
| | 448336 | R53848 | Hs.44976 | ESTs | 5.20 |
| | 429534 | AW976987 | Hs.163327 | ESTs, Weakly similar to 2109260A B cell | 5.20 |
| 35 | 434803 | AW974640 | Hs.303413 | ESTs | 5.20 |
| | 403199 | NA | | NA | 5.20 |
| | 435225 | AI021912 | Hs.187983 | ESTs | 5.20 |
| | 451664 | AA889081 | Hs.153952 | 5' nucleotidase (CD73) | 5.20 |
| | 440385 | AA884283 | Hs.192136 | ESTs | 5.20 |
| 40 | 432328 | AI572739 | Hs.195471 | 6-phosphofructo-2-kinase/fructose-2,6-bi | 5.20 |
| | 400484 | | | NA | 5.20 |
| | 425757 | AA363171 | | gb:EST72986 Ovary II Homo sapiens cDNA 5 | 5.19 |
| | 449841 | AI671602 | Hs.199602 | ESTs | 5.19 |
| | 420303 | AA258282 | Hs.278436 | KIAA1474 protein | 5.19 |
| 45 | 429687 | AI675749 | Hs.211608 | nucleoporin 153kD | 5.19 |
| | 453345 | AA302862 | Hs.90063 | neurocalcin delta | 5.18 |
| | 447499 | AW262580 | Hs.147674 | protocadherin beta 16 | 5.18 |
| | 404913 | | | NA | 5.18 |
| | 405114 | NA | | NA | 5.18 |
| 50 | 431117 | AF003522 | Hs.250500 | delta (Drosophila)-like 1 | 5.18 |
| | 411995 | W49701 | Hs.29667 | ESTs | 5.17 |
| | 401736 | NA | | NA | 5.17 |
| | 425250 | AA353495 | Hs.269762 | ESTs, Weakly similar to A47582 B-cell gr | 5.16 |
| 55 | 454388 | AA630905 | Hs.333300 | hypothetical protein FLJ14026 | 5.16 |
| | 449032 | AA045573 | Hs.22900 | nuclear factor (erythroid-derived 2)-lik | 5.16 |
| | 443646 | AI085198 | Hs.164226 | ESTs | 5.15 |
| | 436032 | AA150797 | Hs.109276 | latexin protein | 5.15 |
| | 456896 | M97639 | Hs.155585 | receptor tyrosine kinase-like orphan rec | 5.15 |
| 60 | 433672 | BE281165 | Hs.288038 | TLS-associated serine-arginine protein 1 | 5.15 |
| | 432826 | X75363 | Hs.250770 | ACO for serine protease homologue | 5.14 |
| | 439441 | W67993 | Hs.323135 | ESTs | 5.14 |
| | 400205 | NA | | NA | 5.14 |
| | 430854 | AW440369 | Hs.47026 | ESTs | 5.14 |
| | 408771 | AW732573 | Hs.47584 | potassium voltage-gated channel, delayed | 5.14 |
| 65 | 456804 | AI421645 | Hs.139851 | caveolin 2 | 5.14 |
| | 424690 | BE538356 | Hs.151777 | eukaryotic translation initiation factor | 5.13 |
| | 449210 | AI635363 | Hs.197636 | ESTs | 5.12 |
| | 419013 | T90378 | Hs.14463 | ESTs | 5.12 |
| | 425843 | BE313280 | Hs.159627 | death associated protein 3 | 5.12 |
| 70 | 422545 | X02761 | Hs.287820 | fibronectin 1 | 5.12 |
| | 424785 | R23519 | Hs.6126 | hypothetical protein dJ1141E15.2 | 5.11 |
| | 442833 | AA328153 | Hs.88201 | ESTs, Weakly similar to A Chain A, Cryst | 5.10 |
| | 422411 | AW749443 | Hs.22511 | ESTs | 5.10 |
| | 457565 | BE294029 | Hs.279903 | Ras homolog enriched in brain 2 | 5.10 |
| 75 | 437722 | AW292947 | Hs.122872 | ESTs, Weakly similar to J00033 hypotheti | 5.10 |
| | 446893 | AI610818 | Hs.7110 | ESTs | 5.10 |
| | 401581 | | | NA | 5.10 |
| | 417511 | AL049176 | Hs.82223 | chordin-like | 5.10 |
| 80 | 422336 | AI761322 | Hs.115285 | dihydrolipoamide S-acetyltransferase (E2 | 5.10 |
| | 437662 | AA765387 | Hs.145095 | ESTs | 5.10 |
| | 429526 | AA454182 | Hs.99360 | ESTs | 5.10 |
| | 447332 | AW445012 | Hs.160918 | ESTs | 5.10 |
| | 436207 | AA334774 | Hs.12845 | hypothetical protein MGC13159 | 5.10 |
| | 428155 | H17012 | Hs.14633 | ESTs | 5.10 |

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|----|--------|-----------|-----------|--|------|
| | 420185 | AL044056 | Hs.158047 | ESTs | 5.10 |
| | 445657 | AW612141 | Hs.279575 | Homo sapiens G-protein coupled receptor | 5.10 |
| | 440913 | AI267491 | Hs.160593 | ESTs | 5.10 |
| 5 | 452943 | BE247449 | Hs.31082 | hypothetical protein FLJ10525 | 5.10 |
| | 428603 | BE241619 | Hs.24541 | cytoskeleton associated protein 2 | 5.10 |
| | 436577 | W84774 | Hs.17643 | ESTs | 5.10 |
| | 400241 | NA | | NA | 5.10 |
| | 437205 | AL110232 | Hs.279243 | Homo sapiens mRNA; cDNA DKFZp564D2071 (f | 5.10 |
| 10 | 423654 | AI674253 | Hs.35828 | ESTs | 5.10 |
| | 417637 | AA204969 | Hs.234863 | Homo sapiens cDNA FLJ12082 fis, clone HE | 5.10 |
| | 430849 | AI940727 | Hs.270556 | ESTs, Highly similar to AF156779 1 ASB-4 | 5.10 |
| | 452605 | AW968557 | Hs.90012 | hypothetical protein FLJ23441 | 5.10 |
| | 440381 | AA917808 | Hs.190495 | ESTs | 5.10 |
| 15 | 441033 | BE562555 | | gb:601335867F1 NIH_MGC_44 Homo sapiens c | 5.10 |
| | 450229 | R18717 | Hs.8929 | hypothetical protein FLJ11362 | 5.10 |
| | 447197 | R36075 | | gb:yh88b01.s1 Soares placenta Nb2HP Homo | 5.10 |
| | 442150 | AI368158 | Hs.70983 | PTPL1-associated RhoGAP 1 | 5.10 |
| | 415651 | AI207162 | Hs.3815 | slathmin-like-protein RB3 | 5.10 |
| 20 | 453655 | AW960427 | Hs.79059 | transforming growth factor, beta recepto | 5.09 |
| | 434442 | AA737415 | Hs.152826 | ESTs | 5.09 |
| | 429389 | AA454779 | Hs.201441 | Homo sapiens cDNA FLJ11079 fis, clone PL | 5.09 |
| | 435419 | AI281068 | Hs.152835 | ESTs | 5.09 |
| | 427620 | NM_003705 | Hs.179866 | solute carrier family 25 (mitochondrial | 5.09 |
| 25 | 445706 | AA305520 | Hs.108812 | hypothetical protein FLJ22004 | 5.08 |
| | 424071 | R71340 | Hs.12876 | ESTs | 5.08 |
| | 428227 | AA321649 | Hs.2248 | small inducible cytokine subfamily B (Cy | 5.08 |
| | 426400 | M78361 | Hs.169743 | Homo sapiens clone Z5121 neuronal offact | 5.08 |
| | 429026 | AA443385 | Hs.221993 | ESTs | 5.08 |
| 30 | 455847 | BE146775 | | gb:QV4-HT0222-181099-013-e04 HT0222 Homo | 5.08 |
| | 416110 | Z42262 | Hs.322844 | hypothetical protein DKFZp564A176 | 5.08 |
| | 436854 | AA749167 | Hs.173911 | ESTs | 5.08 |
| | 421799 | AW972292 | Hs.292998 | ESTs | 5.08 |
| | 452154 | AW953265 | Hs.302746 | MSTP028 protein | 5.06 |
| 35 | 444946 | AW139205 | Hs.156457 | hypothetical protein FLJ22408 | 5.06 |
| | 445950 | AI267957 | Hs.145706 | ESTs | 5.06 |
| | 443124 | AI033500 | Hs.132895 | ESTs | 5.06 |
| | 440698 | AI348455 | Hs.147492 | Homo sapiens cDNA FLJ11777 fis, clone HE | 5.06 |
| | 444713 | AW812074 | Hs.28631 | Homo sapiens cDNA: FLJ22141 fis, clone H | 5.06 |
| 40 | 447970 | AW086109 | Hs.20136 | chromosome X open reading frame 6 | 5.06 |
| | 419307 | AW953190 | Hs.23180 | ESTs | 5.06 |
| | 421954 | AA410245 | Hs.40323 | BUB3 (budding uninhibited by benzimidazo | 5.06 |
| | 451807 | W52854 | Hs.27099 | hypothetical protein FLJ23293 similar to | 5.05 |
| | 421782 | AB029290 | Hs.108258 | actin binding protein; macrophin (microf | 5.05 |
| 45 | 407976 | AI633875 | Hs.77823 | hypothetical protein FLJ21343 | 5.05 |
| | 400869 | | | NA | 5.04 |
| | 416153 | R13894 | | gb:yf62a06.r1 Soares infant brain 1N1B H | 5.04 |
| | 428242 | H55709 | Hs.2250 | leukemia inhibitory factor (cholinergic | 5.04 |
| | 406038 | Y14443 | Hs.88219 | zinc finger protein 200 | 5.03 |
| 50 | 440659 | AF134160 | Hs.7327 | claudin 1 | 5.03 |
| | 425188 | AK002052 | Hs.155071 | hypothetical protein FLJ11190 | 5.02 |
| | 446051 | BE048061 | Hs.37054 | ephrin-A3 | 5.02 |
| | 443387 | BE139135 | Hs.254629 | ESTs | 5.02 |
| | 414407 | AA147026 | Hs.76704 | ESTs | 5.02 |
| 55 | 408349 | BE546947 | Hs.44276 | homeo box C10 | 5.01 |
| | 452510 | Z33566 | Hs.301491 | ESTs | 5.01 |
| | 447245 | AK001713 | Hs.17860 | hypothetical protein FLJ10851 | 5.00 |
| | 413472 | BE242870 | Hs.75379 | solute carrier family 1 (glial high affi | 5.00 |
| | 447857 | AA081218 | Hs.58508 | Homo sapiens cDNA FLJ14206 fis, clone NT | 5.00 |
| 60 | 423648 | AK000456 | Hs.130546 | hypothetical protein FLJ20449 | 5.00 |
| | 412997 | BE046600 | | gb:hn41d08.x1 NCL_CGAP_RDF2 Homo sapiens | 5.00 |
| | 408964 | AF201468 | Hs.49349 | beta-site APP-cleaving enzyme | 5.00 |
| | 411636 | AW855001 | | gb:PM3-CT0263-091299-007-R05 CT0263 Homo | 5.00 |
| | 418111 | R42003 | Hs.106513 | ESTs | 5.00 |
| 65 | 402709 | NA | | NA | 5.00 |
| | 408677 | AI279892 | Hs.46801 | sorting nexin 14 | 5.00 |
| | 411350 | AW877011 | | gb:QV2-PT0010-250300-096-b05 PT0010 Homo | 5.00 |
| | 453382 | AA709285 | Hs.5997 | hypothetical protein FLJ13078 | 5.00 |
| | 458090 | AI282149 | Hs.56213 | ESTs, Highly similar to FXD3_HUMAN FORKH | 5.00 |
| 70 | 408512 | AW902013 | Hs.255937 | ESTs | 5.00 |
| | 453240 | AI969564 | Hs.166254 | hypothetical protein DKFZp566I133 | 5.00 |
| | 440491 | R35252 | Hs.24944 | ESTs, Weakly similar to 2109260A B cell | 5.00 |
| | 423896 | AA332216 | Hs.130584 | ESTs | 5.00 |
| | 429091 | AA935658 | Hs.187939 | ESTs | 5.00 |
| 75 | 410968 | AA199907 | Hs.67397 | homeo box A1 | 5.00 |
| | 436859 | AA732681 | Hs.270053 | ESTs | 5.00 |
| | 452198 | AI097560 | Hs.61210 | ESTs, Weakly similar to I38022 hypotheti | 5.00 |
| | 424511 | BE300512 | Hs.193557 | ESTs, Moderately similar to ALU7_HUMAN A | 5.00 |
| | 414631 | AW970130 | Hs.65406 | ESTs | 5.00 |
| 80 | 405481 | | | NA | 5.00 |
| | 431118 | BE264901 | Hs.250502 | carbonic anhydrase VIII | 5.00 |
| | 421373 | AA808229 | Hs.167771 | ESTs | 5.00 |
| | 424916 | AW867440 | Hs.23096 | ESTs | 5.00 |
| | 433106 | AB002443 | Hs.184418 | ESTs | 5.00 |

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|------------|-------------|---------------------------------------|--|--|------|
| 5 | 427386 | AW836261 | Hs.337717 | ESTs | 5.00 |
| | 441998 | A173236 | Hs.128312 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 5.00 |
| | 420161 | A1683069 | Hs.175319 | ESTs | 5.00 |
| | 430899 | BE018217 | Hs.183528 | hypothetical protein FLJ14906 | 5.00 |
| | 415188 | BE007531 | Hs.258791 | ESTs | 5.00 |
| | 420429 | AW293291 | Hs.255180 | ESTs | 5.00 |
| | 439038 | AV655045 | Hs.8366 | ESTs | 5.00 |
| | 457031 | AM97955 | Hs.304802 | ESTs, Weakly similar to KIAA0944 protein | 5.00 |
| 10 | 430865 | A1073424 | Hs.5232 | HSPC125 protein | 5.00 |
| | 420583 | H77859 | Hs.65450 | reticulum 4 | 5.00 |
| | 432229 | AW290976 | Hs.143587 | ESTs | 5.00 |
| | 455208 | BE180276 | | gb:RC3-HT0622-130400-022-a02 HT0622 Homo | 5.00 |
| | 419263 | AW583874 | Hs.89832 | insulin | 5.00 |
| | 452279 | AA286844 | Hs.61260 | hypothetical protein FLJ13164 | 5.00 |
| 15 | 419100 | AA464362 | Hs.6748 | hypothetical protein PP1665 | 5.00 |
| | 438585 | AA811371 | Hs.123362 | ESTs | 5.00 |
| | 436953 | AW959074 | Hs.23648 | Homo sapiens cDNA FLJ13097 fs, clone NT | 5.00 |
| | 428775 | AA34579 | Hs.143691 | ESTs | 5.00 |
| 20 | 422471 | AA311027 | Hs.271894 | ESTs, Weakly similar to I38022 hypothe | 5.00 |
| | 402524 | | NA | NA | 5.00 |
| TABLE 46B: | | | | | |
| | Playr: | Unique Eos probeset identifier number | | | |
| 25 | CAT number: | Gene cluster number | | | |
| | Accession: | Genbank accession numbers | | | |
| | Playr | CAT number | Accessions | | |
| 30 | 408248 | 1049240_1 | AW854832 AW854798 AW854857 AW854816 AW854834 AW854817 | | |
| | 408432 | 1058667_1 | AW195262 R27868 AW811262 | | |
| | 408744 | 1078309_1 | AW806177 AW806178 AW265775 | | |
| | 409948 | 116139_1 | AA078643 BE535933 AA132607 | | |
| | 410424 | 120166_1 | AA084984 Z18302 AW502279 AW499519 | | |
| | 410444 | 1203699_1 | W73484 AW748569 AW748532 AW748585 | | |
| 35 | 410498 | 120611_1 | AA355749 AA085520 AW966333 AA340319 BE170936 | | |
| | 410784 | 1221005_1 | AW803201 BE079700 BE062940 | | |
| | 410979 | 1228509_1 | BE151480 D63282 AW812615 | | |
| | 411253 | 1236671_1 | AW833897 AW833907 AW833908 AW833920 AW833953 AW833881 AW833878 AW833879 AW833952 AW833919 AW833921 AW833915 | | |
| 40 | 411350 | 1239976_1 | AW877011 AW877066 AW877136 AW876980 AW991827 AW877073 AW877070 AW882665 AW876972 AW877068 AW877064 AW838297 AW877065 | | |
| | 411636 | 1252525_1 | AW855001 AW855031 BE062221 | | |
| | 411861 | 1261785_1 | AW867875 BE067343 BE067301 BE067350 BE067305 BE067347 BE067306 BE067304 BE067303 BE067302 AW938147 | | |
| | 412227 | 1284297_1 | AW902282 AW902508 AW902509 AW902605 AW902606 AW902643 AW902490 | | |
| | 412345 | 1289783_1 | AW938386 AW938411 AW938426 AW938397 | | |
| 45 | 412396 | 1292796_1 | AW947895 AW947891 AW947933 AW947892 AW947930 AW947889 AW947894 AW947931 AW947893 AW947932 AW947929 | | |
| | 412997 | 1343205_1 | BE046600 BE046677 BE046236 | | |
| | 413604 | 1379715_1 | R51767 BE152515 Z44834 H23397 | | |
| | 413894 | 1397740_1 | BE177983 BE178322 | | |
| | 414727 | 1481204_1 | BE466904 W28721 | | |
| 50 | 415308 | 1533673_1 | F05251 R13748 Z44028 H14747 | | |
| | 415371 | 1535066_1 | R15239 Z45189 F06836 | | |
| | 415397 | 1535937_1 | H10818 F07831 Z43072 | | |
| | 415637 | 1540904_1 | R25517 F13222 T75465 | | |
| | 416153 | 1573947_1 | R13894 H23037 R56371 | | |
| 55 | 416190 | 1576789_1 | N54000 H26494 T83818 | | |
| | 416845 | 1624038_1 | H95279 H95331 H95933 | | |
| | 416913 | 163001_1 | AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499 | | |
| | 417352 | 166908_1 | AA195919 D79180 BE543135 BE008355 BE008353 BE008315 BE008317 | | |
| | 417588 | 1688092_1 | Z44510 R24958 R00714 T82024 | | |
| 60 | 418247 | 1733290_1 | R55174 Z19829 X97508 | | |
| | 418553 | 1767393_1 | T88964 R99447 T84773 | | |
| | 418647 | 177521_1 | AA226198 AA226513 AA383773 | | |
| | 418866 | 179788_1 | T65754 AA229857 AA229658 | | |
| | 423172 | 225618_1 | R15652 AA322742 AW961639 AW961637 | | |
| 65 | 423289 | 226804_1 | N77774 AA324125 AW955199 AA452230 | | |
| | 423395 | 227885_1 | AA326613 AA325417 AW962164 | | |
| | 423928 | 233416_1 | AA332680 AA332831 AW962684 | | |
| | 424205 | 236651_1 | AA336825 AA337256 AA337682 AA337525 | | |
| | 425757 | 255956_1 | AA363171 AW963347 AA371863 | | |
| 70 | 428679 | 294049_1 | AA431765 AA432015 | | |
| | 430264 | 315008_1 | AA470519 BE303010 BE302954 BE384120 | | |
| | 430818 | 324239_1 | A1311928 AA936030 T51931 AA609816 AA487195 AA664207 | | |
| | 432494 | 348522_1 | AA551060 AW979274 AA847429 AA878487 | | |
| | 432639 | 351744_1 | AW973785 H60163 AA557608 | | |
| 75 | 433009 | 357371_1 | AA761668 AA573621 R92814 R09670 | | |
| | 434006 | 37855_1 | AF113688 A1114617 | | |
| | 434603 | 38944_1 | AF147384 T60126 T60244 | | |
| | 436411 | 419334_1 | AW674352 AA715374 Z25205 | | |
| | 437092 | 432938_1 | AA744292 AA745577 AW748517 AW748564 AW748511 AW748513 AW748530 AW748574 BE062923 | | |
| 80 | 437237 | 43506_-2 | BE513073 | | |
| | 441033 | 50807_-1 | BE562555 | | |
| | 441761 | 525307_1 | A1222880 A1242392 AA961560 A1242524 A1719648 A1718138 AW275807 | | |
| | 442075 | 532052_1 | AW136928 A1685655 BE218584 BE465078 N68963 AA975338 BE147199 N76377 | | |

| | | |
|--------|-----------|---|
| 445165 | 63181_1 | AV652831 AA191140 AA329706 AJ267893 AJ796986 AW675672 AW195369 BE002835 BE003284 AA190592 AA769594 AW275548 R56781 AA807313 |
| 447197 | 711623_1 | AW169695 N31806 |
| 453685 | 977734_1 | R36075 AJ366546 R36167 |
| 454511 | 1220533_1 | AL110309 AW088119 H22881 |
| 454758 | 1233743_1 | AW948146 AW948135 AW802578 |
| 454835 | 1236507_1 | AW845266 AW845254 AW819440 AW819430 AW819425 AW819423 |
| 455082 | 1252687_1 | AW833763 AW833704 AW833618 |
| 455208 | 1260551_1 | BE148180 AW855210 AW855243 |
| 455212 | 1260678_1 | BE180276 AW866156 BE180165 |
| 455217 | 1261522_1 | AW866330 AW866410 AW866332 AW866411 AW866327 AW866326 AW866335 AW866334 AW866331 AW866333 AW866328 AW866329 |
| 455608 | 1337389_1 | AW867534 AW867539 |
| 455847 | 1375358_1 | BE011437 BE011402 BE011395 BE011428 BE011407 BE011421 BE011406 |
| 455944 | 1385569_1 | BE146775 BE146789 BE146792 BE147010 BE146941 BE146801 BE146998 BE147011 BE146903 BE146901 |
| 457892 | 432526_1 | BE160643 BE160585 |
| 457893 | 432938_1 | AA744389 AA744270 AA744284 AA744299 AA745380 AA744337 AA846905 AA847698 |
| 459279 | 975649_1 | AA744292 AA745577 AW748517 AW748564 AW748511 AW748513 AW748530 AW748574 BE062923 |
| | | AW814996 AL047199 AW850979 |

TABLE 46C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

| Pkey | Ref | Strand | NL_position |
|--------|---------|--------|---|
| 400484 | 8569067 | Minus | 52725-52912 |
| 400570 | 9884797 | Minus | 156787-156862,178082-178208,186819-186957 |
| 400639 | 9887597 | Plus | 23150-23580 |
| 400845 | 9188605 | Plus | 34428-34612 |
| 400860 | 9757499 | Minus | 151830-152104,152649-152744 |
| 400869 | 9838306 | Plus | 29152-30102 |
| 400950 | 7658481 | Minus | 157920-158564 |
| 400977 | 8072510 | Plus | 73950-74364 |
| 401004 | 7229982 | Plus | 62580-62772 |
| 401093 | 8516137 | Minus | 22335-23166 |
| 401183 | 7670214 | Minus | 39921-40601 |
| 401205 | 9743388 | Plus | 167373-167433,167936-168031 |
| 401208 | 7712287 | Plus | 163145-163281 |
| 401244 | 4827300 | Minus | 55359-56376 |
| 401348 | 9930791 | Minus | 9365-9490 |
| 401372 | 9944181 | Plus | 127056-127196 |
| 401424 | 8176894 | Plus | 24223-24428 |
| 401581 | 9502454 | Plus | 9440-10165 |
| 401629 | 8575965 | Minus | 169336-169788 |
| 401708 | 2951946 | Plus | 154511-155298 |
| 401736 | 3219338 | Plus | 1771-1894 |
| 401740 | 2982169 | Plus | 148357-148484,148591-148690 |
| 401747 | 9789672 | Minus | 118596-118816,119119-119244,119509-119761,120422-120990,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011 |
| 401961 | 4581193 | Minus | 124054-124209 |
| 402343 | 8099256 | Plus | 4677-6084 |
| 402363 | 9454515 | Plus | 25693-25991 |
| 402408 | 9796239 | Minus | 110326-110491 |
| 402524 | 9798518 | Minus | 20529-21096 |
| 402709 | 8901246 | Minus | 56847-57055 |
| 402732 | 9211639 | Minus | 147904-148107 |
| 403040 | 3133144 | Minus | 91632-91788,97918-98115 |
| 403137 | 9211494 | Minus | 92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337 |
| 403199 | 9958183 | Minus | 58895-59036,66618-66789 |
| 403278 | 8072597 | Plus | 146823-146986 |
| 403546 | 8078400 | Plus | 94703-94849 |
| 403764 | 7717105 | Minus | 118692-118853 |
| 403776 | 7770611 | Minus | 1414-1513,1624-1756 |
| 403859 | 7708954 | Plus | 113738-113858 |
| 403973 | 8575876 | Plus | 93873-94384 |
| 404012 | 8655948 | Plus | 551356-552233 |
| 404029 | 7671252 | Plus | 108716-111112 |
| 404072 | 9931705 | Plus | 49546-50498 |
| 404117 | 9796029 | Plus | 149723-149920 |
| 404170 | 9930793 | Plus | 168836-169248 |
| 404335 | 9838027 | Minus | 21030-21145,26504-26692 |
| 404440 | 7528051 | Plus | 80430-81581 |
| 404632 | 9796668 | Plus | 45096-45229 |
| 404702 | 7630798 | Plus | 78043-78890 |
| 404913 | 7341740 | Plus | 97717-97976 |
| 404996 | 6007890 | Plus | 37999-38145,38652-38998,39727-39872,40557-40674,42351-42450 |
| 405033 | 7107731 | Minus | 142358-142546 |
| 405065 | 7684500 | Minus | 13855-14027 |
| 405114 | 8096938 | Minus | 97013-97560 |
| 405287 | 3928029 | Plus | 89802-89999 |
| 405352 | 2822162 | Minus | 97253-97742 |
| 405362 | 2337862 | Minus | 105008-105142,105980-106091,140445-140556,142519-142641 |

| | | | | |
|----|--------|---------|-------|---|
| 5 | 405481 | 3688109 | Plus | 5718-5837,8719-8818 |
| | 405511 | 9454623 | Plus | 57731-57852 |
| | 405523 | 9454643 | Plus | 114550-114688,117265-117407,119490-119599,123237-123395,131140-131217 |
| | 405543 | 9857582 | Minus | 104338-104449 |
| | 405545 | 1054740 | Plus | 118677-118807,119091-119296,121626-121823 |
| 10 | 405637 | 6289229 | Plus | 189852-189978 |
| | 405696 | 4309923 | Minus | 1865-2013,2124-2231 |
| | 405770 | 2735037 | Plus | 61057-62075 |
| | 406465 | 9795550 | Plus | 94502-94706,96776-96914,98795-98928,102423-102576,105087-105191,107023-107127,108852-108992 |
| | | | | |

TABLE 47A: ABOUT 370 GENES SIGNIFICANTLY DOWN-REGULATED IN STOMACH CANCER COMPARED TO NORMAL STOMACH

Table 47A lists about 370 genes significantly down-regulated in stomach cancer compared to normal stomach. These were selected as for Table 46A, except that the numerator and denominator were switched and the ratio was equal to or less than 0.33.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal body tissue

| Pkey | ExAccn | UnigenelD | Unigene Title | R1 |
|--------|-----------|-----------|---|------|
| 412859 | NM_000705 | Hs.813 | ATPase, H ⁺ /K ⁺ exchanging, beta polypept | 0.02 |
| 423371 | AU076819 | Hs.1650 | solute carrier family 26, member 3 | 0.02 |
| 425607 | U09860 | Hs.158333 | protease, serine, 7 (enterokinase) | 0.04 |
| 429050 | X81333 | Hs.194777 | meprin A, beta | 0.04 |
| 421996 | AW583807 | Hs.1460 | glucagon | 0.05 |
| 441212 | AW242447 | Hs.146182 | cytosolic beta-glucosidase | 0.05 |
| 429093 | NM_000253 | Hs.195799 | microsomal triglyceride transfer protein | 0.06 |
| 403697 | NA | | NA | 0.07 |
| 402760 | NA | | NA | 0.08 |
| 428285 | AW340797 | Hs.98434 | ESTs | 0.08 |
| 419279 | AA235900 | Hs.87500 | ESTs | 0.08 |
| 422459 | K02100 | Hs.117050 | ornithine carbamoyltransferase | 0.09 |
| 422992 | AF016833 | Hs.122785 | maltase-glucoamylase (alpha-glucosidase) | 0.09 |
| 430867 | M16404 | Hs.248099 | cholinergic receptor, muscarinic 2 | 0.09 |
| 453989 | M63962 | Hs.36992 | ATPase, H ⁺ /K ⁺ exchanging, alpha polypept | 0.10 |
| 443022 | AL046485 | Hs.207604 | ESTs | 0.10 |
| 413382 | BE090689 | | gb:RC1-BT0720-280300-011-408 BT0720 Homo | 0.10 |
| 450769 | AA057418 | Hs.33654 | ESTs | 0.10 |
| 428070 | T63918 | Hs.182313 | retinol-binding protein 2, cellular | 0.10 |
| 415447 | Z97171 | Hs.78454 | myocilin, trabecular meshwork inducible | 0.11 |
| 430073 | U86136 | Hs.232070 | telomerase-associated protein 1 | 0.11 |
| 431716 | D89053 | Hs.268012 | fatty-acid-Coenzyme A ligase, long-chain | 0.12 |
| 416889 | AW250318 | Hs.80395 | mal, T-cell differentiation protein | 0.12 |
| 405650 | NA | | NA | 0.12 |
| 419219 | AW583139 | Hs.89717 | carboxypeptidase A2 (pancreatic) | 0.12 |
| 401623 | NA | | NA | 0.12 |
| 400811 | AF219139 | Hs.87726 | KIAA0154 protein; ADP-ribosylation facto | 0.13 |
| 455826 | BE144228 | | gb:MR0-HT0165-140200-009-d04 HT0165 Homo | 0.13 |
| 414949 | C15314 | Hs.323349 | ESTs | 0.13 |
| 407486 | S69741 | | gb:hSCG-3=stomach cancer gene-3 (oncogen | 0.13 |
| 407494 | U10072 | | gb:Human forkhead family (AFX1) mRNA, pa | 0.13 |
| 401015 | NA | | NA | 0.13 |
| 426651 | AU076646 | Hs.171683 | nuclear receptor subfamily 1, group H, m | 0.14 |
| 450926 | A1744361 | Hs.205591 | ESTs, Weakly similar to T45608 zinc fing | 0.14 |
| 443564 | A1921685 | Hs.199713 | ESTs | 0.14 |
| 457955 | A1208986 | Hs.143945 | ESTs | 0.14 |
| 457345 | A1699933 | Hs.192175 | ESTs | 0.14 |
| 417118 | U38654 | Hs.50477 | RAB27A, member RAS oncogene family | 0.14 |
| 408518 | BE162203 | Hs.314758 | ESTs | 0.14 |
| 444938 | AW470690 | Hs.148814 | ESTs | 0.15 |
| 403670 | NA | | NA | 0.15 |
| 432440 | X63597 | Hs.2996 | sucrase-isomaltase | 0.15 |
| 428492 | AW662740 | Hs.259391 | ESTs | 0.15 |
| 443607 | A1452512 | Hs.134069 | ESTs | 0.15 |
| 446914 | BE044496 | Hs.166994 | FAT tumor suppressor (Drosophila) homolo | 0.15 |
| 424596 | AB020639 | Hs.151017 | estrogen-related receptor gamma | 0.15 |
| 430350 | BE169639 | | gb:PM1-HT0527-280200-005-a05 HT0527 Homo | 0.16 |
| 431094 | AW972276 | Hs.116195 | ESTs | 0.16 |
| 401683 | NA | | NA | 0.16 |
| 419278 | AU076799 | Hs.1247 | apolipoprotein A-IV | 0.16 |
| 455071 | BE145826 | | gb:MR0-HT0208-101299-202-e12 HT0208 Homo | 0.16 |
| 454282 | AW296422 | | gb:U1-H-BW0-aio-h-05-0-U1.s1 NCI_CGAP_Su | 0.16 |
| 428848 | NM_000230 | Hs.194236 | leptin (murine obesity homolog) | 0.16 |
| 451729 | AW160725 | Hs.312469 | ESTs | 0.16 |
| 451103 | RS2804 | Hs.25956 | DKFZP564D206 protein | 0.16 |
| 428602 | AL137479 | Hs.186655 | Homo sapiens mRNA; cDNA DKFZp434M0223 (f | 0.16 |
| 437157 | BE048860 | Hs.120655 | ESTs | 0.17 |
| 422731 | AL138411 | | gb:DKFZp434A1229_r1 434 (synonym: htes3) | 0.17 |
| 402015 | NA | | NA | 0.17 |
| 414758 | H82022 | Hs.282847 | pregnancy specific beta-1-glycoprotein 3 | 0.17 |
| 412793 | AW997986 | | gb:RC1-BN0056-230200-021-e11 BN0056 Homo | 0.17 |
| 438152 | AW292520 | Hs.122082 | ESTs | 0.17 |

| | | | | |
|----|--------|-----------|--|------|
| | 401685 | NA | NA | 0.17 |
| | 441519 | AA972740 | ESTs | 0.17 |
| | 438327 | H87407 | chorionic gonadotropin, beta polypeptide | 0.17 |
| 5 | 402761 | BE387621 | chaperonin containing TCP1, subunit 7 (e | 0.17 |
| | 424268 | AA397653 | Human DNA sequence from clone 495010 on | 0.18 |
| | 414507 | AW102637 | Homo sapiens cDNA FLJ14647 fis, clone NT | 0.18 |
| | 413808 | J00287 | Homo sapiens mRNA for caldesmon, 3' UTR | 0.18 |
| | 401132 | NA | NA | 0.18 |
| 10 | 412374 | X01388 | apolipoprotein C-III | 0.18 |
| | 423417 | AP000365 | potassium large conductance calcium-acti | 0.18 |
| | 447677 | AI419235 | gb:U21d02.x1 NCI_CGAP_Bm23 Homo sapien | 0.18 |
| | 448828 | AI580296 | ESTs, Weakly similar to KIAA1437 protein | 0.18 |
| | 424122 | AA335593 | ESTs | 0.18 |
| 15 | 417332 | AW972717 | hypothetical protein FLJ21511 | 0.18 |
| | 434597 | AW974668 | gb:EST386757 MAGE resequences, MAGM Homo | 0.19 |
| | 428804 | AK000713 | hypothetical protein FLJ20706 | 0.19 |
| | 410280 | AA083558 | ESTs | 0.19 |
| | 408382 | AA071244 | gb:zm73g03.r1 Stratagene neuroepithelium | 0.19 |
| 20 | 428062 | AA420683 | hypothetical protein FLJ14103 | 0.19 |
| | 426069 | H10807 | Homo sapiens cDNA FLJ14028 fis, clone HE | 0.19 |
| | 430135 | NM_000035 | aldolase B, fructose-bisphosphate | 0.19 |
| | 414802 | AI793107 | Ris | 0.19 |
| | 457432 | NM_005136 | potassium voltage-gated channel, Isk-rel | 0.19 |
| 25 | 446909 | AA004895 | ESTs | 0.19 |
| | 435447 | AI872932 | gb:wm72e03.x1 NCI_CGAP_U12 Homo sapiens | 0.20 |
| | 408611 | NM_004367 | chemokine (C-C motif) receptor 6 | 0.20 |
| | 423577 | AW810107 | Homo sapiens cDNA: FLJ22145 fis, clone H | 0.20 |
| | 439328 | W07411 | ESTs, Moderately similar to ALU3_HUMAN A | 0.20 |
| 30 | 436741 | AA860163 | ESTs | 0.20 |
| | 426635 | BE395109 | hypothetical protein MGC13057 | 0.20 |
| | 418277 | AW135221 | ESTs | 0.20 |
| | 448871 | BE616709 | kruppel-related zinc finger protein hckr | 0.20 |
| | 459370 | AA889982 | ESTs, Weakly similar to I38022 hypotheti | 0.21 |
| 35 | 427469 | AA403084 | ESTs, Weakly similar to 2109260A B cell | 0.21 |
| | 432887 | AI926047 | ESTs | 0.21 |
| | 421296 | NM_002666 | peritropin | 0.21 |
| | 449216 | AW295417 | ESTs | 0.21 |
| | 414835 | AA156720 | ESTs | 0.21 |
| 40 | 459233 | AI939966 | gb:MRO-CT0015-160799-002-b06 CT0015 Homo | 0.21 |
| | 439756 | AL359651 | Homo sapiens mRNA full length insert cDN | 0.21 |
| | 427167 | AI239607 | hypothetical protein MGC11324 | 0.21 |
| | 400410 | AF154915 | homeo box D12 | 0.21 |
| | 409828 | AW501137 | gb:U1-HF-BP0p-ait-e-12-0-U1.r1 NIH_MGC_5 | 0.22 |
| 45 | 428470 | AC002301 | Homo sapiens Chromosome 16 BAC clone CIT | 0.22 |
| | 455968 | BE168828 | gb:QV1-HT0517-020400-145-f04 HT0517 Homo | 0.22 |
| | 404145 | NA | NA | 0.22 |
| | 454011 | M31008 | alkaline phosphatase, intestinal | 0.22 |
| | 430588 | AI741461 | ESTs | 0.22 |
| 50 | 403652 | NA | NA | 0.22 |
| | 440410 | AW204436 | ESTs | 0.22 |
| | 453871 | BE300380 | Homo sapiens cDNA FLJ12758 fis, clone NT | 0.22 |
| | 458567 | AI222075 | ESTs | 0.22 |
| | 436004 | AA703332 | folate transporter/carrier | 0.22 |
| 55 | 417408 | F17211 | Homo sapiens skeletal myosin light chain | 0.22 |
| | 448643 | AI557531 | gb:pt2.1-06.D06.r tumor2 Homo sapiens cD | 0.22 |
| | 404401 | NA | NA | 0.22 |
| | 428088 | AA421130 | EST | 0.22 |
| | 427074 | AA527435 | hepatocellular carcinoma antigen gene 52 | 0.22 |
| 60 | 421972 | M18185 | gastric inhibitory polypeptide | 0.22 |
| | 429001 | AF098951 | ATP-binding cassette, sub-family G (WHIT | 0.22 |
| | 441155 | AW161008 | GABA(A) receptor-associated protein | 0.22 |
| | 402750 | NA | NA | 0.22 |
| | 438587 | AA811450 | ESTs | 0.22 |
| 65 | 404848 | NA | NA | 0.22 |
| | 427833 | AA416615 | ESTs | 0.23 |
| | 439907 | AA853978 | ESTs | 0.23 |
| | 414373 | AW162907 | proline-rich protein with nuclear target | 0.23 |
| | 446817 | AI700684 | ESTs | 0.23 |
| 70 | 437333 | AA748898 | gb:ny76h10.s1 NCI_CGAP_GCB1 Homo sapiens | 0.23 |
| | 404097 | NA | NA | 0.23 |
| | 446393 | AW014174 | zinc finger protein | 0.23 |
| | 456328 | T41368 | gb:ph1d1_19/1TV Outward Alu-primed hncDN | 0.23 |
| | 401042 | NA | NA | 0.23 |
| 75 | 458441 | AW842283 | cyclin I | 0.23 |
| | 435547 | AW117431 | ESTs | 0.23 |
| | 429060 | AW139155 | hypothetical protein DKFZp434O0320 | 0.23 |
| | 425158 | AW954631 | t-complex-associated-testis-expressed 1- | 0.23 |
| | 448758 | AB018311 | KIAA0768 protein | 0.23 |
| 80 | 441240 | AA923749 | ESTs | 0.23 |
| | 436562 | H71937 | ESTs, Weakly similar to I38022 hypotheti | 0.23 |
| | 424104 | AA669515 | ESTs | 0.23 |
| | 447452 | BE618258 | Homo sapiens, clone IMAGE:3869590, mRNA, | 0.23 |
| | 444515 | AW204908 | ESTs | 0.24 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 433084 | M18079 | Hs.282265 | fatty acid binding protein 2, intestinal | 0.24 |
| | 406560 | NA | | NA | 0.24 |
| | 432408 | N39127 | Hs.332557 | ESTs, Weakly similar to A46010 X-linked | 0.24 |
| 5 | 455699 | BE068121 | | gb:CM1-BT0368-061299-060-a02 BT0368 Homo | 0.24 |
| | 453979 | M68895 | Hs.76800 | alcohol dehydrogenase 6 (class V) | 0.24 |
| | 439657 | W93589 | | gb:zd95g05.s1 Soares_fetal_heart_NbHH19W | 0.24 |
| | 407512 | X15674 | | gb:Human pTR5 mRNA for repetitive sequen | 0.24 |
| | 440875 | AW138036 | Hs.201788 | ESTs | 0.24 |
| 10 | 404753 | NA | | NA | 0.24 |
| | 411119 | MG0627 | Hs.753 | formyl peptide receptor 1 | 0.24 |
| | 418692 | AK000268 | Hs.87383 | hypothetical protein | 0.24 |
| | 415327 | H22769 | | gb:ym54c02.r1 Soares infant brain 1NIB H | 0.24 |
| | 429446 | AJ547111 | | gb:PN2.1_A01_G12.r mynorm Homo sapiens c | 0.24 |
| 15 | 455391 | BE156230 | | gb:QV0-HT0367-310100-102-c11 HT0367 Homo | 0.25 |
| | 422818 | AA404290 | Hs.97848 | ESTs | 0.25 |
| | 435338 | AA678071 | Hs.194300 | ESTs, Weakly similar to I38022 hypotheti | 0.25 |
| | 414203 | BE262170 | Hs.78629 | ATPase, Na ⁺ /K ⁺ transporting, beta 1 poly | 0.25 |
| | 403941 | NA | | NA | 0.25 |
| 20 | 414383 | BE279406 | | gb:601157981F1 NIH_MGC_21 Homo sapiens c | 0.25 |
| | 412008 | NM_001841 | Hs.73037 | cannabinoid receptor 2 (macrophage) | 0.25 |
| | 424985 | AJ907236 | Hs.279935 | Homo sapiens cDNA FLJ11780 fs, clone HE | 0.25 |
| | 450736 | AW970060 | | gb:EST382140 MAGE resequences, MAGK Homo | 0.25 |
| | 431185 | H02767 | Hs.28944 | ESTs | 0.25 |
| 25 | 455308 | AW893949 | | gb:RC4-NN0027-060400-011-a09 NN0027 Homo | 0.25 |
| | 435464 | BE548300 | Hs.192999 | ESTs, Moderately similar to KIAA0961 pro | 0.25 |
| | 418525 | AW450369 | Hs.86937 | ESTs | 0.25 |
| | 402790 | | | NA | 0.25 |
| | 411869 | W20027 | Hs.23439 | ESTs | 0.25 |
| 30 | 400332 | S66407 | Hs.248032 | FLT4 | 0.25 |
| | 424884 | AW299437 | Hs.225717 | ESTs | 0.25 |
| | 414376 | BE393856 | Hs.66915 | ESTs, Weakly similar to 16.7Kd protein [| 0.25 |
| | 439780 | AL109688 | | gb:Homo sapiens mRNA full length insert | 0.25 |
| | 408947 | AL080093 | Hs.49117 | Homo sapiens mRNA; cDNA DKFZp564N1662 (f | 0.25 |
| 35 | 404900 | NA | | NA | 0.25 |
| | 441918 | AJ733373 | Hs.128119 | ESTs | 0.25 |
| | 441639 | AJ133287 | Hs.303953 | ESTs | 0.25 |
| | 459396 | AJ907536 | Hs.103869 | ESTs | 0.25 |
| | 452755 | AW138937 | Hs.213436 | ESTs, Weakly similar to A34087 hypotheti | 0.25 |
| 40 | 422183 | AA431698 | Hs.112794 | Human DNA sequence from clone 1068E13 on | 0.25 |
| | 415186 | AA160945 | Hs.14479 | Homo sapiens cDNA FLJ14199 fs, clone NT | 0.26 |
| | 429450 | AA824451 | Hs.94292 | hypothetical protein FLJ23311 | 0.26 |
| | 455615 | BE045344 | Hs.274923 | ESTs, Moderately similar to unnamed prot | 0.26 |
| | 454633 | AW811380 | | gb:IL3-ST0143-290999-019-D05 ST0143 Homo | 0.26 |
| 45 | 424853 | BE549737 | Hs.132967 | Human EST clone 122887 mariner transposo | 0.26 |
| | 455802 | BE141491 | | gb:MR0-HT0080-011099-002-h06 HT0080 Homo | 0.26 |
| | 414003 | AA134472 | | gb:zo13c01.s1 Stratagene colon (937204) | 0.26 |
| | 436363 | AA843926 | Hs.124434 | ESTs | 0.26 |
| | 456074 | BE409525 | Hs.902 | neurofibromin 2 (bilateral acoustic neur | 0.26 |
| 50 | 430569 | AF241254 | Hs.178098 | angiotensin I converting enzyme (peptidy | 0.26 |
| | 445635 | AJ769774 | Hs.209831 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 0.26 |
| | 405953 | NA | | NA | 0.26 |
| | 411021 | F00055 | Hs.172004 | titin | 0.26 |
| 55 | 428443 | BE618106 | Hs.184326 | CDC10 (cell division cycle 10, S. cerevi | 0.26 |
| | 434345 | AF127772 | | gb:Homo sapiens cell-line E8CASS clone E | 0.26 |
| | 455743 | BE073754 | | gb:RC0-BT0561-210100-032-d07 BT0561 Homo | 0.26 |
| | 451138 | W92287 | Hs.40268 | ESTs | 0.26 |
| | 449528 | H63337 | Hs.38178 | hypothetical protein FLJ23468 | 0.26 |
| | 441040 | AW449782 | Hs.178803 | ESTs | 0.26 |
| 60 | 458830 | AW501248 | Hs.250824 | Homo sapiens cDNA: FLJ23435 fs, clone H | 0.26 |
| | 428861 | AW352234 | Hs.269365 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 0.26 |
| | 435469 | AW388237 | Hs.191204 | ESTs | 0.27 |
| | 427562 | R56424 | Hs.26534 | ESTs | 0.27 |
| | 434779 | AF153815 | Hs.50151 | potassium inwardly-rectifying channel, s | 0.27 |
| 65 | 423528 | AB011137 | Hs.300938 | KIAA0565 gene product | 0.27 |
| | 406589 | | | NA | 0.27 |
| | 450059 | BE220223 | Hs.279626 | ESTs | 0.27 |
| | 417296 | L36196 | Hs.81884 | sulfotransferase family, cytosolic, 2A, | 0.27 |
| 70 | 454007 | AW015870 | Hs.232081 | ESTs | 0.27 |
| | 426062 | N57014 | Hs.75874 | pregnancy-associated plasma protein A | 0.27 |
| | 441665 | AJ301355 | Hs.151285 | ESTs | 0.27 |
| | 405037 | NA | | NA | 0.27 |
| | 446820 | AW295037 | Hs.254986 | ESTs | 0.27 |
| | 448487 | AJ523720 | Hs.172567 | ESTs | 0.27 |
| 75 | 447567 | AW474513 | Hs.224397 | ESTs, Weakly similar to I38931 Wiskott-A | 0.27 |
| | 408540 | L13220 | Hs.639 | calbindin 3, (vitamin D-dependent calciu | 0.27 |
| | 407601 | AC002300 | Hs.37129 | sodium channel, nonvoltage-gated 1, beta | 0.27 |
| | 432501 | BE546532 | Hs.25682 | Homo sapiens mRNA for KIAA1863 protein, | 0.27 |
| | 401350 | NA | | NA | 0.27 |
| 80 | 417569 | R00271 | Hs.144651 | ESTs | 0.27 |
| | 443542 | AJ927065 | Hs.146040 | ESTs | 0.27 |
| | 437105 | AA744554 | Hs.222127 | ESTs | 0.27 |
| | 432119 | T80289 | Hs.302041 | Homo sapiens clone 24762 mRNA sequence | 0.27 |
| | 419056 | M89957 | Hs.89575 | CD79B antigen (immunoglobulin-associated | 0.28 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 427812 | AA770424 | Hs.98162 | ESTs | 0.28 |
| | 423557 | AB011176 | Hs.129801 | KIAA0604 gene product | 0.28 |
| | 445311 | AW027556 | Hs.156286 | ESTs | 0.28 |
| | 402758 | NA | | NA | 0.28 |
| 5 | 448240 | AJ478345 | Hs.191034 | ESTs | 0.28 |
| | 401333 | NA | | NA | 0.28 |
| | 444107 | T46839 | Hs.10319 | UDP glycosyltransferase 2 family, polype | 0.28 |
| | 454738 | BE072139 | | gb:PM1-BT0533-291299-002-b05 BT0533 Homo | 0.28 |
| 10 | 442896 | R37725 | Hs.261108 | ESTs | 0.28 |
| | 447949 | AJ446820 | Hs.165839 | EST | 0.28 |
| | 435625 | H50654 | Hs.113999 | ESTs | 0.28 |
| | 415817 | U88967 | Hs.78867 | protein tyrosine phosphatase, receptor-t | 0.28 |
| | 438380 | T06430 | Hs.6194 | chondroitin sulfate proteoglycan BEHAB/b | 0.28 |
| 15 | 442967 | AJ025460 | Hs.220977 | ESTs | 0.28 |
| | 448062 | AW295923 | Hs.255472 | KIAA1843 protein | 0.28 |
| | 425860 | L29339 | Hs.1964 | solute carrier family 5 (sodium/glucose | 0.28 |
| | 451839 | AJ820516 | Hs.16857 | ESTs | 0.28 |
| | 446000 | AV656052 | Hs.1504 | hemopexin | 0.28 |
| 20 | 443506 | H10661 | Hs.192124 | ESTs, Weakly similar to I38022 hypotheti | 0.28 |
| | 418345 | AJ001696 | Hs.241407 | serine (or cysteine) proteinase inhibito | 0.28 |
| | 445481 | AW661846 | Hs.148836 | ESTs | 0.28 |
| | 409337 | H71289 | Hs.220535 | ESTs | 0.28 |
| | 411414 | AW897236 | | gb:CM0-NN0057-150400-335-c06 NN0057 Homo | 0.28 |
| 25 | 427642 | R40761 | Hs.9834 | ESTs | 0.28 |
| | 456392 | W28766 | | gb:51d3 Human retina cDNA randomly prime | 0.28 |
| | 409920 | BE169746 | Hs.12504 | likely ortholog of mouse Arkadia | 0.28 |
| | 410285 | AA083609 | | gb:zm63d05.r1 Stratagene fibroblast (937 | 0.28 |
| | 442496 | R55073 | Hs.124130 | ESTs | 0.28 |
| 30 | 423770 | AW976766 | Hs.132776 | Homo sapiens cDNA FLJ10077 fis, clone HE | 0.28 |
| | 423467 | AK000214 | Hs.129014 | hypothetical protein FLJ20207 | 0.29 |
| | 458716 | N99013 | Hs.16762 | Homo sapiens mRNA; cDNA DKFZp564B2062 (f | 0.29 |
| | 423235 | AW410698 | Hs.169917 | neurabin II | 0.29 |
| | 431087 | H12723 | Hs.290791 | ESTs | 0.29 |
| 35 | 459106 | AW589793 | Hs.224713 | ESTs | 0.29 |
| | 414870 | N72264 | Hs.300670 | KIAA1204 protein | 0.29 |
| | 402243 | | | NA | 0.29 |
| | 432628 | R02394 | Hs.269436 | ESTs, Moderately similar to PC4259 ferri | 0.29 |
| | 404364 | NA | | NA | 0.29 |
| 40 | 400480 | | | NA | 0.29 |
| | 456083 | U46922 | Hs.77252 | fragile histidine triad gene | 0.29 |
| | 446598 | AW250546 | | gb:2821774.5prime NIH_MGC_7 Homo sapiens | 0.29 |
| | 422201 | NM_001505 | Hs.113207 | G protein-coupled receptor 30 | 0.29 |
| | 443919 | AJ091284 | Hs.135224 | ESTs, Weakly similar to A47582 B-cell gr | 0.29 |
| 45 | 453948 | AJ970797 | Hs.64859 | ESTs | 0.29 |
| | 403792 | NA | | NA | 0.29 |
| | 418957 | AJ792615 | Hs.188712 | ESTs | 0.29 |
| | 457960 | AA771881 | Hs.298149 | ESTs | 0.29 |
| | 404269 | | | NA | 0.29 |
| 50 | 439309 | AF090097 | Hs.6524 | Homo sapiens clone IMAGE 25997 | 0.29 |
| | 458239 | BE439877 | Hs.283389 | ESTs | 0.30 |
| | 414941 | C14865 | Hs.332341 | ESTs | 0.30 |
| | 404954 | | | NA | 0.30 |
| | 441609 | AA946764 | Hs.133460 | ESTs | 0.30 |
| 55 | 426895 | AA416880 | Hs.225738 | ESTs | 0.30 |
| | 403182 | NA | | NA | 0.30 |
| | 402319 | | | NA | 0.30 |
| | 429699 | AJ383469 | Hs.159300 | ESTs | 0.30 |
| | 405669 | NA | | NA | 0.30 |
| 60 | 459312 | AF107457 | Hs.37035 | homeo box HB9 | 0.30 |
| | 431853 | AA521034 | Hs.70834 | ESTs | 0.30 |
| | 449768 | AJ972746 | Hs.102945 | ESTs, Weakly similar to I78885 serine/th | 0.30 |
| | 443609 | AV650231 | Hs.282941 | ESTs, Highly similar to A Chain A, Human | 0.30 |
| | 454293 | H49739 | Hs.134013 | ESTs, Moderately similar to HK61_HUMAN H | 0.30 |
| 65 | 447569 | AJ393202 | Hs.147554 | hypothetical protein FLJ23392 | 0.30 |
| | 400128 | NA | | NA | 0.30 |
| | 423208 | AA323191 | Hs.137064 | cytoplasmic polyadenylation element bind | 0.30 |
| | 434227 | AF119893 | Hs.63382 | hypothetical protein PRO2714 | 0.30 |
| | 424208 | AW583123 | Hs.143113 | pancreatic lipase-related protein 2 | 0.30 |
| 70 | 401165 | NA | | NA | 0.30 |
| | 415394 | R19249 | Hs.22654 | sodium channel, voltage-gated, type I, a | 0.30 |
| | 443110 | AW352243 | Hs.132665 | ESTs | 0.30 |
| | 426724 | AA383623 | Hs.293616 | ESTs | 0.30 |
| | 416035 | H42314 | | gb:yo09e02.s1 Soares adult brain N2b5HB5 | 0.30 |
| 75 | 409753 | AA234847 | | gb:zs37b10.r1 Soares_NhHMPu_S1 Homo sapi | 0.31 |
| | 459221 | BE246522 | Hs.306121 | leukocyte receptor cluster (LRC) encoded | 0.31 |
| | 408895 | AA058730 | Hs.191464 | ESTs | 0.31 |
| | 405110 | NA | | NA | 0.31 |
| | 432430 | AW079984 | Hs.262480 | ESTs, Weakly similar to PIHUB6 salivary | 0.31 |
| 80 | 426442 | AA378656 | Hs.106510 | ESTs, Moderately similar to ALU2_HUMAN A | 0.31 |
| | 411765 | H43346 | | gb:yp09a04.r1 Soares breast 3NbHBst Homo | 0.31 |
| | 431854 | AA383550 | Hs.271699 | polymerase (DNA directed) iota | 0.31 |
| | 457553 | AJ861895 | Hs.304505 | ESTs | 0.31 |
| | 412301 | AW936328 | | gb:QV4-DT0021-281299-070-07 DT0021 Homo | 0.31 |

| | | | | | |
|----|--------|----------|-----------|--|------|
| 5 | 418626 | AW299508 | Hs.135230 | ESTs | 0.31 |
| | 416156 | Z41922 | | gb:HSC03B101 normalized infant brain cDN | 0.31 |
| | 416275 | H42823 | Hs.155742 | glyoxylate reductase/hydroxypyruvate red | 0.31 |
| | 419091 | T85332 | Hs.178294 | ESTs | 0.31 |
| | 420118 | AW295297 | Hs.182585 | KIAA1276 protein | 0.31 |
| | 451094 | A1949825 | Hs.260395 | ESTs | 0.31 |
| | 403214 | NA | | NA | 0.31 |
| | 412717 | W00973 | Hs.334728 | ESTs | 0.31 |
| 10 | 428782 | X12830 | Hs.193400 | interleukin 6 receptor | 0.31 |
| | 449202 | AW295154 | Hs.255396 | ESTs | 0.31 |
| | 433138 | AB029496 | Hs.59729 | semaphorin sem2 | 0.31 |
| | 436602 | A1793222 | Hs.166817 | ESTs | 0.31 |
| | 424844 | D61524 | | gb:HUM413E07B Clontech human fetal brain | 0.32 |
| 15 | 435253 | W91884 | | gb:zh47D8.s1 Soares_fetal_liver_spleen_ | 0.32 |
| | 455350 | AW901809 | | gb:QV0-NN1020-170400-195-h02 NN1020 Homo | 0.32 |
| | 416320 | H47867 | Hs.34024 | ESTs | 0.32 |
| | 406333 | | | NA | 0.32 |
| | 443652 | A1080692 | Hs.134229 | ESTs, Weakly similar to I54401 hypertens | 0.32 |
| 20 | 457103 | A1421187 | Hs.189192 | ESTs, Weakly similar to T COMPLEX TESTIS | 0.32 |
| | 423593 | AA328144 | | gb:EST31752 Embryo, 12 week 1 Homo sapie | 0.32 |
| | 453242 | T98327 | Hs.18343 | ESTs | 0.32 |
| | 456281 | AA284166 | Hs.84113 | cyclin-dependent kinase inhibitor 3 (CDK | 0.32 |
| | 403847 | NA | | NA | 0.32 |
| 25 | 458711 | AL036877 | Hs.282878 | ESTs | 0.32 |
| | 406242 | NA | | NA | 0.32 |
| | 433493 | AA594915 | Hs.155087 | ESTs | 0.32 |
| | 458147 | AW752597 | | gb:IL3-CT0214-161299-045-B06 CT0214 Homo | 0.32 |
| 30 | 437403 | A1208149 | Hs.121196 | ESTs | 0.32 |
| | 407823 | D44744 | Hs.247447 | ESTs | 0.32 |
| | 457300 | AW297436 | Hs.158849 | Homo sapiens cDNA: FLJ21663 fs, clone C | 0.32 |
| | 436089 | AA804957 | Hs.119840 | ESTs | 0.32 |
| | 457463 | AW877031 | Hs.272321 | hypothetical protein FLJ12571 | 0.32 |
| | 433370 | A1084343 | Hs.122310 | ESTs | 0.32 |
| 35 | 436298 | AW293496 | Hs.180138 | ESTs | 0.32 |
| | 419768 | T72104 | Hs.93194 | apolipoprotein A-I | 0.32 |
| | 449428 | A1651280 | Hs.195685 | ESTs | 0.33 |
| | 406291 | NA | | NA | 0.33 |
| 40 | 409699 | BE154650 | | gb:PM3-HT0344-071299-003-c08 HT0344 Homo | 0.33 |
| | 418162 | T11958 | | gb:A802R Heart Homo sapiens cDNA clone A | 0.33 |
| | 408316 | AW807771 | | gb:MR4-ST0098-090300-003-c05 ST0098 Homo | 0.33 |
| | 404187 | NA | | NA | 0.33 |
| | 452992 | A1792376 | Hs.31290 | Homo sapiens clone 23832 mRNA sequence | 0.33 |
| 45 | 448355 | A1493734 | Hs.329374 | ESTs | 0.33 |
| | 442423 | BE326264 | Hs.246842 | ESTs | 0.33 |
| | 439474 | A1824060 | Hs.211501 | ESTs | 0.33 |
| | 457149 | AA429575 | Hs.297493 | ESTs | 0.33 |
| | 448623 | BE613468 | Hs.107515 | ESTs, Weakly similar to T00329 hypotheti | 0.33 |
| | 454790 | AW820852 | | gb:RC2-ST0301-120200-011-f12 ST0301 Homo | 0.33 |
| 50 | 419372 | W28781 | | gb:51h3 Human retina cDNA randomly prime | 0.33 |
| | 406293 | NA | | NA | 0.33 |
| | 422933 | AF073931 | Hs.122359 | calcium channel, voltage-dependent, alph | 0.33 |
| | 451818 | A1819018 | Hs.339668 | ESTs | 0.33 |
| | 441912 | AA971484 | Hs.159938 | ESTs | 0.33 |
| 55 | 429013 | AJ012590 | Hs.194728 | hexose-6-phosphate dehydrogenase (glucos | 0.33 |
| | 422304 | AK002016 | Hs.114727 | Homo sapiens, clone MGC:16327, mRNA, com | 0.33 |
| | 457394 | M86528 | Hs.266902 | neurotrophin 5 (neurotrophin 4/5) | 0.33 |
| | 406597 | | | NA | 0.33 |
| | 451636 | AW173270 | Hs.140444 | ESTs | 0.33 |
| 60 | 424226 | N94153 | Hs.19155 | ESTs | 0.33 |

TABLE 47B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

| | | | |
|----|--------|------------|---|
| 65 | Pkey | CAT Number | Accession |
| | 408316 | 1051210_1 | AW807771 AW179260 AW807851 AW179240 AW845961 AW807693 BE141176 AW807594 AW807772 AW846003 AW845963 AW179239 |
| | 409382 | 112508_1 | AA071244 AA071477 |
| 70 | 409699 | 1149033_1 | BE154650 BE154785 AW468343 BE154816 BE154667 |
| | 409753 | 115305_1 | AA234847 AA077472 |
| | 409828 | 1155571_1 | AW501137 AW501295 AW501212 |
| | 410285 | 119128_1 | AA083609 AA083790 AA112048 |
| | 411414 | 1245024_1 | AW897236 AW845406 |
| 75 | 411765 | 125700_1 | H43346 AA248302 AA095182 |
| | 412301 | 1288123_1 | AW936328 AW936539 |
| | 412793 | 1327636_-1 | AW997986 |
| | 413382 | 1365954_1 | BE090689 BE090685 BE090697 BE090680 BE090691 BE090696 BE090698 BE090686 |
| | 414003 | 140888_1 | AA134472 R76288 AW750262 |
| 80 | 414383 | 1440279_1 | BE279406 BE280100 |
| | 415327 | 1534137_1 | H22769 R35182 Z43545 F05783 N92089 H71928 |
| | 416035 | 1567254_1 | H42314 H43080 H45217 H15384 |
| | 416156 | 1573980_1 | Z41922 H23072 T77322 |
| | 418162 | 1725383_1 | T11958 T11756 T11816 T20135 T19729 R45874 |

| | | | |
|----|--------|-----------|--|
| 5 | 419372 | 1842942_1 | W28781 W26588 W26377 |
| | 422731 | 220507_1 | AL138411 AL138412 AA315860 |
| | 423593 | 229555_1 | AA328144 AW962385 N30457 |
| | 424844 | 244291_1 | D61524 AA347654 AW961758 |
| | 429446 | 304683_1 | AI547111 AW973749 AA558007 |
| | 430350 | 316401_1 | BE169639 AA476976 |
| | 434345 | 38411_1 | AF127772 AF062358 AF060217 AA652270 F23288 |
| | 434597 | 389383_1 | AW974668 AA651959 AA649572 AA640401-AA640402 |
| 10 | 435253 | 403478_1 | W91884 W95119 AA676941 |
| | 435447 | 406400_1 | AI872932 AA682306 BE220163 W88695 T81307 H91447 |
| | 437333 | 436167_1 | AA748898 AW997701 AW997703 |
| | 439657 | 47499_1 | W93589 W93487 AF086493 |
| | 439780 | 47673_1 | AL109688 R23665 R26578 |
| 15 | 446598 | 68463_1 | AW250546 BE257108 BE251006 BE255957 BE250926 BE513012 AV659318 |
| | 447677 | 732252_1 | AM19235 AW05016 BE007490 BE550241 |
| | 448643 | 773566_-1 | AI557531 |
| | 450736 | 844652_1 | AW970060 AI732366 AI792313 AW839644 |
| | 454282 | 1091035_1 | AW296422 H72616 H63825 |
| 20 | 454633 | 1227504_1 | AW811380 AW811385 |
| | 454738 | 1232449_1 | BE072139 BE157977 BE157974 AW857974 AW817778 |
| | 454790 | 1234752_1 | AW820852 AW820773 AW821088 |
| | 455071 | 1252281_1 | BE145826 BE145815 BE145822 AW854707 BE145912 |
| | 455308 | 1278147_1 | AW893949 AW893960 AW893966 |
| 25 | 455350 | 1283853_1 | AW901809 AW901787 AW901795 AW901792 AW901744 AW901753 AW901807 AW901798 |
| | 455391 | 1288067_1 | BE156230 BE156239 AW936260 |
| | 455699 | 1351258_1 | BE068121 BE068090 BE068153 BE068128 BE068197 BE068136 BE068140 BE068185 BE068105 |
| | 455743 | 1354978_1 | BE073754 BE073753 BE073755 BE073756 BE073752 BE073795 BE073796 BE073704 BE073791 BE073733 BE073695 |
| | 455802 | 1370828_1 | BE141491 BE141016 BE141479 |
| 30 | 455826 | 1373392_1 | BE144228 BE144291 |
| | 455968 | 1391117_1 | BE168828 BE168830 BE168823 BE168928 BE168820 BE168826 |
| | 456328 | 1789791_1 | T41368 T41369 T41294 |
| | 456392 | 1843059_1 | W28766 W26500 |
| | 458147 | 488021_1 | AW752597 AW848781 AW849062 AW848490 AW752699 AW752604 AW752700 |
| 35 | 459233 | 944881_1 | AI939966 AI939988 AI939951 AI939981 AI939976 AI939959 |

TABLE 47C:

| | |
|--------------|---|
| Pkey: | Unique number corresponding to an Eos probeset |
| Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. |
| Strand: | Indicates DNA strand from which exons were predicted. |
| Nt_position: | Indicates nucleotide positions of predicted exons. |

| | | | | |
|----|--------|---------|--------|---|
| 45 | Pkey | Ref | Strand | Nt_position |
| | 400480 | 8439796 | Minus | 110553-111119 |
| | 401015 | 8117441 | Plus | 72260-72369 |
| | 401042 | 8117611 | Plus | 151364-151606 |
| | 401132 | 8705350 | Minus | 85679-85795 |
| | 401165 | 9438376 | Minus | 168244-168423 |
| 50 | 401333 | 9884881 | Plus | 13852-14861 |
| | 401350 | 9931226 | Plus | 14471-14623 |
| | 401623 | 8575907 | Plus | 163249-163623 |
| | 401683 | 7689961 | Plus | 2934-3446 |
| | 401685 | 7689961 | Minus | 8038-8319 |
| 55 | 402015 | 7417802 | Minus | 48791-49043,50038-50205,51530-51672,54448-54565,55933-56073 |
| | 402243 | 7690137 | Minus | 196521-196721 |
| | 402319 | 7582559 | Plus | 116589-117549 |
| | 402750 | 7210067 | Plus | 69466-69678,71139-71284,71572-71865 |
| | 402758 | 9213869 | Plus | 87638-87924 |
| 60 | 402760 | 9213869 | Plus | 136829-136952,137336-137521 |
| | 402790 | 4835258 | Minus | 147744-147861 |
| | 403182 | 9838273 | Plus | 102163-102345,102545-102725 |
| | 403214 | 7630945 | Minus | 76723-77027,79317-79484 |
| | 403652 | 8705848 | Minus | 49991-50129 |
| 65 | 403670 | 7259739 | Minus | 88377-88537 |
| | 403697 | 3962501 | Minus | 102965-103174 |
| | 403792 | 7230192 | Minus | 149707-149873 |
| | 403847 | 7708844 | Plus | 317240-317391,317913-318032 |
| | 403941 | 7454203 | Plus | 114876-115342 |
| 70 | 404097 | 7770701 | Plus | 55512-55781 |
| | 404145 | 9863643 | Plus | 30607-31266 |
| | 404187 | 4481839 | Plus | 7644-7991 |
| | 404269 | 9711443 | Plus | 70261-70404,72944-73063 |
| | 404364 | 9964977 | Minus | 32966-33202 |
| 75 | 404401 | 7259738 | Plus | 71066-71326 |
| | 404753 | 7637341 | Plus | 14770-14931 |
| | 404848 | 8248647 | Minus | 23955-24034,25143-25264 |
| 80 | 404900 | 7331453 | Plus | 22032-22219 |
| | 404954 | 7387327 | Plus | 131720-132042 |
| | 405037 | 7543748 | Minus | 127374-127578 |
| | 405110 | 8096888 | Minus | 118940-119100 |
| | 405650 | 4926905 | Minus | 71743-72291 |
| | 405669 | 4508140 | Plus | 14130-14270 |
| | 405953 | 7960374 | Minus | 65101-65574 |

| | | | | |
|---|--------|---------|-------|--|
| 5 | 406242 | 7417725 | Minus | 36736-36951 |
| | 406291 | 5686274 | Plus | 9582-9867 |
| | 406293 | 5686274 | Minus | 17646-17953 |
| | 406333 | 9213235 | Plus | 64689-64798 |
| | 406560 | 7711569 | Minus | 35162-35292 |
| | 406589 | 8224211 | Plus | 38805-38989 |
| | 406597 | 8248613 | Minus | 132738-132985, 134266-134425, 135034-135192, 135471-135608, 137345-137478, 138768-138912 |

10 TABLE 48A: ABOUT 426 GENES UPREGULATED IN MELANOMA RELATIVE TO NORMAL BODY TISSUES
Table 48A lists about 426 genes upregulated in melanoma relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

15 Key: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Mean of melanoma AIs divided by the mean of normal tissue AIs, where the minimum value for the numerator and denominator was set to 1.0

| | | | | | |
|----|--------|-----------|-----------|--|--------|
| 20 | Key | ExAccn | UnigeneID | Unigene Title | R1 |
| | 426555 | NM 000372 | Hs.2053 | tyrosinase (oculocutaneous albinism IA) | 376.61 |
| | 428855 | H05769 | Hs.188757 | Homo sapiens, clone MGC:5564, mRNA, comp | 324.36 |
| | 430377 | NM 001922 | Hs.301865 | dopachrome tautomerase (dopachrome delta | 231.30 |
| 25 | 453344 | BE349075 | Hs.44571 | ESTs | 180.67 |
| | 425289 | AW139342 | Hs.155530 | interferon, gamma-inducible protein 16 | 107.36 |
| | 417166 | AA431323 | Hs.42146 | ESTs | 97.76 |
| | 425234 | AW152225 | Hs.165909 | ESTs, Weakly similar to I38022 hypothesi | 96.76 |
| | 434826 | AF155661 | Hs.22265 | pyruvate dehydrogenase phosphatase | 94.52 |
| 30 | 427528 | AU077143 | Hs.179565 | minichromosome maintenance deficient (S. | 90.88 |
| | 438209 | AL120659 | Hs.6111 | aryl-hydrocarbon receptor nuclear trans | 87.91 |
| | 443983 | H04482 | Hs.163724 | ESTs | 85.55 |
| | 428513 | BE220806 | Hs.184697 | Homo sapiens clone 23785 mRNA sequence | 85.03 |
| | 419956 | AL137939 | Hs.40096 | cadherin 19, type 2 | 84.27 |
| 35 | 423605 | AF047826 | Hs.129887 | cadherin 19, type 2 | 80.88 |
| | 430540 | AW245422 | | Homo sapiens cDNA: FLJ22105 fis, clone H | 80.64 |
| | 416975 | NM 004131 | Hs.1051 | granzyme B (granzyme 2, cytotoxic T-lymp | 79.09 |
| | 421633 | AF121860 | Hs.106260 | sorting nexin 10 | 71.52 |
| | 442064 | AI422867 | Hs.88594 | ESTs | 69.88 |
| 40 | 418310 | AA814100 | Hs.86693 | ESTs | 67.94 |
| | 423799 | AW026300 | Hs.132906 | 19A24 protein | 67.64 |
| | 432886 | BE159028 | Hs.279704 | chromatin accessibility complex 1 | 63.24 |
| | 456508 | AA502764 | Hs.123469 | ESTs, Weakly similar to AF208855 1 BM-01 | 63.18 |
| | 432882 | NM 013257 | Hs.279696 | serum/glucocorticoid regulated kinase-II | 62.33 |
| 45 | 454088 | AW062425 | | gb:CMO-CT0042-090899-018-f01 CT0042 Homo | 61.62 |
| | 430838 | N46664 | Hs.169395 | hypothetical protein FLJ12015 | 60.52 |
| | 422363 | T55979 | Hs.115474 | replication factor C (activator 1) 3 (38 | 59.73 |
| | 407748 | AL079409 | Hs.38176 | KIAA0606 protein; SCN Circadian Oscillat | 59.33 |
| | 450800 | BE395161 | Hs.1390 | proteasome (prosome, macropain) subunit, | 59.00 |
| 50 | 441224 | AU076964 | Hs.7753 | calumenin | 58.27 |
| | 408418 | AW963897 | Hs.44743 | KIAA1435 protein | 56.79 |
| | 428001 | H97428 | Hs.219907 | ESTs, Moderately similar to Transforming | 56.45 |
| | 456373 | BE247706 | Hs.89751 | membrane-spanning 4-domains, subfamily A | 56.29 |
| 55 | 420674 | NM 000055 | Hs.1327 | butyrylcholinesterase | 56.15 |
| | 407856 | AA045281 | Hs.266175 | phosphoprotein associated with GEMs | 55.82 |
| | 420552 | AK000492 | Hs.98806 | hypothetical protein | 55.39 |
| | 442355 | AA456539 | Hs.8262 | lysosomal-associated membrane protein 2 | 54.97 |
| | 429747 | M87507 | Hs.2490 | caspase 1, apoptosis-related cysteine pr | 52.85 |
| | 410174 | AA306007 | Hs.59461 | DKFZP434C245 protein | 52.00 |
| 60 | 437396 | BE140396 | Hs.21621 | hypothetical protein DKFZp7620076 | 51.97 |
| | 409557 | BE182896 | Hs.3686 | ESTs | 51.64 |
| | 420301 | AA767526 | Hs.22030 | paired box gene 5 (B-cell lineage specif | 51.42 |
| | 414403 | AW963551 | Hs.76064 | ribosomal protein L27a | 50.58 |
| | 452958 | AA883929 | Hs.40527 | ESTs | 50.21 |
| 65 | 458997 | AW937420 | | ESTs | 49.97 |
| | 458079 | AI796870 | Hs.54277 | DNA segment on chromosome X (unique) 992 | 49.85 |
| | 435905 | AW997484 | Hs.5003 | KIAA0456 protein | 48.76 |
| | 424800 | AL035588 | Hs.153203 | MyoD family inhibitor | 48.33 |
| 70 | 426827 | AW067805 | Hs.172665 | methylene tetrahydrofolate dehydrogenase | 47.91 |
| | 408548 | AA055449 | Hs.63187 | ESTs, Weakly similar to ALUC_HUMAN !!! | 47.45 |
| | 420000 | AB036063 | Hs.94262 | p53-inducible ribonucleotide reductase s | 46.52 |
| | 419465 | AA489023 | Hs.99807 | ESTs, Weakly similar to unnamed protein | 45.79 |
| | 451134 | AA318315 | Hs.25999 | hypothetical protein FLJ22195 | 45.52 |
| | 430066 | AI929659 | Hs.237825 | signal recognition particle 72kD | 45.45 |
| 75 | 417427 | M90391 | Hs.82127 | interleukin 16 (lymphocyte chemoattracta | 44.58 |
| | 450447 | AF212223 | Hs.25010 | hypothetical protein P15-2 | 43.36 |
| | 446019 | AI362520 | | histone deacetylase 3 | 43.03 |
| | 430015 | AW768399 | | ESTs | 42.45 |
| 80 | 446880 | AU811807 | Hs.108546 | Homo sapiens cDNA FLJ14934 fis, clone PL | 42.36 |
| | 409327 | L41162 | Hs.53563 | collagen, type IX, alpha 3 | 42.30 |
| | 425390 | AI092634 | Hs.156114 | protein tyrosine phosphatase, non-recept | 41.42 |
| | 411088 | BE247593 | Hs.145053 | ESTs | 41.21 |
| | 408527 | AL135018 | Hs.33074 | Homo sapiens, clone IMAGE:3606519, mRNA, | 40.94 |
| | 441590 | AI623207 | Hs.190537 | ESTs | 40.66 |

| | | | | | |
|----|--------|-----------|-----------|---|-------|
| | 457465 | AW301344 | Hs.122908 | DNA replication factor | 39.91 |
| | 430280 | AA361258 | Hs.237858 | interleukin 7 receptor | 38.91 |
| | 410700 | AA352335 | Hs.65641 | hypothetical protein FLJ20073 | 38.70 |
| 5 | 421282 | AA286914 | Hs.40782 | ESTs | 38.55 |
| | 448275 | BE514434 | Hs.20830 | kinesin-like 2 | 38.00 |
| | 453912 | AL121031 | | SWI/SNF related, matrix associated, acti | 37.94 |
| | 414844 | AA295874 | Hs.77494 | deoxyguanosine kinase | 37.88 |
| | 421305 | BE397354 | Hs.324830 | diphtheria toxin resistance protein requi | 37.70 |
| 10 | 439352 | BE614347 | Hs.169615 | hypothetical protein FLJ20989 | 37.64 |
| | 409078 | AW327515 | | ESTs | 37.30 |
| | 449845 | AW971183 | Hs.6019 | DnaJ (Hsp40) homolog, subfamily C, membe | 37.27 |
| | 444184 | T87841 | Hs.282990 | Human DNA sequence from clone RP1-28H20 | 37.21 |
| | 445819 | AJ767472 | Hs.146290 | ESTs, Weakly similar to putative p150 [H | 37.21 |
| 15 | 451418 | BE387790 | Hs.26369 | hypothetical protein FLJ20287 | 37.00 |
| | 433226 | AW503733 | Hs.9414 | KIAA1488 protein | 36.88 |
| | 445784 | AJ253155 | Hs.146065 | ESTs | 35.36 |
| | 454117 | BE410100 | Hs.40368 | adaptor-related protein complex 1, sigma | 33.09 |
| | 407756 | AA116021 | Hs.38260 | ubiquitin specific protease 18 | 32.05 |
| 20 | 447937 | AL109716 | Hs.20034 | Homo sapiens mRNA full length insert cDN | 31.00 |
| | 438549 | BE385801 | Hs.21858 | trinucleotide repeat containing 3 | 30.76 |
| | 429083 | Y09397 | Hs.227817 | BCL2-related protein A1 | 30.73 |
| | 444670 | H58373 | Hs.332938 | hypothetical protein MGC5370 | 28.45 |
| | 446839 | BE091926 | Hs.16244 | mitotic spindle coiled-coil related prot | 27.62 |
| 25 | 433576 | BE080715 | Hs.161091 | ESTs | 27.42 |
| | 422173 | BE385828 | Hs.250619 | phorbol-in-like protein MDS019 (CEM15) | 27.36 |
| | 408962 | BE386436 | Hs.44317 | SRY (sex determining region Y)-box 10 | 26.66 |
| | 442757 | AJ739528 | Hs.28345 | ESTs | 25.94 |
| 30 | 414646 | AA353776 | Hs.901 | CD48 antigen (B-cell membrane protein) | 25.39 |
| | 433675 | AW977653 | Hs.75319 | ribonucleotide reductase M2 polypeptide | 24.55 |
| | 438461 | AW075485 | Hs.285049 | phosphoserine aminotransferase | 22.48 |
| | 427581 | NM 014788 | Hs.179703 | KIAA0129 gene product | 22.15 |
| | 435256 | AF193766 | Hs.13872 | cytokine-like protein C17 | 20.61 |
| | 409988 | N27687 | Hs.334334 | transcription factor AP-2 alpha (activat | 19.79 |
| 35 | 444863 | AW384082 | Hs.104879 | serine (or cysteine) proteinase inhibito | 19.73 |
| | 417404 | NM 007350 | Hs.82101 | pleckstrin homology-like domain, family | 19.27 |
| | 458098 | BE550224 | | metallothionein 1E (functional) | 18.09 |
| | 417018 | M16038 | Hs.80887 | v-yes-1 Yamaguchi sarcoma viral related | 16.95 |
| | 446054 | AB014537 | Hs.13604 | KIAA0637 gene product | 15.67 |
| 40 | 432606 | NM 002104 | Hs.3056 | granzyme K (serine protease, granzyme 3; | 15.54 |
| | 414696 | AF002020 | Hs.76918 | Niemann-Pick disease, type C1 | 15.06 |
| | 457211 | AW972565 | Hs.32399 | ESTs, Weakly similar to S51797 vasodilat | 14.89 |
| | 414821 | M63835 | Hs.77424 | Fc fragment of IgG, high affinity Ia, re | 14.84 |
| | 422486 | BE514492 | Hs.117487 | gene near HD on 4p16.3 with homology to | 14.61 |
| 45 | 424308 | AW975531 | Hs.154443 | minichromosome maintenance deficient (S. | 14.12 |
| | 421334 | BE297729 | | gb:601175625F1 NIH_MGC_17 Homo sapiens c | 13.94 |
| | 422423 | AF283777 | Hs.116481 | CD72 antigen | 13.77 |
| | 408996 | AJ979168 | Hs.344096 | glycoprotein (transmembrane) nmb | 13.33 |
| | 416406 | D86961 | Hs.79299 | lipoma HMGIC fusion partner-like 2 | 12.76 |
| 50 | 427536 | BE277141 | Hs.115803 | gb:601178666F1 NIH_MGC_20 Homo sapiens c | 12.76 |
| | 423198 | M81933 | Hs.1634 | cell division cycle 25A | 12.65 |
| | 430770 | AA765694 | Hs.123296 | ESTs | 12.58 |
| | 407833 | AW955632 | Hs.66666 | ESTs, Weakly similar to S19560 proline-r | 12.09 |
| | 430822 | AJ005371 | Hs.248017 | glyceraldehyde-3-phosphate dehydrogenase | 11.46 |
| 55 | 424259 | AK001776 | Hs.143954 | hypothetical protein FLJ10914 | 10.58 |
| | 446950 | AA305800 | Hs.5672 | hypothetical protein AF140225 | 10.04 |
| | 420956 | AA351584 | Hs.100543 | Homo sapiens clone 24505 mRNA sequence | 9.98 |
| | 448356 | AL120837 | Hs.20993 | high-glucose-regulated protein 8 | 9.88 |
| | 428799 | AJ478619 | Hs.104677 | ESTs | 9.56 |
| 60 | 437271 | AL137445 | Hs.28846 | Homo sapiens mRNA; cDNA DKFZp5660134 (fr | 9.03 |
| | 447769 | AW873704 | Hs.320831 | Homo sapiens cDNA FLJ14597 fis, clone NT | 9.01 |
| | 408393 | AW015318 | Hs.23165 | ESTs | 8.99 |
| | 407966 | AA295052 | Hs.38516 | Homo sapiens, clone MGC:15887, mRNA, com | 8.99 |
| | 450534 | AJ570189 | Hs.25132 | KIAA0470 gene product | 8.91 |
| 65 | 410101 | AJ388045 | Hs.203559 | hypothetical protein FLJ12701 | 8.90 |
| | 417129 | AJ381800 | Hs.300684 | calcitonin gene-related peptide-receptor | 8.86 |
| | 453507 | AF083217 | Hs.33085 | WD repeat domain 3 | 8.68 |
| | 442739 | NM 007274 | Hs.8679 | cytosolic acyl coenzyme A thioester hydr | 8.46 |
| 70 | 456249 | AJ206144 | Hs.82508 | HRHFB2206 protein | 8.38 |
| | 437786 | BE142681 | Hs.155573 | polymerase (DNA directed), eta | 8.35 |
| | 448410 | AK000227 | Hs.21126 | hypothetical protein FLJ20220 | 8.20 |
| | 442711 | AF151073 | Hs.8645 | hypothetical protein | 8.14 |
| | 408405 | AK001332 | Hs.44672 | hypothetical protein FLJ10470 | 7.96 |
| | 420208 | BE276055 | Hs.95972 | silver (mouse homolog) like | 7.88 |
| 75 | 415929 | AA724373 | Hs.49344 | hypothetical protein FLJ11006 | 7.79 |
| | 449217 | AA278536 | Hs.23262 | ribonuclease, RNase A family, k6 | 7.66 |
| | 451239 | H24302 | Hs.23127 | ESTs | 7.50 |
| | 442426 | AJ373062 | Hs.332938 | hypothetical protein MGC5370 | 7.40 |
| | 447233 | AW246333 | Hs.17901 | Homo sapiens, clone IMAGE:3937015, mRNA, | 7.39 |
| 80 | 439574 | AJ469788 | | ESTs | 7.13 |
| | 431360 | NM 000427 | Hs.251680 | ionixin | 7.12 |
| | 412438 | AJ087928 | Hs.110741 | ESTs | 6.96 |
| | 452882 | AW972990 | Hs.196270 | folate transporter/carrier | 6.87 |
| | 436581 | AA725726 | Hs.180213 | ESTs | 6.64 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| | 431317 | AA502682 | | gb:ng23d01.s1 NCI_CGAP_Ov2 Homo sapiens | 6.63 |
| | 443264 | BE221477 | Hs.132137 | ESTs, Moderately similar to A47582 B-cel | 6.58 |
| | 412490 | AW803564 | Hs.288850 | Homo sapiens cDNA: FLJ22528 fts, clone H | 6.53 |
| 5 | 408367 | AK001178 | Hs.44424 | homolog of rat orphan transporter v7-3 | 6.52 |
| | 413283 | R78669 | Hs.23756 | hypothetical protein similar to swine ac | 6.50 |
| | 453878 | AW964440 | Hs.19025 | DC32 | 6.48 |
| | 424148 | BE242274 | Hs.1741 | integrin, beta 7 | 6.44 |
| | 407876 | NM 004519 | Hs.40866 | potassium voltage-gated channel, KQT-Jik | 6.44 |
| 10 | 409512 | AW979187 | Hs.293591 | melanoma differentiation associated prot | 6.39 |
| | 427951 | AJ826125 | Hs.43546 | ESTs | 6.32 |
| | 448664 | AJ879317 | Hs.334691 | splicing factor 3a, subunit 1, 120kD | 6.03 |
| | 416640 | BE262478 | Hs.79404 | neuron-specific protein | 6.01 |
| | 446830 | BE179030 | | Human DNA sequence from clone RPS-1174N9 | 5.98 |
| 15 | 452629 | W02772 | Hs.180178 | Homo sapiens, clone IMAGE:3947276, mRNA, | 5.93 |
| | 427390 | AJ432163 | Hs.268231 | Homo sapiens cDNA: FLJ23111 fts, clone L | 5.73 |
| | 427853 | AJ569798 | Hs.98260 | ESTs | 5.55 |
| | 434398 | AA121098 | Hs.3838 | serum-inducible kinase (SNK) | 5.54 |
| | 450256 | AA286887 | Hs.24724 | MFH-amplified sequences with leucine-ric | 5.54 |
| | 428524 | AA429772 | | ESTs | 5.53 |
| 20 | 431797 | BE169641 | Hs.270134 | hypothetical protein FLJ20280 | 5.50 |
| | 418403 | D86978 | Hs.84790 | KIAA0225 protein | 5.50 |
| | 411524 | AW850303 | | gb:IL3-CT0219-191199-030-F09 CT0219 Homo | 5.47 |
| | 426158 | NM 001982 | Hs.199067 | v-erb-b2 avian erythroblastic leukemia v | 5.40 |
| 25 | 443086 | AW977125 | | sine oculus homeobox (Drosophila) homolo | 5.38 |
| | 447735 | AA775268 | Hs.6127 | Homo sapiens cDNA: FLJ23020 fts, clone L | 5.38 |
| | 406843 | AW196933 | Hs.119598 | ribosomal protein L3 | 5.36 |
| | 430594 | AK000790 | Hs.246885 | hypothetical protein FLJ20783 | 5.35 |
| | 447674 | BE270640 | Hs.19192 | cyclin-dependent kinase 2 | 5.23 |
| 30 | 410491 | AA465131 | Hs.64001 | Homo sapiens clone 25218 mRNA sequence | 5.23 |
| | 420338 | AA825595 | Hs.88269 | Homo sapiens, clone MGC:17339, mRNA, com | 5.09 |
| | 409264 | NM 014937 | Hs.52463 | KIAA0966 protein | 5.03 |
| | 414734 | AA151712 | Hs.82572 | ESTs | 5.01 |
| | 426759 | AJ590401 | Hs.21213 | ESTs | 4.99 |
| 35 | 426793 | X89887 | Hs.172350 | HIR (histone cell cycle regulation defec | 4.98 |
| | 428612 | AA770001 | | ESTs | 4.97 |
| | 413550 | W03011 | Hs.306881 | MSTP043 protein | 4.92 |
| | 447349 | AJ375546 | | gb:tc23d04.x1 Soares_tetal_fetus_Nb2HF8_ | 4.86 |
| | 403328 | | | Target Exon | 4.85 |
| 40 | 452840 | AJ097393 | Hs.43481 | hypothetical protein DKFZp564K192 | 4.83 |
| | 439310 | AF086120 | Hs.102793 | ESTs | 4.82 |
| | 451281 | AJ768965 | Hs.292708 | ESTs | 4.82 |
| | 431183 | NM 006855 | Hs.250696 | KDEL (Lys-Asp-Glu-Leu) endoplasmic retic | 4.81 |
| | 427871 | AW992405 | Hs.59622 | Homo sapiens, clone IMAGE:3507281, mRNA, | 4.74 |
| 45 | 435963 | AF271212 | Hs.322901 | disrupter of silencing 10 | 4.67 |
| | 418699 | BE539639 | Hs.173030 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 4.66 |
| | 414770 | BE257224 | | Homo sapiens, clone IMAGE:3873720, mRNA | 4.66 |
| | 419628 | H67546 | Hs.49758 | ESTs | 4.64 |
| | 420258 | AA477514 | Hs.96247 | translin-associated factor X | 4.63 |
| 50 | 446341 | AL040763 | Hs.310735 | ESTs, Moderately similar to ALU7_HUMAN A | 4.58 |
| | 420267 | N37030 | Hs.173337 | ESTs | 4.57 |
| | 412228 | AW503785 | Hs.73792 | complement component (3d/Epstein Barr vi | 4.55 |
| | 432888 | T86823 | | gb:yd81a08.s1 Soares fetal liver spleen | 4.55 |
| | 453258 | AW293134 | Hs.32597 | ring finger protein (C3H2C3 type) 6 | 4.53 |
| 55 | 418340 | NM 013286 | Hs.84162 | chromosome 3p21.1 gene sequence | 4.50 |
| | 409038 | T97490 | Hs.50002 | small inducible cytokine subfamily A (Cy | 4.44 |
| | 447484 | AA464839 | Hs.292566 | hypothetical protein FLJ14697 | 4.42 |
| | 452036 | NM 003966 | Hs.27621 | sema domain, seven thrombospondin repeat | 4.41 |
| | 406903 | K03121 | | gb:Human glycerate dehydro-3-phosphate dehy | 4.40 |
| 60 | 405451 | | | dihydropyrimidinase-like 3 | 4.34 |
| | 434203 | BE262677 | Hs.283558 | hypothetical protein PRO1855 | 4.33 |
| | 450088 | AW292933 | Hs.254110 | ESTs | 4.31 |
| | 421535 | AB002359 | Hs.105478 | phosphoribosylformylglycinamide syntha | 4.31 |
| | 415912 | H08859 | Hs.206469 | ESTs, Weakly similar to ALU6_HUMAN ALU S | 4.30 |
| 65 | 451259 | NM 006052 | Hs.26146 | Down syndrome critical region gene 3 | 4.29 |
| | 452548 | AL050321 | Hs.301532 | CRP2 binding protein | 4.28 |
| | 432195 | AJ243669 | Hs.8127 | KIAA0144 gene product | 4.24 |
| | 445101 | T75202 | Hs.12314 | Homo sapiens mRNA; cDNA DKFZp586C1019 (f | 4.22 |
| | 425913 | AA365799 | | SEC22, vesicle trafficking protein (S. c | 4.19 |
| 70 | 423494 | AW504365 | Hs.24143 | Wiskott-Aldrich syndrome protein interac | 4.18 |
| | 442092 | AW578669 | | hypothetical protein FLJ12439 | 4.16 |
| | 424954 | NM 000546 | Hs.1846 | tumor protein p53 (Li-Fraumeni syndrome) | 4.05 |
| | 427719 | AJ393122 | Hs.134726 | ESTs | 4.04 |
| | 415310 | R16313 | | gb:y93h09.r1 Soares infant brain 1N1B H | 4.04 |
| 75 | 416058 | L08895 | Hs.78995 | MADS box transcription enhancer factor 2 | 4.03 |
| | 427828 | AJ024471 | Hs.98232 | ESTs | 3.93 |
| | 410079 | U94362 | Hs.58589 | glycogenin 2 | 3.92 |
| | 420265 | AA766209 | Hs.88087 | ESTs | 3.92 |
| | 426181 | AA371422 | Hs.334371 | hypothetical protein MGC13096 | 3.90 |
| 80 | 431639 | AK000680 | Hs.266175 | phosphoprotein associated with GEMs | 3.89 |
| | 410275 | U85658 | Hs.61796 | transcription factor AP-2 gamma (activat | 3.88 |
| | 422150 | AJ867118 | | calpastatin | 3.87 |
| | 429238 | NM 002849 | Hs.198288 | protein tyrosine phosphatase, receptor t | 3.86 |
| | 418827 | BE327311 | Hs.47166 | HT021 | 3.84 |

| | | | | | |
|----|--------|-----------|-----------|---|------|
| 5 | 425050 | BE391854 | Hs.7970 | gb:601285394F1 NIH_MGC_44 Homo sapiens c | 3.82 |
| | 442271 | AF000652 | Hs.8180 | syndecan binding protein (syntenin) | 3.81 |
| | 410235 | AA082977 | | gb:zn07h10.r1 Stratagene hNT neuron (937 | 3.79 |
| | 408636 | BE294925 | Hs.46680 | CGI-12 protein | 3.78 |
| | 424624 | AB032947 | Hs.151301 | Ca2+-dependent activator protein for secr | 3.76 |
| | 411400 | AA311919 | Hs.69851 | nucleolar protein family A, member 1 (H/ | 3.74 |
| | 458215 | AA928160 | | gb:zn06f10.s1 Soares_NFL_T_GBC_S1 Homo s | 3.73 |
| | 452874 | AK001061 | Hs.30925 | hypothetical protein FLJ10199 | 3.72 |
| 10 | 442643 | U82756 | | PRP4/STK/WD splicing factor | 3.70 |
| | 447471 | AF039843 | Hs.18576 | sprouty (Drosophila) homolog 2 | 3.70 |
| | 447644 | AW861622 | Hs.108646 | Homo sapiens cDNA FLJ14934 fis, clone PL | 3.67 |
| | 422616 | BE300330 | Hs.118725 | selenophosphate synthetase 2 | 3.64 |
| | 433160 | AW207002 | Hs.134342 | TASP for testis-specific adriamycin sens | 3.64 |
| 15 | 418180 | BE618087 | Hs.83724 | hypothetical protein MGC5466 | 3.62 |
| | 423032 | AI684746 | Hs.119274 | RAS p21 protein activator (GTPase activa | 3.62 |
| | 425569 | AA359597 | Hs.301701 | Homo sapiens cDNA FLJ12073 fis, clone HE | 3.62 |
| | 412156 | H29487 | Hs.17110 | Homo sapiens mRNA; cDNA DKFZp434C2016 (f | 3.61 |
| | 417426 | NM 002291 | Hs.82124 | laminin, beta 1 | 3.61 |
| 20 | 407188 | AA457592 | | gb:aa92f11.s1 Stratagene fetal retina 93 | 3.61 |
| | 426600 | NM 003378 | Hs.171014 | VEGF nerve growth factor inducible | 3.61 |
| | 440760 | AK001145 | Hs.284216 | hypothetical protein FLJ10283 | 3.60 |
| | 448481 | W15284 | Hs.74832 | ESTs | 3.59 |
| | 414111 | BE047679 | Hs.152982 | hypothetical protein FLJ13117 | 3.59 |
| 25 | 437862 | AW978107 | Hs.5884 | Homo sapiens mRNA; cDNA DKFZp586C0224 (f | 3.59 |
| | 409703 | NM 006187 | Hs.56009 | Z-5'-oligoadenylate synthetase 3 (100 k | 3.59 |
| | 406981 | S71129 | | acetylcholinesterase (YT blood group) | 3.59 |
| | 431586 | AW971100 | Hs.293189 | ESTs | 3.58 |
| | 415173 | AW501735 | Hs.180059 | ESTs | 3.57 |
| 30 | 430512 | AF182294 | Hs.241578 | U6 snRNA-associated Sm-like protein LSm8 | 3.57 |
| | 446126 | AW085909 | | pleckstrin homology domain interacting p | 3.57 |
| | 409305 | AA070078 | | gb:zm60f05.r1 Stratagene fibroblast (937 | 3.57 |
| | 433867 | AK000596 | Hs.3518 | hippocalcin-like 1 | 3.56 |
| | 459721 | AI299050 | Hs.143835 | gb:qn14d12.x1 NCI_CGAP_Lu5 Homo sapiens | 3.56 |
| 35 | 441412 | AI393657 | Hs.159750 | ESTs | 3.55 |
| | 416114 | AI695549 | Hs.183868 | glucuronidase, beta | 3.55 |
| | 454870 | AW836081 | | gb:PM0-LT0019-090300-002-e11 LT0019 Homo | 3.54 |
| | 443105 | X96753 | Hs.9004 | chondroitin sulfate proteoglycan 4 (meta | 3.53 |
| | 444680 | AI186671 | Hs.22670 | ESTs | 3.51 |
| 40 | 413949 | AA316077 | Hs.75639 | Human TB1 gene mRNA, 3' end | 3.51 |
| | 437033 | AW248364 | Hs.5409 | RNA polymerase I subunit | 3.50 |
| | 412141 | AI183838 | Hs.48938 | hypothetical protein FLJ21802 | 3.49 |
| | 437158 | AW090198 | | KIAA1150 protein | 3.48 |
| | 432642 | BE297635 | Hs.3069 | heat shock 70kD protein 9B (mortalin-2) | 3.47 |
| 45 | 440634 | AA921767 | Hs.132447 | ESTs | 3.47 |
| | 445652 | AL117473 | Hs.13036 | DKFZP727A071 protein | 3.46 |
| | 429500 | X78565 | Hs.289114 | hexabrachion (tenascin C, cytotoxic) | 3.43 |
| | 420460 | AA262331 | Hs.48376 | Homo sapiens clone HB-2 mRNA sequence | 3.43 |
| | 426141 | C05886 | Hs.293972 | ESTs | 3.40 |
| 50 | 424321 | W74048 | Hs.1765 | lymphocyte-specific protein tyrosine kin | 3.40 |
| | 449209 | BE616830 | Hs.294145 | ESTs | 3.39 |
| | 408304 | AW810279 | | gb:MR4-ST0125-151299-029-a09 ST0125 Homo | 3.37 |
| | 416561 | D87328 | Hs.79375 | holocarboxylase synthetase (biotin-prop | 3.35 |
| | 422947 | AA306782 | Hs.122552 | G-2 and S-phase expressed 1 | 3.34 |
| 55 | 453005 | AW055308 | Hs.31803 | ESTs, Weakly similar to N-WASP [H.sapien | 3.34 |
| | 409430 | R21945 | Hs.346735 | splicing factor, arginine/serine-rich 5 | 3.32 |
| | 417386 | AL037228 | Hs.82043 | D123 gene product | 3.32 |
| | 440999 | AI951562 | Hs.126370 | ESTs, Weakly similar to CNE3_HUMAN COPIN | 3.31 |
| | 407516 | X64974 | | gb:H.sapiens mRNA HTPCRH02 for olfactory | 3.31 |
| 60 | 450065 | AL050107 | Hs.24341 | transcriptional co-activator with PDZ-bi | 3.31 |
| | 416902 | AA375634 | Hs.288974 | hypothetical protein FLJ12528 | 3.28 |
| | 432878 | BE386490 | Hs.279663 | Pirin | 3.28 |
| | 443296 | AI765286 | Hs.313342 | ESTs | 3.27 |
| | 429954 | AI918130 | Hs.21374 | ESTs | 3.25 |
| 65 | 428044 | AA093322 | Hs.301404 | RNA binding motif protein 3 | 3.25 |
| | 425317 | AW205118 | Hs.210546 | interleukin 21 receptor | 3.25 |
| | 418064 | BE387287 | Hs.83384 | S100 calcium-binding protein, beta (neur | 3.25 |
| | 432917 | NM 014125 | Hs.241517 | PRO0327 protein | 3.24 |
| | 447871 | BE297946 | Hs.239052 | ESTs | 3.24 |
| 70 | 414829 | AA321568 | Hs.77436 | pleckstrin | 3.24 |
| | 426996 | AW968934 | Hs.173108 | Homo sapiens cDNA: FLJ21897 fis, clone H | 3.23 |
| | 416188 | BE157260 | Hs.79070 | v-myc avian myelocytomatosis viral oncog | 3.22 |
| | 429530 | AA454191 | Hs.99362 | Human DNA sequence from clone RP11-530N1 | 3.21 |
| | 445174 | AV652850 | Hs.172004 | titin | 3.19 |
| 75 | 459227 | AW167599 | | ESTs | 3.19 |
| | 439039 | AI656707 | Hs.48713 | ESTs | 3.15 |
| | 418803 | U50079 | Hs.88556 | histone deacetylase 1 | 3.15 |
| | 420005 | AW271106 | Hs.133294 | ESTs | 3.15 |
| | 422511 | AU076442 | Hs.117938 | collagen, type XVII, alpha 1 | 3.14 |
| 80 | 452480 | AI903526 | | gb:RC-BT031-090199-063 BT031 Homo sapien | 3.14 |
| | 445701 | AF055581 | Hs.13131 | lymphocyte adaptor protein | 3.14 |
| | 410678 | BE540516 | Hs.293732 | hypothetical protein MGC3195 | 3.14 |
| | 458664 | AI300427 | | gb:qo18h07.x1 NCI_CGAP_Lu5 Homo sapiens | 3.13 |
| | 436315 | BE390513 | Hs.27935 | hypothetical protein MGC4837 | 3.13 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| | 430441 | BE398091 | | desmoplakin (DPI, DPII) | 3.12 |
| | 435080 | AI831760 | Hs.155111 | hypothetical protein FLJ14428 | 3.12 |
| | 425606 | U52112 | Hs.158331 | renin-binding protein | 3.11 |
| 5 | 432978 | AF126743 | Hs.279884 | DNAJ domain-containing | 3.11 |
| | 452826 | BE245286 | Hs.301636 | peroxisomal biogenesis factor 6 | 3.10 |
| | 446627 | AJ973016 | Hs.15725 | hypothetical protein SBB148 | 3.10 |
| | 427647 | W19744 | Hs.180059 | Homo sapiens cDNA FLJ20653 fis, clone KA | 3.09 |
| | 417211 | T97617 | Hs.269092 | ESTs | 3.08 |
| 10 | 448140 | AF146761 | Hs.20450 | BCM-like membrane protein precursor | 3.08 |
| | 448752 | AA593867 | Hs.300842 | KIAA1608 protein | 3.07 |
| | 416355 | H49875 | Hs.268906 | ESTs | 3.07 |
| | 425345 | AU077297 | Hs.155894 | protein tyrosine phosphatase, non-recept | 3.07 |
| | 410321 | Y12860 | Hs.62245 | solute carrier family 25 (mitochondrial | 3.07 |
| 15 | 411395 | AA889673 | Hs.7542 | KIAA1802 protein | 3.07 |
| | 416065 | BE267931 | Hs.78996 | proliferating cell nuclear antigen | 3.06 |
| | 432343 | NM 002960 | Hs.2961 | S100 calcium-binding protein A3 | 3.06 |
| | 457991 | BE539951 | Hs.306996 | Homo sapiens, clone IMAGE:3447073, mRNA, | 3.05 |
| | 433201 | AB040896 | Hs.21104 | KIAA1463 protein | 3.03 |
| 20 | 416178 | AB808527 | Hs.192822 | serologically defined breast cancer anti | 3.02 |
| | 411975 | AJ916058 | Hs.144583 | ESTs | 3.01 |
| | 448719 | AA033627 | Hs.21858 | trinucleotide repeat containing 3 | 3.00 |
| | 419870 | AW403911 | Hs.266175 | phosphoprotein associated with GEMs | 3.00 |
| | 409601 | AF237621 | Hs.80828 | keratin 1 (epidermolytic hyperkeratosis) | 2.94 |
| 25 | 415668 | AW957684 | Hs.306814 | hypothetical protein FLJ21889 | 2.93 |
| | 453256 | AI585587 | Hs.32556 | KIAA0379 protein | 2.81 |
| | 436856 | AI469355 | Hs.127310 | ESTs | 2.75 |
| | 417880 | BE241595 | Hs.82848 | selectin L (lymphocyte adhesion molecule | 2.60 |
| | 408209 | NM 004454 | Hs.43697 | ets variant gene 5 (ets-related molecule | 2.59 |
| 30 | 440457 | BE387593 | Hs.21321 | Homo sapiens clone FLB9213 PRO2474 mRNA, | 2.55 |
| | 415314 | N88802 | Hs.5422 | glycoprotein M6B | 2.51 |
| | 434276 | AF123659 | Hs.93505 | leucine zipper, putative tumor suppresso | 2.50 |
| | 424085 | NM 002914 | Hs.139226 | replication factor C (activator 1) 2 (40 | 2.48 |
| | 410600 | AW575742 | | ESTs, Moderately similar to S65657 alpha | 2.48 |
| 35 | 439180 | AI393742 | Hs.199067 | v-erb-b2 avian erythroblastic leukemia v | 2.43 |
| | 444809 | BE207568 | Hs.208219 | ocutspanin | 2.39 |
| | 453837 | AL138387 | Hs.256126 | baculoviral IAP repeat-containing 7 (liv | 2.39 |
| | 410290 | AA402307 | Hs.322844 | hypothetical protein DKFZp564A176 | 2.37 |
| | 411358 | R47479 | Hs.94761 | KIAA1691 protein | 2.35 |
| 40 | 427550 | BE242818 | Hs.311609 | nuclear RNA helicase, DECD variant of DE | 2.34 |
| | 426312 | AF028939 | Hs.181874 | interferon-induced protein with tetratri | 2.29 |
| | 448569 | BE382657 | Hs.21486 | signal transducer and activator of trans | 2.27 |
| | 418661 | NM 001949 | Hs.1189 | E2F transcription factor 3 | 2.24 |
| 45 | 459373 | BE408266 | Hs.301406 | hypothetical protein PP3501 | 2.21 |
| | 417437 | U52682 | Hs.82132 | interferon regulatory factor 4 | 2.21 |
| | 436700 | AI693690 | Hs.301406 | hypothetical protein PP3501 | 2.18 |
| | 450690 | AA296696 | Hs.333418 | FXFD domain-containing ion transport reg | 2.15 |
| | 432800 | BE391046 | Hs.278962 | AIM-1 protein | 2.15 |
| | 421773 | W69233 | Hs.112457 | ESTs | 2.09 |
| 50 | 409415 | AA579258 | Hs.6083 | Homo sapiens cDNA: FLJ21028 fis, clone C | 2.03 |
| | 433364 | AI075407 | Hs.296083 | ESTs, Moderately similar to IS4374 gene | 2.02 |
| | 412609 | Z48804 | Hs.74124 | ocular albinism 1 (Nettleship-Falls) | 2.01 |
| | 443950 | NM 001425 | Hs.9999 | epithelial membrane protein 3 | 2.01 |
| | 451537 | R56631 | Hs.26550 | retinoid X receptor, gamma | 2.00 |
| 55 | 427080 | AW068287 | Hs.301175 | ras-related C3 botulinum toxin substrate | 1.96 |
| | 413190 | AA151802 | Hs.40368 | adaptor-related protein complex 1, sigma | 1.94 |
| | 412926 | AI879076 | Hs.75061 | macrophage myristoylated alanine-rich C | 1.91 |
| | 453779 | N35187 | Hs.43388 | 28kD interferon responsive protein | 1.86 |
| | 453107 | NM 016113 | Hs.279746 | vanilloid receptor-like protein 1 | 1.86 |
| 60 | 430637 | BE160081 | Hs.256290 | S100 calcium-binding protein A11 (calgiz | 1.86 |
| | 408561 | AI308037 | Hs.84120 | hypothetical protein MGC13016 | 1.84 |
| | 413171 | AA318325 | Hs.75219 | tyrosinase-related protein 1 | 1.83 |
| | 406016 | | | Target Exon | 1.82 |
| | 446644 | NM 003272 | Hs.15791 | transmembrane 7 superfamily member 1 (up | 1.81 |
| 65 | 431836 | AF178532 | Hs.271411 | beta-site APP-cleaving enzyme 2 | 1.77 |
| | 439496 | BE616501 | Hs.32343 | Homo sapiens, Similar to RIKEN cDNA 1110 | 1.77 |
| | 447604 | AW089933 | Hs.301342 | hypothetical protein MGC4342 | 1.76 |
| | 438866 | U44385 | Hs.325495 | tissue inhibitor of metalloproteinase 2 | 1.74 |
| | 440672 | AF083811 | Hs.7345 | MAD1 (mitotic arrest deficient, yeast, h | 1.70 |
| 70 | 416091 | AF295370 | Hs.283082 | defensin, beta 3 | 1.69 |
| | 446291 | BE397753 | Hs.14623 | interferon, gamma-inducible protein 30 | 1.67 |
| | 422532 | AL008726 | Hs.118126 | protective protein for beta-galactosidas | 1.67 |
| | 418918 | X07871 | Hs.89476 | CD2 antigen (p50), sheep red blood cell | 1.67 |
| | 412580 | AA113262 | Hs.17901 | Homo sapiens, clone IMAGE:3937015, mRNA, | 1.67 |
| 75 | 448258 | BE386983 | Hs.343214 | hypothetical protein FLJ20396 | 1.66 |
| | 414945 | BE076358 | Hs.77667 | lymphocyte antigen 6 complex, locus E | 1.66 |
| | 425262 | D87119 | Hs.155418 | GSJ955 protein | 1.65 |
| | 439237 | AW408158 | Hs.318893 | ESTs, Weakly similar to A47582 B-cell gr | 1.64 |
| 80 | 427923 | AW274357 | Hs.301406 | hypothetical protein PP3501 | 1.63 |
| | 424825 | AF207069 | Hs.153357 | procollagen-lysine, 2-oxoglutarate 5-dio | 1.62 |
| | 441859 | AW194364 | Hs.94814 | interleukin-4 induced gene-1 protein (FI | 1.60 |
| | 445982 | BE410233 | Hs.13501 | pescadillo (zebrafish) homolog 1, contai | 1.58 |
| | 412939 | AW411491 | Hs.75069 | eukaryotic translation elongation factor | 1.58 |
| | 417237 | H86385 | Hs.81737 | palmitoyl-protein thioesterase 2 | 1.56 |

| | | | | | |
|----|--------|-----------|-----------|--|------|
| 5 | 412856 | BE386745 | Hs.74631 | basigin (OK blood group) | 1.56 |
| | 447200 | BE543146 | Hs.281434 | Homo sapiens cDNA FLJ14028 fis, clone HE | 1.54 |
| | 409614 | BE297412 | Hs.55189 | hypothetical protein | 1.53 |
| | 450663 | H43540 | Hs.25292 | ribonuclease H1, large subunit | 1.53 |
| | 423397 | NM_001838 | Hs.1652 | chemokine (C-C motif) receptor 7 | 1.49 |
| | 425535 | AB007937 | Hs.158287 | KIAA0468 gene product | 1.48 |
| | 409340 | BE174629 | Hs.321130 | hypothetical protein MGC2771 | 1.46 |
| | 446755 | AW451473 | Hs.16134 | serine/threonine kinase 10 | 1.46 |
| 10 | 454429 | BE273437 | Hs.301406 | hypothetical protein PP3501 | 1.46 |
| | 425722 | AI659076 | Hs.97031 | hypothetical protein MGC13047 | 1.45 |
| | 414509 | AW161311 | Hs.76294 | CD63 antigen (melanoma 1 antigen) | 1.44 |
| | 452203 | X57522 | | transporter 1, ATP-binding cassette, sub | 1.43 |
| | 436378 | AJ227874 | Hs.99244 | ESTs | 1.42 |
| 15 | 424218 | AF031824 | Hs.143212 | cystatin F (leukocystatin) | 1.42 |
| | 436456 | AW292677 | Hs.248122 | G protein-coupled receptor 24 | 1.42 |
| | 439740 | AL365512 | Hs.6657 | hypothetical protein bK1048E9.5 | 1.42 |
| | 429359 | W08482 | Hs.2399 | matrix metalloproteinase 14 (membrane-in | 1.42 |
| | 427634 | AI399745 | Hs.18449 | hypothetical protein MGC10820 | 1.40 |
| 20 | 403409 | | | NM_005929:Homo sapiens antigen p97 (meta | 1.40 |
| | 434262 | AF121858 | Hs.12169 | sorting nexin 8 | 1.34 |
| | 413566 | AW604451 | Hs.285814 | sprouty (Drosophila) homolog 4 | 1.32 |
| | 427730 | AW250549 | Hs.180577 | granulin | 1.32 |
| | 411742 | AW247593 | Hs.71819 | eukaryotic translation initiation factor | 1.31 |
| 25 | 450395 | BE048545 | Hs.161757 | ESTs | 1.30 |
| | 413291 | NM_006278 | Hs.75268 | sialyltransferase 4C (beta-galactosidase | 1.26 |
| | 442609 | AL020996 | Hs.8518 | selenoprotein N | 1.24 |
| | 416929 | N20535 | | melastatin 1 | 1.21 |
| | 421975 | AW961017 | Hs.6459 | hypothetical protein FLJ11856 | 1.21 |
| 30 | 454478 | AW805749 | | superoxide dismutase 2, mitochondrial | 1.20 |
| | 437723 | AI672731 | Hs.13256 | ESTs | 1.18 |
| | 416350 | AF188625 | Hs.189507 | phospholipase A2, group IID | 1.08 |

TABLE 48B:

| | |
|-------------|---------------------------------------|
| Pkey: | Unique Eos probeset identifier number |
| CAT number: | Gene cluster number |
| Accession: | Genbank accession numbers |

| | | | |
|----|--------|------------|--|
| 40 | Pkey | CAT Number | Accession |
| | 430540 | 713_2 | BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 BM045810 AU120387 BG770238 BG686740 BG913323 B1759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 AJ770171 BF196861 BE856897 AA463876 AJ375927 AA648810 AA948193 AA490916 AJ459893 AJ458188 AJ240408 AJ191843 AJ131029 AW768399 AI365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903567 BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610 BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 BE298109 AW245422 AJ423847 AI914618 H80534 BE301004 AL531791 AJ435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296 AI359493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AJ421728 BG767231 BM462953 BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512 W58732 W85690 BG958989 AI205206 H19721 W17051 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114 AI243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103 AW008188 R07703 AA989120 AA746235 AW026983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809 BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591 AW062425 AW062411 BM453041 AA760783 BE218582 AJ340046 AW166131 BF515854 AI630296 AA461307 AI090881 AW023059 AA155797 AA115486 AL597396 AW889004 AW937420 AA137082 AA013374 BG619478 BG401839 AI362520 D25917 AI670784 AI742347 AW269789 AI270700 AW610541 AW793036 AW793035 AW610540 AW362220 AW362166 AW362214 AW362225 AW362228 AL119827 |
| 45 | | | BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 BM045810 AU120387 BG770238 BG686740 BG913323 B1759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 AJ770171 BF196861 BE856897 AA463876 AJ375927 AA648810 AA948193 AA490916 AJ459893 AJ458188 AJ240408 AJ191843 AJ131029 AW768399 AI365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903567 BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610 BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 BE298109 AW245422 AJ423847 AI914618 H80534 BE301004 AL531791 AJ435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296 AI359493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AJ421728 BG767231 BM462953 BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512 W58732 W85690 BG958989 AI205206 H19721 W17051 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114 AI243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103 AW008188 R07703 AA989120 AA746235 AW026983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809 BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591 AW062425 AW062411 BM453041 AA760783 BE218582 AJ340046 AW166131 BF515854 AI630296 AA461307 AI090881 AW023059 AA155797 AA115486 AL597396 AW889004 AW937420 AA137082 AA013374 BG619478 BG401839 AI362520 D25917 AI670784 AI742347 AW269789 AI270700 AW610541 AW793036 AW793035 AW610540 AW362220 AW362166 AW362214 AW362225 AW362228 AL119827 |
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| 65 | | | BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 BM045810 AU120387 BG770238 BG686740 BG913323 B1759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 AJ770171 BF196861 BE856897 AA463876 AJ375927 AA648810 AA948193 AA490916 AJ459893 AJ458188 AJ240408 AJ191843 AJ131029 AW768399 AI365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903567 BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610 BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 BE298109 AW245422 AJ423847 AI914618 H80534 BE301004 AL531791 AJ435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296 AI359493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AJ421728 BG767231 BM462953 BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512 W58732 W85690 BG958989 AI205206 H19721 W17051 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114 AI243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103 AW008188 R07703 AA989120 AA746235 AW026983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809 BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591 AW062425 AW062411 BM453041 AA760783 BE218582 AJ340046 AW166131 BF515854 AI630296 AA461307 AI090881 AW023059 AA155797 AA115486 AL597396 AW889004 AW937420 AA137082 AA013374 BG619478 BG401839 AI362520 D25917 AI670784 AI742347 AW269789 AI270700 AW610541 AW793036 AW793035 AW610540 AW362220 AW362166 AW362214 AW362225 AW362228 AL119827 |
| 70 | | | BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 BM045810 AU120387 BG770238 BG686740 BG913323 B1759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 AJ770171 BF196861 BE856897 AA463876 AJ375927 AA648810 AA948193 AA490916 AJ459893 AJ458188 AJ240408 AJ191843 AJ131029 AW768399 AI365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903567 BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610 BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 BE298109 AW245422 AJ423847 AI914618 H80534 BE301004 AL531791 AJ435581 |

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|----|--------------|--|--|-----------------------|
| | 446830 | 41421_1 | BC020595 BI488430 BG168023 BE179030 AW294203 BF849776 AA459064 AI917452 AW403072 W27419 BF914568 BF798468 AW370558 T35055 AW370623 AA339232 AA214221 AW802987 BF902228 AW370622 BF819597 AW370567 BF914313 AW954040 BF060706 AA194237 T25074 C01285 BI489433 | |
| 5 | 428524 | 1382184_1 | AI208080 AA442862 AA429772 | |
| | 411524 | 1089114_1 | AW850587 AW850589 AW850318 AW850303 | |
| | 443086 | 25669_4 | BE896316 BG819393 AA187888 AW753122 | |
| | 428612 | 1383189_1 | AA770001 AA431112 AA432126 | |
| | 447349 | 1063443_1 | BE743847 AW809603 BM469626 AI375546 | |
| 10 | 414770 | 41721_1 | AK056926 BG473673 BG482256 AI135566 AW419211 BF949370 AL120313 AV703730 H82569 BG012696 R27084 AA304583 BM452908 BF516419 BF515687 BG036572 BG696740 AW953552 AW859437 AA306038 AI754064 AA608729 AA664163 H65119 AW272606 BF942099 AW130458 BI089467 BG821499 AA152403 BF310450 BF314240 BG830310 BF803223 BG764269 BE542645 BE259142 R26953 BE257224 BG475461 BF677821 R33048 | |
| | 432888 | 2155976_1 | T86823 AA570737 AI821425 AA569589 AI732232 | |
| 15 | 425913 | 4123_2 | AV703649 AW959818 AI582119 AI523459 AI674473 AW663543 AA825476 AI935231 BF742805 AA426156 AI253626 AA846477 AI024230 BF221780 AI493027 AW006841 AA814699 H99650 AI088977 AA442691 AI783526 BF207915 AI752847 AA782635 AI978980 AA788634 BG119454 BF678528 AI627829 BG993975 AV701283 | |
| | 442092 | 22756_2 | BM449821 BM069895 BM023170 AW025563 BG152606 BM023452 AI862106 BG959957 | |
| | 415310 | 1869807_1 | R16313 Z45351 R14838 F05290 R14821 R16277 | |
| 20 | 422150 | 782_1 | BI086421 BF059136 AW003898 BF446659 AI632891 AI628067 AI703179 AI961149 BF111022 AW614154 BE674215 AA687350 AA779426 BF591963 AW243344 AI356530 AI492508 AI694049 AI090422 AA465307 AI273387 BE674625 AW271971 AA699153 AW468593 AA984014 AI817491 AA970258 AI914450 AI018697 AW577591 AW577616 AA382101 AW954455 AI867266 AI707995 AI337384 BF208406 BF037100 BF223433 BF195517 BE673984 BF224124 BE813387 BG036579 BI553906 AA304995 AW361269 AW754160 AW361276 AW361271 AI867118 AW805555 AW361284 AW954458 AW585551 BG681507 H79011 AW205696 AW134957 AA747667 AW753296 BF939060 AW958549 BF910827 BG573750 BG168639 | |
| 25 | 410235 | 2930253_1 | AA082977 AA082955 | |
| | 458215 | 540112_3 | BE176902 BE177058 | |
| | 442643 | 2736_1 | BC001588 BC007424 AF016369 NM_004697 BI756186 BE257019 BG500792 BI862776 AL121371 BG574833 AA703250 AA179511 AW052006 AI280150 AI914000 AI358319 AI081204 AI082594 AA992449 AI470821 AI655744 AW237529 AA678858 AI984430 BF433055 BE467594 BE467573 AA035630 AI289987 AI184802 AI681391 AW592416 AI138377 AI139266 AA961714 AI800163 AA418751 AW451928 AA668676 AI273444 AW94387 BE046912 AI276555 BF196021 AA700055 AA609305 AA772596 AI635758 AI635749 H95459 AW610290 BE464994 AA527136 BF374802 AI800175 AW195227 AI189676 BF802049 AI513632 AL554911 AL538845 BE297273 AA315321 BM451920 BE269268 BE292835 BE018128 BG755713 BM041095 BG677009 AL039691 BF995709 BE735586 BE296453 BG393609 BG824453 AI567522 AI745257 AW388641 AW301265 AI141144 AW029280 AU149362 AU152328 AA418960 AL121009 AI890398 AL528748 H13050 T47086 BI000575 BF334914 BF109661 R44450 H13259 T47087 AW388646 BF305834 AL577515 BM041600 BE889299 BF239768 | |
| 30 | 446126 | 610_2 | BF946219 BF946218 BF851494 AL536879 AA457150 AI590194 AI582629 AA464515 AA916242 AA337109 AA336509 N46906 AA336322 AA336407 AA337222 AA319240 BI027058 AL536880 AI693827 AA651730 AI701013 BM068789 AW339506 AA293021 BF891108 AI458885 AW361203 AW974652 AI761251 AI655763 AA628063 BE047125 AW085916 AI129587 N52070 AW172361 AA052951 AW085909 AI000008 AA962570 AI371342 AI364207 AA464514 AI962506 AI824603 AW376300 AA058439 AW361192 AV656660 N50282 BF820514 BF891008 H40784 BF891112 BE708029 AW043567 AA056762 | |
| 35 | | | AA071475 AA112236 AA070648 AA071243 AA081725 AA085187 AA070078 | |
| 40 | 409305 | 109927_1 | AW836081 BF854404 AW578594 AW578581 BF507971 AW196760 AA779923 AA707233 AI655913 AA948295 AW089222 AW291883 | |
| | 454870 | 2170_9 | AL050068 AA160485 AW173544 AW296506 AW439860 AI521563 AI702529 AI393606 AW138323 AA570109 H19504 BM021968 BF063327 BF593552 | |
| | 437158 | 59575_1 | AA630766 AI597717 AI807128 AA523012 AI356250 AW451857 AA974203 AI762577 BF512552 AW007307 BE675286 AW450602 AA962057 AW516069 AI582546 BF221924 BF222543 AI801808 AW468599 AW000736 AI866625 AW235356 BM021837 AA911956 AI680606 W86516 T03370 AW611634 H41653 AI468349 H19588 AW090198 AW043993 R39847 | |
| 45 | 408304 | 645409_1 | AW810279 BE146684 AW810193 AW810515 AW178835 AW810516 BE146689 AW178842 BE146693 BE146694 AW810208 AW810258 AW810447 AW810443 AW810330 AW810211 AW810328 AW810327 AW810288 AW810265 AW810257 AW810263 AW810567 AW178838 AW810323 AW810358 AW810281 AW810321 AW178837 AW810635 BE062400 AW810198 AW810325 AW810513 BE062434 BE146679 AW810441 AW846649 AW810536 AW178857 AW810185 BE146653 AW810636 AW810322 BE146674 AW810359 AW810293 AW810472 AW178852 AW810356 AW810514 AW810289 BE146652 AW810566 | |
| 50 | 459227 | 639802_1 | AW167599 AI971179 AI934948 | |
| | 452480 | 3144986_1 | AI903574 AI903572 AI903526 AI903571 | |
| | 458664 | 2139033_1 | BF432937 R07053 AI300427 W57876 | |
| | 430441 | 1438_6 | BG108218 BE560548 AW380115 BE269629 AI911518 AW380113 AA902964 AA455001 AI276529 AI685597 AA970496 D61084 AW380068 AW380080 R00283 C15236 AW327776 D80759 | |
| 55 | 410600 | 497855_1 | BF347859 AW499616 AA191322 AW499617 AL601010 AW575742 AA729043 BE463447 AA086179 BE459623 AI335824 AW408712 BM149172 | |
| | 452203 | 2630_1 | BC014081 NM_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL546423 AL560492 AL556882 AL541576 AL550654 BI823519 BI770023 AL554969 BI489906 AI304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 T12630 BM423610 AL561518 BM009470 BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 AI569894 AW073296 AI361433 AA554644 AA487429 BE858232 AA838610 AI539114 AI719375 AI829129 BG057675 AI423422 AU158860 BM300655 AW170777 AA586956 AL571889 AI556850 AL576404 AL582800 BI256544 BF342301 BC875994 AA054458 AA353161 AI940434 BE816522 AL577636 AI479650 AW150377 AU154395 AW951271 AI032220 AI819778 AI346733 AW771150 AW512525 AI249904 AA279809 AI352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 BI819184 AV660190 AL556475 AI520020 AW089888 AW079179 Z21518 AA687601 F04651 AI783961 T57198 AI433367 T78652 AL554968 AA365648 AL582619 BE874601 BF804669 AL574458 BM145502 AI266514 AI538823 AI475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256 AW361447 BE788505 AI682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 W79997 AW366665 AW366601 AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI560216 BI753586 | |
| 60 | | | BC017849 BC005892 N42983 BF691239 N42991 N29240 N40292 N33322 N33330 N20535 | |
| 65 | 416929 | 14596_3 | AW796921 AW798102 AW805749 AW805872 BF985060 AW794380 BF380449 AW794466 AW794538 | |
| | 454478 | 4273_16 | | |
| 70 | TABLE 48C: | | | |
| | Pkey: | Unique number corresponding to an Eos probe set | | |
| | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. | | |
| | Strand: | Indicates DNA strand from which exons were predicted. | | |
| 75 | Nt_position: | Indicates nucleotide positions of predicted exons. | | |
| | Pkey | Ref | Strand | Nt_position |
| | 403328 | 8469086 | Minus | 120428-120703 |
| | 405451 | 7622517 | Minus | 145949-146227 |
| | 406016 | 8272661 | Plus | 41341-41940 |
| 80 | 403409 | 9438598 | Plus | 6860-7054,12573-12771 |

TABLE 49A: ABOUT 1127 GENES UPREGULATED IN PRIMARY MELANOMA AND/OR MELANOMA METASTASES RELATIVE TO NORMAL BODY TISSUES

Table 49A lists about 1127 genes upregulated in primary melanoma and/or melanoma metastases relative to normal body tissues. These genes were selected from 59680 probesets on the Eos/Alfymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

| | | | | | | | |
|----|----------------|--|-----------|---|-------|-------|-------|
| 5 | Pkey: | Unique Eos probeset identifier number | | | | | |
| | ExAccn: | Exemplar Accession number, Genbank accession number | | | | | |
| | UnigeneID: | Unigene number | | | | | |
| | Unigene Title: | Unigene gene title | | | | | |
| | R1: | 90th percentile of primary melanoma and melanoma metastasis AIs divided by the 90th percentile of normal tissue AIs | | | | | |
| 10 | R2: | 90th percentile of primary melanoma and melanoma metastasis AIs divided by the 90th percentile of normal tissue AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator | | | | | |
| | R3: | 90th percentile of primary melanoma and melanoma metastasis AIs divided by the 90th percentile of heart, liver, lung, and kidney AIs | | | | | |
| | Pkey | ExAccn | UnigeneID | Unigene Title | R1 | R2 | R3 |
| 15 | 452838 | U65011 | Hs.30743 | preferentially expressed antigen in meta | 14.05 | 11.83 | 14.05 |
| | 426555 | NM_000372 | Hs.2053 | tyrosinase (oculocutaneous albinism IA) | 13.15 | 13.27 | 13.15 |
| | 430377 | NM_001922 | Hs.301865 | dopachrome tautomerase (dopachrome delta | 11.77 | 7.43 | 11.77 |
| | 420208 | BE276055 | Hs.95972 | silver (mouse homolog) like | 10.53 | 19.95 | 10.27 |
| | 431360 | NM_000427 | Hs.251680 | loricin | 9.78 | 7.09 | 0.89 |
| 20 | 430822 | AJ005371 | Hs.248017 | glyceraldehyde-3-phosphate dehydrogenase | 9.40 | 7.20 | 8.84 |
| | 422168 | AA586894 | Hs.112408 | S100 calcium-binding protein A7 (psorias | 8.03 | 10.27 | 12.84 |
| | 419628 | H67546 | Hs.49768 | ESTs | 7.56 | 8.92 | 6.49 |
| | 438549 | BE386801 | Hs.21858 | trinucleotide repeat containing 3 | 7.52 | 5.47 | 16.47 |
| | 430686 | NM_001942 | Hs.2633 | desmoglein 1 | 6.06 | 4.13 | 3.31 |
| 25 | 409601 | AF237621 | Hs.80828 | keratin 1 (epidermolytic hyperkeratosis) | 5.86 | 9.22 | 0.77 |
| | 429170 | NM_001394 | Hs.2359 | dual specificity phosphatase 4 | 5.84 | 3.46 | 5.84 |
| | 428227 | AA321649 | Hs.2248 | small inducible cytokine subfamily B (Cy | 5.82 | 3.94 | 5.82 |
| | 414812 | X72755 | Hs.77367 | monokine induced by gamma interferon | 5.81 | 3.33 | 6.79 |
| | 453344 | BE349075 | Hs.44571 | ESTs | 5.78 | 3.07 | 5.98 |
| 30 | 425088 | AA663372 | Hs.169395 | hypothetical protein FLJ12015 | 5.60 | 3.92 | 5.60 |
| | 402075 | | | ENSP00000251056*-Plasma membrane calcium | 5.12 | 4.22 | 5.12 |
| | 416975 | NM_004131 | Hs.1051 | granzyme B (granzyme 2, cytotoxic T-lymp | 5.09 | 3.33 | 4.14 |
| | 420602 | AF060877 | Hs.99236 | regulator of G-protein signaling 20 | 5.06 | 5.78 | 5.06 |
| | 426600 | NM_003378 | Hs.171014 | VEGF nerve growth factor inducible | 5.04 | 6.77 | 9.42 |
| 35 | 430838 | N46664 | Hs.169395 | hypothetical protein FLJ12015 | 5.03 | 3.06 | 5.03 |
| | 417542 | J04129 | Hs.82269 | progesterone-associated endometrial prote | 4.93 | 8.13 | 5.41 |
| | 425234 | AW152225 | Hs.165909 | ESTs, Weakly similar to I38022 hypotheti | 4.78 | 2.93 | 4.78 |
| | 408962 | BE386436 | Hs.44317 | SRY (sex determining region Y)-box 10 | 4.75 | 3.28 | 5.30 |
| | 410361 | BE391804 | Hs.62661 | guanylate binding protein 1, interferon- | 4.70 | 3.11 | 4.70 |
| 40 | 429903 | AL134197 | Hs.93597 | cyclin-dependent kinase 5, regulatory su | 4.68 | 2.27 | 4.68 |
| | 407756 | AA116021 | Hs.38260 | ubiquitin specific protease 18 | 4.65 | 3.21 | 3.31 |
| | 417166 | AA431323 | Hs.42146 | ESTs | 4.56 | 5.23 | 4.56 |
| | 421773 | W69233 | Hs.112457 | ESTs | 4.52 | 11.11 | 0.96 |
| | 442711 | AF151073 | Hs.8645 | hypothetical protein | 4.37 | 3.70 | 4.30 |
| 45 | 457211 | AW972565 | Hs.32399 | ESTs, Weakly similar to S51797 vasodilat | 4.37 | 3.08 | 6.75 |
| | 428513 | BE220806 | Hs.184697 | Homo sapiens clone 23785 mRNA sequence | 4.32 | 2.61 | 4.32 |
| | 447937 | AL109716 | Hs.20034 | Homo sapiens mRNA full length insert cDN | 4.31 | 3.13 | 4.31 |
| | 451099 | R52795 | Hs.25954 | interleukin 13 receptor, alpha 2 | 4.28 | 2.89 | 2.17 |
| | 433658 | L03678 | Hs.156110 | immunoglobulin kappa constant | 4.18 | 2.68 | 5.92 |
| 50 | 420301 | AA767526 | Hs.22030 | paired box gene 5 (B-cell lineage specif | 4.16 | 2.57 | 4.16 |
| | 433447 | U29195 | Hs.3281 | neuronal pentraxin II | 4.15 | 2.26 | 6.46 |
| | 446341 | AL040763 | Hs.310735 | ESTs, Moderately similar to ALU7_HUMAN A | 4.10 | 4.04 | 4.64 |
| | 408380 | AF123050 | Hs.44532 | diubiquitin | 4.02 | 2.46 | 5.33 |
| | 421379 | Y15221 | Hs.103982 | small inducible cytokine subfamily B (Cy | 4.02 | 3.48 | 3.19 |
| 55 | 421633 | AF121850 | Hs.106260 | sorting nexin 10 | 4.01 | 2.61 | 3.36 |
| | 454117 | BE410100 | Hs.40368 | adaptor-related protein complex 1, sigma | 3.96 | 2.68 | 3.96 |
| | 417355 | D13168 | Hs.82002 | endothelin receptor type B | 3.95 | 2.46 | 3.66 |
| | 420267 | N37030 | Hs.173337 | ESTs | 3.88 | 3.87 | 3.88 |
| | 412228 | AW503785 | Hs.73792 | complement component (3d/Epstein Barr vi | 3.81 | 3.04 | 7.94 |
| 60 | 427528 | AU077143 | Hs.179565 | minichromosome maintenance deficient (S, | 3.79 | 2.23 | 3.79 |
| | 405451 | | | dihydropyrimidinase-like 3 | 3.78 | 3.74 | 4.06 |
| | 449078 | AK001256 | Hs.22975 | KIAA1576 protein | 3.76 | 2.83 | 3.76 |
| | 423799 | AW026300 | Hs.132906 | 19A24 protein | 3.75 | 2.36 | 3.75 |
| | 456373 | BE247706 | Hs.89751 | membrane-spanning 4-domains, subfamily A | 3.73 | 2.59 | 6.97 |
| 65 | 444863 | AW384082 | Hs.104879 | serine (or cysteine) proteinase inhibito | 3.72 | 2.15 | 3.92 |
| | 427666 | AI791495 | Hs.180142 | calmodulin-like skin protein (CLSP) | 3.69 | 4.17 | 1.18 |
| | 415817 | U88967 | Hs.78867 | protein tyrosine phosphatase, receptor-t | 3.64 | 2.08 | 3.64 |
| | 422423 | AF283777 | Hs.116481 | CD72 antigen | 3.64 | 2.94 | 3.64 |
| | 419956 | AL137939 | Hs.40096 | cadherin 19, type 2 | 3.56 | 2.22 | 4.68 |
| 70 | 420338 | AA825595 | Hs.88269 | Homo sapiens, clone MGC:17339, mRNA, com | 3.55 | 2.96 | 4.70 |
| | 412140 | AA219691 | Hs.73625 | RAB6 interacting, kinesin-like (rabkines | 3.54 | 1.96 | 3.54 |
| | 458079 | AI796870 | Hs.54277 | DNA segment on chromosome X (unique) 992 | 3.53 | 2.18 | 3.27 |
| | 444381 | BE387335 | Hs.283713 | ESTs, Weakly similar to S64054 hypotheti | 3.48 | 2.83 | 11.00 |
| | 449722 | BE280074 | Hs.23960 | cyclin B1 | 3.48 | 2.10 | 4.64 |
| 75 | 438380 | T06430 | Hs.6194 | chondroitin sulfate proteoglycan BEHAB/b | 3.47 | 3.90 | 4.98 |
| | 452744 | AI267652 | Hs.246107 | Homo sapiens mRNA; cDNA DKFZp434E082 (fr | 3.45 | 2.38 | 3.45 |
| | 447210 | AF035269 | Hs.17752 | phosphatidylserine-specific phospholipas | 3.44 | 3.83 | 2.09 |
| | 428804 | AK000713 | Hs.193736 | hypothetical protein FLJ20706 | 3.43 | 2.39 | 3.43 |
| | 407846 | AA426202 | Hs.40403 | Cbp/p300-interacting transactivator, wit | 3.41 | 4.33 | 5.41 |
| 80 | 423605 | AF047826 | Hs.129887 | cadherin 19, type 2 | 3.40 | 1.97 | 4.06 |
| | 421508 | NM_004833 | Hs.105115 | absent in melanoma 2 | 3.38 | 2.77 | 5.46 |
| | 428001 | H97428 | Hs.219907 | ESTs, Moderately similar to Transforming | 3.36 | 2.41 | 3.36 |
| | 430770 | AA765694 | Hs.123296 | ESTs | 3.36 | 2.08 | 3.83 |
| | 445784 | AI253155 | Hs.146065 | ESTs | 3.32 | 2.02 | 3.80 |

| | | | | | | | |
|----|--------|-----------|-----------|--|------|------|-------|
| 5 | 414646 | AA353776 | Hs.901 | CD48 antigen (B-cell membrane protein) | 3.32 | 1.87 | 3.76 |
| | 448966 | AW372914 | Hs.86149 | phosphoinositol 3-phosphate-binding prot | 3.31 | 2.10 | 3.31 |
| | 441224 | AU076964 | Hs.7753 | calumenin | 3.28 | 2.04 | 3.28 |
| | 428242 | H55709 | Hs.2250 | leukemia inhibitory factor (cholinergic | 3.26 | 2.43 | 3.56 |
| | 413385 | M34455 | Hs.840 | indoleamine-pyrrole 2,3 dioxygenase | 3.24 | 2.94 | 2.85 |
| | 416636 | N32536 | Hs.42645 | solute carrier family 16 (monocarboxylic | 3.23 | 1.84 | 3.87 |
| | 415668 | AW957684 | Hs.306814 | hypothetical protein FLJ21889 | 3.22 | 3.10 | 3.13 |
| | 442757 | AI739528 | Hs.28345 | ESTs | 3.22 | 3.41 | 1.45 |
| 10 | 426317 | AA312350 | Hs.169294 | transcription factor 7 (T-cell specific, | 3.18 | 2.50 | 3.18 |
| | 432874 | W94322 | Hs.279651 | melanoma inhibitory activity | 3.18 | 5.31 | 4.55 |
| | 412561 | NM_002286 | Hs.74011 | lymphocyte activation gene 3 | 3.17 | 3.09 | 4.28 |
| | 443983 | H04482 | Hs.163724 | ESTs | 3.16 | 2.21 | 3.16 |
| | 429732 | U20158 | Hs.2488 | lymphocyte cytosolic protein 2 (SH2 doma | 3.14 | 1.74 | 3.25 |
| 15 | 422363 | T55979 | Hs.115474 | replication factor C (activator 1) 3 (38 | 3.14 | 2.07 | 3.33 |
| | 422424 | AI186431 | Hs.296638 | prostate differentiation factor | 3.10 | 3.20 | 2.15 |
| | 435256 | AF193766 | Hs.13872 | cytokine-like protein C17 | 3.10 | 2.23 | 3.10 |
| | 401747 | | | Homo sapiens keratin 17 (KRT17) | 3.10 | 2.10 | 3.02 |
| 20 | 447674 | BE270640 | Hs.19192 | cyclin-dependent kinase 2 | 3.08 | 3.08 | 4.00 |
| | 419870 | AW403911 | Hs.266175 | phosphoprotein associated with GEMs | 3.07 | 3.16 | 3.07 |
| | 432878 | BE386490 | Hs.279663 | Pirin | 3.06 | 2.92 | 4.20 |
| | 401454 | | | NM_014226: Homo sapiens renal tumor an | 3.05 | 1.96 | 3.05 |
| | 410079 | U94362 | Hs.58589 | glycogenin 2 | 3.01 | 2.26 | 3.27 |
| 25 | 426501 | AW043782 | Hs.293616 | ESTs | 3.01 | 2.00 | 3.68 |
| | 418310 | AA814100 | Hs.86693 | ESTs | 3.00 | 2.35 | 6.76 |
| | 422283 | AW411307 | Hs.114311 | CDC45 (cell division cycle 45, S.cerevis | 2.96 | 2.31 | 3.78 |
| | 422309 | U79745 | Hs.114924 | solute carrier family 16 (monocarboxylic | 2.96 | 2.49 | 4.74 |
| | 408418 | AW963897 | Hs.44743 | KIAA1435 protein | 2.94 | 1.80 | 2.94 |
| 30 | 432882 | NM_013257 | Hs.279696 | serum/glucocorticoid regulated kinase-ii | 2.93 | 1.74 | 2.93 |
| | 416640 | BE262478 | Hs.79404 | neuron-specific protein | 2.93 | 2.78 | 3.09 |
| | 443264 | BE221477 | Hs.132137 | ESTs, Moderately similar to A47582 B-cel | 2.92 | 2.35 | 4.27 |
| | 410491 | AA465131 | Hs.64001 | Homo sapiens clone 25218 mRNA sequence | 2.91 | 2.83 | 3.84 |
| | 405545 | | | Target Exon | 2.90 | 2.44 | 2.90 |
| 35 | 451537 | R56631 | Hs.26550 | retinoid X receptor, gamma | 2.90 | 4.09 | 3.40 |
| | 439926 | AW014875 | Hs.137007 | ESTs | 2.90 | 2.43 | 2.90 |
| | 406673 | M34996 | Hs.198253 | major histocompatibility complex, class | 2.89 | 3.22 | 1.44 |
| | 418007 | M13509 | Hs.83169 | matrix metalloproteinase 1 (interstitial | 2.89 | 3.90 | 2.89 |
| | 440065 | W03476 | Hs.266331 | hypothetical protein MGC4595 | 2.89 | 4.40 | 3.05 |
| 40 | 442739 | NM_007274 | Hs.8679 | cytosolic acyl coenzyme A thioester hydr | 2.88 | 2.36 | 4.54 |
| | 424620 | AA101043 | Hs.151254 | kallikrein 7 (chymotryptic, stratum corn | 2.86 | 3.23 | 1.95 |
| | 407856 | AA045281 | Hs.266175 | phosphoprotein associated with GEMs | 2.84 | 1.84 | 2.84 |
| | 430540 | AW245422 | | Homo sapiens cDNA: FLJ22105 fs, clone H | 2.84 | 1.80 | 2.92 |
| | 424153 | AA451737 | Hs.141496 | MAGE-like 2 | 2.84 | 2.26 | 2.84 |
| | 420798 | W93774 | Hs.99936 | keratin 10 (epidermolytic hyperkeratosis | 2.81 | 2.91 | 0.83 |
| 45 | 431317 | AA502682 | | gb:ng23d01.s1 NCI_CGAP_Ov2 Homo sapiens | 2.81 | 2.17 | 2.96 |
| | 424800 | AL035588 | Hs.153203 | MyoD family inhibitor | 2.80 | 2.06 | 4.10 |
| | 448111 | AA053486 | Hs.20315 | interferon-induced protein with tetratri | 2.79 | 1.85 | 2.42 |
| | 431183 | NM_006855 | Hs.250696 | KDEL (Lys-Asp-Glu-Leu) endoplasmic retic | 2.78 | 2.34 | 6.53 |
| | 448719 | AA033627 | Hs.21858 | trinucleotide repeat containing 3 | 2.78 | 3.75 | 4.01 |
| 50 | 427951 | AI826125 | Hs.43546 | ESTs | 2.78 | 1.99 | 2.70 |
| | 453912 | AL121031 | | SWI/SNF related, matrix associated, acti | 2.77 | 2.28 | 2.77 |
| | 426711 | AA383471 | Hs.343800 | conserved gene amplified in osteosarcoma | 2.75 | 1.98 | 2.75 |
| | 409430 | R21945 | Hs.346735 | splicing factor, arginine/serine-rich 5 | 2.74 | 3.18 | 3.60 |
| 55 | 409041 | AB033025 | Hs.50081 | Hypothetical protein, XP_051860 (KIAA119 | 2.72 | 2.24 | 2.72 |
| | 442117 | AW664964 | Hs.128899 | ESTs; hypothetical protein for IMAGE:447 | 2.72 | 2.31 | 3.59 |
| | 420552 | AK000492 | Hs.98806 | hypothetical protein | 2.72 | 1.85 | 2.72 |
| | 409103 | AF251237 | Hs.112208 | XAGE-1 protein | 2.72 | 2.18 | 2.72 |
| | 439963 | AW247529 | Hs.6793 | platelet-activating factor acetylhydrola | 2.71 | 2.20 | 4.48 |
| 60 | 413171 | AA318325 | Hs.75219 | tyrosinase-related protein 1 | 2.71 | 5.74 | 2.62 |
| | 436700 | AI693690 | Hs.301406 | hypothetical protein PP3501 | 2.71 | 3.37 | 3.32 |
| | 419098 | AA234041 | Hs.87271 | ESTs | 2.70 | 3.53 | 1.35 |
| | 436608 | AA628980 | Hs.192371 | down syndrome critical region protein DS | 2.69 | 2.48 | 2.69 |
| | 418067 | AI127958 | Hs.83393 | cystatin E/M | 2.68 | 3.04 | 0.56 |
| 65 | 439453 | BE264974 | Hs.6566 | thyroid hormone receptor interactor 13 | 2.67 | 2.36 | 3.16 |
| | 437723 | AI672731 | Hs.13256 | ESTs | 2.66 | 2.16 | 2.66 |
| | 411252 | AB018549 | Hs.69328 | MD-2 protein | 2.66 | 1.81 | 2.66 |
| | 424321 | W74048 | Hs.1765 | lymphocyte-specific protein tyrosine kin | 2.66 | 2.43 | 3.92 |
| | 453837 | AL138387 | Hs.256126 | baculoviral IAP repeat-containing 7 (liv | 2.65 | 3.71 | 2.80 |
| 70 | 434826 | AF155661 | Hs.22265 | pyruvate dehydrogenase phosphatase | 2.64 | 1.85 | 4.72 |
| | 414696 | AF002020 | Hs.76918 | Niemann-Pick disease, type C1 | 2.64 | 2.07 | 2.64 |
| | 444371 | BE540274 | Hs.239 | forkhead box M1 | 2.64 | 2.82 | 4.46 |
| | 436291 | BE568452 | Hs.344037 | protein regulator of cytokinesis 1 | 2.63 | 1.81 | 2.95 |
| | 439310 | AF086120 | Hs.102793 | ESTs | 2.62 | 2.38 | 10.12 |
| | 420218 | AW958037 | | ribosomal protein L4 | 2.62 | 2.80 | 2.62 |
| 75 | 438746 | AI885815 | Hs.184727 | Human melanoma-associated antigen p97 (m | 2.60 | 3.27 | 2.12 |
| | 432828 | AB042326 | Hs.287402 | chondroitin 4-sulfotransferase | 2.60 | 2.67 | 3.03 |
| | 408367 | AK001178 | Hs.44424 | homolog of rat orphan transporter v7-3 | 2.59 | 3.22 | 2.59 |
| | 408527 | AL135018 | Hs.33074 | Homo sapiens, clone IMAGE:3606519, mRNA, | 2.58 | 1.69 | 2.05 |
| | 444809 | BE207568 | Hs.208219 | oculopainin | 2.58 | 2.77 | 2.88 |
| 80 | 432886 | BE159028 | Hs.279704 | chromatin accessibility complex 1 | 2.58 | 1.83 | 2.58 |
| | 434276 | AF123659 | Hs.93605 | leucine zipper, putative tumor suppresso | 2.55 | 3.70 | 3.28 |
| | 412326 | R07566 | Hs.73817 | small inducible cytokine A3 (homologous | 2.55 | 2.14 | 1.62 |
| | 410174 | AA305007 | Hs.59461 | DKFZP434C245 protein | 2.55 | 2.07 | 2.55 |
| | 447735 | AA775268 | Hs.6127 | Homo sapiens cDNA: FLJ23020 fs, clone L | 2.54 | 2.17 | 4.01 |

| | | | | | | | |
|----|--------|-----------|-----------|---|------|------|------|
| 5 | 422173 | BE385828 | Hs.250619 | phorbol-like protein MDS019 (CEM15) | 2.53 | 1.68 | 3.16 |
| | 418506 | AA084248 | Hs.85339 | G protein-coupled receptor 39 | 2.53 | 2.74 | 3.93 |
| | 437396 | BE140396 | Hs.21621 | hypothetical protein DKFZp762O076 | 2.52 | 1.62 | 3.17 |
| | 448140 | AF146761 | Hs.20450 | BCM-like membrane protein precursor | 2.51 | 2.67 | 1.88 |
| | 442426 | AI373062 | Hs.332938 | hypothetical protein MGC5370 | 2.51 | 2.08 | 4.57 |
| 10 | 417427 | M90391 | Hs.82127 | interleukin 16 (lymphocyte chemoattractant) | 2.51 | 1.74 | 2.68 |
| | 427581 | NM_014788 | Hs.179703 | KIAA0129 gene product | 2.51 | 1.67 | 2.24 |
| | 432800 | BE391046 | Hs.278962 | AIM-1 protein | 2.51 | 5.55 | 2.42 |
| | 408996 | AI979168 | Hs.344096 | glycoprotein (transmembrane) nmb | 2.50 | 1.95 | 2.41 |
| | 410326 | AI368909 | Hs.47650 | ESTs | 2.50 | 2.85 | 2.63 |
| 15 | 452833 | BE559681 | Hs.30736 | KIAA0124 protein | 2.50 | 3.14 | 3.07 |
| | 410016 | AA297977 | Hs.57907 | small inducible cytokine subfamily A (Cy) | 2.49 | 3.38 | 2.91 |
| | 429083 | Y09397 | Hs.227817 | BCL2-related protein A1 | 2.48 | 1.85 | 2.70 |
| | 418460 | M26315 | Hs.85258 | CD8 antigen, alpha polypeptide (p32) | 2.48 | 2.33 | 2.99 |
| | 409142 | AL136877 | Hs.50758 | SMC4 (structural maintenance of chromosome) | 2.47 | 1.88 | 4.14 |
| 20 | 412970 | AB026436 | Hs.177534 | dual specificity phosphatase 10 | 2.46 | 2.00 | 0.98 |
| | 401780 | | | NM_005557: Homo sapiens keratin 16 (foca) | 2.44 | 2.30 | 1.39 |
| | 416426 | AA180256 | Hs.210473 | Homo sapiens cDNA FLJ14872 fis, clone PL | 2.44 | 1.57 | 0.88 |
| | 432606 | NM_002104 | Hs.3086 | granzyme K (serine protease, granzyme 3; | 2.42 | 1.91 | 2.56 |
| | 417880 | BE241595 | Hs.82848 | selectin L (lymphocyte adhesion molecule) | 2.42 | 2.31 | 4.27 |
| 25 | 415929 | AA724373 | Hs.49344 | hypothetical protein FLJ11006 | 2.41 | 2.73 | 2.41 |
| | 415752 | BE314524 | Hs.78776 | putative transmembrane protein | 2.41 | 2.07 | 3.41 |
| | 409703 | NM_006187 | Hs.56009 | 2'-5'-oligoadenylate synthetase 3 (100 k | 2.41 | 2.34 | 3.26 |
| | 414004 | AA737033 | Hs.7155 | ESTs, Moderately similar to 2115357A TYK | 2.40 | 1.65 | 2.40 |
| | 453857 | AL080235 | Hs.35861 | DKFZP586E1621 protein | 2.40 | 2.18 | 8.13 |
| 30 | 410290 | AA402307 | Hs.322844 | hypothetical protein DKFZp564A176 | 2.40 | 2.88 | 2.46 |
| | 403328 | | | Target Exon | 2.39 | 2.00 | 1.95 |
| | 427540 | R12014 | Hs.20976 | ESTs | 2.39 | 1.73 | 3.24 |
| | 449523 | NM_000579 | Hs.54443 | chemokine (C-C motif) receptor 5 | 2.39 | 1.96 | 2.39 |
| | 433848 | AF095719 | Hs.93764 | carboxypeptidase A4 | 2.38 | 2.45 | 2.65 |
| 35 | 438501 | Z44110 | Hs.86149 | phosphoinositide 3-phosphate-binding prot | 2.38 | 1.85 | 2.38 |
| | 430066 | AI929659 | Hs.237825 | signal recognition particle 72kD | 2.38 | 1.60 | 2.79 |
| | 447343 | AA256641 | Hs.235894 | ESTs, Highly similar to S02392 alpha-2-m | 2.37 | 1.99 | 6.23 |
| | 450447 | AF212223 | Hs.25010 | hypothetical protein P15-2 | 2.37 | 1.72 | 3.24 |
| | 458997 | AW937420 | | ESTs | 2.37 | 1.57 | 3.27 |
| 40 | 451446 | AI826288 | Hs.171637 | hypothetical protein MGC2628 | 2.35 | 1.90 | 2.39 |
| | 408838 | AI669535 | Hs.40369 | ESTs | 2.35 | 1.59 | 2.71 |
| | 448275 | BE514434 | Hs.20830 | kinesin-like 2 | 2.35 | 2.19 | 2.35 |
| | 424148 | BE242274 | Hs.1741 | integrin, beta 7 | 2.35 | 1.89 | 3.07 |
| | 410700 | AA352335 | Hs.65641 | hypothetical protein FLJ20073 | 2.35 | 1.65 | 2.35 |
| 45 | 409105 | AW467539 | Hs.255877 | ESTs | 2.35 | 2.50 | 2.35 |
| | 452882 | AW972990 | Hs.196270 | folate transporter/carrier | 2.34 | 2.12 | 2.90 |
| | 425606 | U52112 | Hs.158331 | renin-binding protein | 2.34 | 2.69 | 1.69 |
| | 433576 | BE080715 | Hs.161091 | ESTs | 2.34 | 3.74 | 2.34 |
| | 423494 | AW504365 | Hs.24143 | Wiskott-Aldrich syndrome protein interac | 2.34 | 2.08 | 4.48 |
| 50 | 431620 | AA126109 | Hs.264981 | 2'-5'-oligoadenylate synthetase 2 (69-71 | 2.33 | 2.43 | 2.66 |
| | 436614 | AW104388 | Hs.149091 | ESTs | 2.33 | 3.37 | 2.33 |
| | 425289 | AW139342 | Hs.155530 | interferon, gamma-inducible protein 16 | 2.33 | 1.67 | 4.28 |
| | 426827 | AW067805 | Hs.172665 | methylene tetrahydrofolate dehydrogenase | 2.33 | 1.58 | 0.40 |
| | 430015 | AW768399 | | ESTs | 2.33 | 1.76 | 2.33 |
| 55 | 421282 | AA286914 | Hs.40782 | ESTs | 2.32 | 1.65 | 2.49 |
| | 447737 | AK000643 | Hs.19404 | DKFZP564L0862 protein | 2.32 | 2.16 | 1.48 |
| | 432540 | AI821517 | Hs.105866 | ESTs | 2.32 | 1.58 | 2.35 |
| | 418064 | BE387287 | Hs.83384 | S100 calcium-binding protein, beta (neur | 2.32 | 2.46 | 9.99 |
| | 414829 | AA321568 | Hs.77436 | pleckstrin | 2.32 | 1.91 | 2.32 |
| 60 | 425390 | AI092634 | Hs.156114 | protein tyrosine phosphatase, non-recept | 2.31 | 1.63 | 2.31 |
| | 448569 | BE382657 | Hs.21486 | signal transducer and activator of trans | 2.31 | 2.79 | 2.41 |
| | 428819 | AL135623 | Hs.193914 | KIAA0575 gene product | 2.30 | 1.60 | 2.95 |
| | 409512 | AW979187 | Hs.293591 | melanoma differentiation associated prot | 2.30 | 1.95 | 3.66 |
| | 425231 | AA527161 | | ESTs | 2.28 | 1.96 | 2.36 |
| 65 | 416091 | AF295370 | Hs.283082 | defensin, beta 3 | 2.28 | 2.76 | 2.18 |
| | 418478 | U38945 | Hs.1174 | cyclin-dependent kinase inhibitor 2A (me | 2.27 | 2.88 | 2.46 |
| | 427719 | AI393122 | Hs.134726 | ESTs | 2.27 | 1.88 | 2.29 |
| | 431830 | Y16645 | Hs.271387 | small inducible cytokine subfamily A (Cy | 2.27 | 2.16 | 4.09 |
| | 457465 | AW301344 | Hs.122908 | DNA replication factor | 2.26 | 2.23 | 2.26 |
| 70 | 431639 | AK000680 | Hs.266175 | phosphoprotein associated with GEMs | 2.26 | 2.13 | 3.16 |
| | 442485 | BE092285 | Hs.29724 | hypothetical protein FLJ13187 | 2.26 | 1.75 | 2.84 |
| | 424687 | J05070 | Hs.151738 | matrix metalloproteinase 9 (gelatinase B | 2.26 | 3.38 | 2.56 |
| | 449317 | AW293413 | Hs.132906 | 19A24 protein | 2.26 | 2.04 | 2.73 |
| | 429922 | Z97630 | Hs.226117 | H1 histone family, member D | 2.26 | 1.59 | 2.38 |
| 75 | 441362 | BE614410 | Hs.23044 | RAD51 (S. cerevisiae) homolog (E. coli Ra | 2.25 | 1.86 | 3.07 |
| | 425388 | AA329384 | Hs.156110 | immunoglobulin kappa constant | 2.25 | 1.91 | 2.25 |
| | 417282 | AA195203 | | RAB5C, member RAS oncogene family | 2.25 | 2.23 | 3.20 |
| | 406687 | M31126 | | matrix metalloproteinase 11 (stromelysin | 2.24 | 2.69 | 2.78 |
| | 437862 | AW978107 | Hs.5884 | Homo sapiens mRNA; cDNA DKFZp586C0224 (f | 2.23 | 2.20 | 2.51 |
| 80 | 408015 | AW136771 | Hs.244349 | epidermal differentiation complex protei | 2.23 | 4.59 | 2.47 |
| | 442503 | AF147078 | Hs.150853 | p53-responsive gene 5 | 2.23 | 3.62 | 0.85 |
| | 429747 | M87507 | Hs.2490 | caspase 1, apoptosis-related cysteine pr | 2.22 | 1.60 | 1.69 |
| | 424825 | AF207069 | Hs.153357 | procollagen-lysine, 2-oxoglutarate 5-dio | 2.22 | 5.53 | 2.46 |
| | 417693 | AW959741 | Hs.40368 | adaptor-related protein complex 1, sigma | 2.21 | 2.40 | 4.37 |
| | 422947 | AA306782 | Hs.122552 | G-2 and S-phase expressed 1 | 2.21 | 2.06 | 2.32 |
| | 445875 | AF070524 | Hs.13410 | Homo sapiens clone 24453 mRNA sequence | 2.20 | 2.69 | 2.91 |
| | 417366 | BE185289 | Hs.1076 | small proline-rich protein 1B (corniflin) | 2.20 | 2.26 | 3.79 |

| | | | | | | | |
|----|--------|-----------|-----------|---|------|------|------|
| 5 | 450065 | AL050107 | Hs.24341 | transcriptional co-activator with PDZ-bi | | | |
| | 423397 | NM_001838 | Hs.1652 | chemokine (C-C motif) receptor 7 | 2.20 | 1.96 | 2.44 |
| | 427051 | BE178110 | Hs.173374 | Homo sapiens cDNA FLJ10500 fis, clone NT | 2.20 | 3.28 | 2.99 |
| | 418203 | X54942 | Hs.83758 | CDC28 protein kinase 2 | 2.20 | 1.98 | 3.40 |
| | 409354 | N68188 | Hs.159472 | Homo sapiens cDNA: FLJ22224 fis, clone H | 2.20 | 1.44 | 2.31 |
| | 418941 | AA452970 | Hs.239527 | E1B-55kDa-associated protein 5 | 2.18 | 2.44 | 2.70 |
| | 424723 | BE409813 | Hs.152337 | protein arginine N-methyltransferase 3(h | 2.18 | 1.75 | 2.70 |
| | 430132 | AA204686 | Hs.234149 | hypothetical protein FLJ20647 | 2.18 | 1.55 | 2.44 |
| 10 | 452194 | AJ694413 | | Ubiquitin-like protein FAT107?? - diubiq | 2.18 | 1.43 | 2.37 |
| | 417933 | X02308 | Hs.82962 | thymidylate synthetase | 2.17 | 3.07 | 1.76 |
| | 420137 | AA306478 | Hs.95327 | CD3D antigen, delta polypeptide (TIT3 co | 2.17 | 1.86 | 4.15 |
| | 425317 | AW205118 | Hs.210546 | interleukin 21 receptor | 2.17 | 2.38 | 2.91 |
| | 447769 | AW873704 | Hs.320831 | Homo sapiens cDNA FLJ14597 fis, clone NT | 2.17 | 2.02 | 2.22 |
| 15 | 407748 | AL079409 | Hs.38176 | KIAA0606 protein; SCN Circadian Oscillat | 2.16 | 1.87 | 2.49 |
| | 452958 | AA883929 | Hs.40527 | ESTs | 2.16 | 1.55 | 2.26 |
| | 440325 | NM_003812 | Hs.7164 | a disintegrin and metalloproteinase doma | 2.15 | 1.56 | 2.84 |
| | 426153 | AF057169 | Hs.182771 | vitelliform macular dystrophy (Best dise | 2.15 | 1.76 | 2.97 |
| | 430580 | AA806105 | Hs.300697 | immunoglobulin heavy constant gamma 3 (G | 2.15 | 1.85 | 2.74 |
| 20 | 451952 | AL120173 | Hs.301663 | ESTs | 2.14 | 1.88 | 4.99 |
| | 450534 | AJ570189 | Hs.25132 | KIAA0470 gene product | 2.13 | 2.08 | 2.13 |
| | 449217 | AA278536 | Hs.23262 | ribonuclease, RNase A family, k5 | 2.12 | 1.67 | 3.41 |
| | 432734 | AA837396 | Hs.263925 | LIS1-interacting protein NUDE1, rat homo | 2.12 | 1.75 | 2.27 |
| | 413190 | AA151802 | Hs.40368 | adaptor-related protein complex 1, sigma | 2.12 | 2.14 | 2.49 |
| 25 | 443991 | NM_002250 | Hs.10082 | potassium intermediate/small conductance | 2.12 | 2.46 | 2.67 |
| | 429624 | AA458648 | Hs.99476 | ESTs, Weakly similar to 1313184B alpha1 | 2.12 | 2.16 | 2.82 |
| | 447178 | AW594641 | Hs.192417 | ESTs | 2.11 | 2.01 | 0.68 |
| | 423017 | AW178761 | Hs.227948 | serine (or cysteine) proteinase inhibito | 2.10 | 2.52 | 2.10 |
| | 452110 | T47667 | Hs.28005 | Homo sapiens cDNA FLJ11309 fis, clone PL | 2.10 | 1.52 | 4.01 |
| 30 | 436797 | AA731491 | Hs.334477 | hypothetical protein MGC14879 | 2.10 | 1.53 | 2.10 |
| | 453256 | AJ565587 | Hs.32556 | KIAA0379 protein | 2.10 | 1.55 | 2.41 |
| | 405547 | | | NM_018833: Homo sapiens transporter 2, A | 2.09 | 2.13 | 2.89 |
| | 434203 | BE262677 | Hs.283558 | hypothetical protein PRO1855 | 2.09 | 2.61 | 2.09 |
| | 412609 | Z48804 | Hs.74124 | ocular albinism 1 (Nettleship-Falls) | 2.09 | 1.76 | 4.10 |
| 35 | 414821 | M63835 | Hs.77424 | Fc fragment of IgG, high affinity Ia, re | 2.09 | 3.91 | 2.38 |
| | 417576 | AA339449 | Hs.82285 | phosphoribosylglycinamide formyltransfer | 2.09 | 1.62 | 1.28 |
| | 447377 | X77343 | Hs.334334 | transcription factor AP-2 alpha | 2.08 | 1.86 | 2.08 |
| | 423198 | M81933 | Hs.1634 | cell division cycle 25A | 2.08 | 2.83 | 2.08 |
| | 433068 | NM_006456 | Hs.288215 | sialyltransferase | 2.08 | 1.66 | 2.23 |
| 40 | 409038 | T97490 | Hs.50002 | small inducible cytokine subfamily A (Cy | 2.08 | 1.94 | 2.60 |
| | 452392 | L20815 | Hs.507 | corneodesmosin | 2.07 | 1.91 | 3.62 |
| | 403532 | | | NM_024638: Homo sapiens hypothetical prot | 2.07 | 3.96 | 0.97 |
| | 439859 | AW292872 | Hs.124554 | ESTs | 2.07 | 1.88 | 2.68 |
| | 428484 | AF104032 | Hs.184601 | solute carrier family 7 (cationic amino | 2.07 | 1.72 | 2.22 |
| 45 | 442643 | U82756 | | PRP4/STK4WD splicing factor | 2.07 | 2.26 | 4.22 |
| | 426312 | AF026939 | Hs.181874 | interferon-induced protein with tetratin | 2.07 | 1.74 | 1.90 |
| | 409988 | N27687 | Hs.334334 | transcription factor AP-2 alpha (activat | 2.06 | 2.08 | 1.43 |
| | 408548 | AA055449 | Hs.63187 | ESTs, Weakly similar to ALUC_HUMAN !!!! | 2.06 | 2.12 | 2.06 |
| | 442271 | AF000652 | Hs.8180 | syndecan binding protein (syntenin) | 2.06 | 1.65 | 2.91 |
| 50 | 414142 | AW368397 | Hs.334485 | hemicentin (fibulin 6) | 2.06 | 1.97 | 2.42 |
| | 420931 | AF044197 | Hs.100431 | small inducible cytokine B subfamily (Cy | 2.05 | 2.44 | 2.05 |
| | 450325 | AJ935962 | Hs.91973 | ESTs | 2.05 | 2.37 | 2.05 |
| | 424080 | X99699 | Hs.139262 | XIAP associated factor-1 | 2.05 | 1.67 | 1.82 |
| | 438209 | AL120659 | Hs.6111 | aryl-hydrocarbon receptor nuclear transi | 2.05 | 1.56 | 1.99 |
| 55 | 413794 | AF234532 | Hs.61638 | myosin X | 2.04 | 1.52 | 2.07 |
| | 414945 | BE076358 | Hs.77667 | lymphocyte antigen 6 complex, locus E | 2.04 | 2.02 | 2.11 |
| | 425580 | L11144 | Hs.1907 | galanin | 2.04 | 4.57 | 1.64 |
| | 420052 | AA418850 | Hs.44410 | ESTs | 2.04 | 1.67 | 2.26 |
| | 415947 | U04045 | Hs.78934 | mutS (E. coli) homolog 2 (colon cancer, | 2.03 | 1.90 | 2.21 |
| 60 | 416406 | D86961 | Hs.79299 | lipoma HMGIC fusion partner-like 2 | 2.03 | 1.53 | 2.31 |
| | 426759 | AJ590401 | Hs.21213 | ESTs | 2.02 | 1.73 | 2.02 |
| | 432435 | BE218886 | Hs.282070 | ESTs | 2.02 | 1.86 | 5.47 |
| | 444184 | T87841 | Hs.282990 | Human DNA sequence from clone RP1-28H20 | 2.02 | 1.39 | 1.67 |
| | 421574 | AJ000152 | Hs.105924 | defensin, beta 2 | 2.02 | 1.57 | 2.02 |
| 65 | 411358 | R47479 | Hs.94761 | KIAA1691 protein | 2.02 | 2.22 | 2.15 |
| | 408209 | NM_004454 | Hs.43697 | ets variant gene 5 (ets-related molecule | 2.01 | 2.55 | 1.75 |
| | 409262 | AK000631 | Hs.52256 | hypothetical protein FLJ20624 | 2.01 | 2.58 | 2.39 |
| | 400750 | | | Target Exon | 2.01 | 1.50 | 2.01 |
| | 439496 | BE616501 | Hs.32343 | Homo sapiens, Similar to RIKEN cDNA 1110 | 2.01 | 1.73 | 2.09 |
| 70 | 420460 | AA262331 | Hs.48376 | Homo sapiens clone HB-2 mRNA sequence | 2.01 | 2.42 | 0.78 |
| | 446839 | BE091926 | Hs.16244 | mitotic spindle coiled-coil related prot | 2.01 | 1.65 | 1.72 |
| | 427647 | W19744 | Hs.180059 | Homo sapiens cDNA FLJ20653 fis, clone KA | 2.01 | 1.61 | 1.03 |
| | 436200 | R51386 | Hs.124881 | ESTs | 2.00 | 2.11 | 2.33 |
| | 414175 | AJ308876 | Hs.103849 | hypothetical protein DKFZp761D112 | 2.00 | 1.89 | 2.24 |
| 75 | 420005 | AW271106 | Hs.133294 | ESTs | 1.99 | 1.50 | 1.99 |
| | 417848 | AA206581 | Hs.116586 | ESTs, Weakly similar to JCS314 CDC28cdc | 1.99 | 2.03 | 2.59 |
| | 435545 | AA687415 | Hs.28107 | ESTs | 1.99 | 1.42 | 2.17 |
| | 443426 | AF098158 | Hs.93329 | chromosome 20 open reading frame 1 | 1.99 | 1.89 | 1.99 |
| | 444342 | NM_014398 | Hs.10887 | similar to lysosome-associated membrane | 1.99 | 2.23 | 3.44 |
| 80 | 453905 | NM_002314 | Hs.35566 | LIM domain kinase 1 | 1.99 | 2.05 | 0.32 |
| | 453884 | AA355925 | Hs.36232 | KIAA0186 gene product | 1.98 | 2.48 | 2.79 |
| | 459373 | BE408266 | Hs.301406 | hypothetical protein PP3501 | 1.98 | 1.93 | 1.98 |
| | 422809 | AK001379 | Hs.121028 | hypothetical protein FLJ10549 | 1.98 | 2.22 | 1.91 |
| | 452840 | AJ097393 | Hs.43481 | hypothetical protein DKFZp564K192 | 1.98 | 1.68 | 1.98 |
| | | | | | 1.98 | 1.67 | 2.18 |

| | | | | | | | |
|----|--------|-----------|-----------|--|------|------|------|
| 5 | 409178 | BE393948 | Hs.50915 | kallikrein 5 | 1.98 | 3.76 | 1.37 |
| | 420991 | AW504814 | Hs.287379 | Homo sapiens mRNA for FLJ001111 protein, | 1.98 | 1.90 | 2.63 |
| | 414020 | NM_002984 | Hs.75703 | small inducible cytokine A4 (homologous | 1.97 | 1.88 | 1.23 |
| | 443105 | X96753 | Hs.9004 | chondroitin sulfate proteoglycan 4 (mela | 1.97 | 1.95 | 5.55 |
| | 413450 | Z99716 | Hs.75372 | N-acetylgalactosaminidase, alpha- | 1.97 | 1.77 | 1.97 |
| | 431574 | AW572659 | Hs.261373 | hypothetical protein dJ434O14.3 | 1.97 | 1.73 | 3.89 |
| | 408561 | AI308037 | Hs.84120 | hypothetical protein MGC13016 | 1.97 | 2.89 | 2.08 |
| | 421855 | M24470 | Hs.1435 | guanosine monophosphate reductase | 1.97 | 1.95 | 2.65 |
| | 405506 | | | Target Exon | 1.96 | 1.72 | 2.27 |
| 10 | 412490 | AW803564 | Hs.288850 | Homo sapiens cDNA: FLJ22528 fis, clone H | 1.96 | 1.74 | 2.35 |
| | 437379 | AL359575 | Hs.23765 | Homo sapiens mRNA; cDNA DKFZp547M123 (fr | 1.95 | 2.09 | 2.77 |
| | 448356 | AL120837 | Hs.20993 | high-glucose-regulated protein 8 | 1.95 | 1.66 | 2.58 |
| | 453931 | AL121278 | Hs.25144 | ESTs | 1.95 | 2.38 | 1.95 |
| | 424308 | AW975531 | Hs.154443 | minichromosome maintenance deficient (S. | 1.95 | 1.63 | 2.82 |
| 15 | 429547 | AW009166 | Hs.99376 | FGENESH predicted novel secreted protein | 1.94 | 2.02 | 1.35 |
| | 442064 | AI422867 | Hs.88594 | ESTs | 1.94 | 1.49 | 2.21 |
| | 400533 | | | ENSP00000209376::PRED65 protein (Fragmen | 1.94 | 1.69 | 1.94 |
| | 448752 | AA593867 | Hs.300842 | KIAA1608 protein | 1.94 | 1.71 | 2.40 |
| 20 | 408636 | BE294925 | Hs.46680 | CGI-12 protein | 1.94 | 1.69 | 2.93 |
| | 439569 | AW602166 | Hs.222399 | CEGP1 protein | 1.93 | 1.62 | 3.21 |
| | 405779 | | | NM_005367:Homo sapiens melanoma antigen, | 1.93 | 1.83 | 1.99 |
| | 444670 | H58373 | Hs.332938 | hypothetical protein MGC5370 | 1.93 | 1.97 | 1.93 |
| | 446950 | AA305800 | Hs.5672 | hypothetical protein AF140225 | 1.93 | 1.56 | 1.61 |
| 25 | 409185 | AW961601 | Hs.252406 | hypothetical protein FLJ12296 similar to | 1.93 | 2.12 | 2.63 |
| | 409098 | AA132672 | Hs.7984 | pleckstrin homology, Sec7 and coiled/coi | 1.92 | 2.12 | 2.51 |
| | 413916 | N49813 | Hs.75615 | apolipoprotein C-II | 1.92 | 1.98 | 0.22 |
| | 429609 | AF002246 | Hs.210863 | cell adhesion molecule with homology to | 1.92 | 1.65 | 6.39 |
| | 402994 | | | NM_002463::Homo sapiens myxovirus (influ | 1.92 | 2.45 | 1.89 |
| 30 | 425722 | AI659076 | Hs.97031 | hypothetical protein MGC13047 | 1.92 | 2.69 | 2.30 |
| | 421958 | AA357185 | Hs.109918 | ras homolog gene family, member H | 1.92 | 2.10 | 2.93 |
| | 412584 | X54870 | Hs.74085 | DNA segment on chromosome 12 (unique) 24 | 1.91 | 1.57 | 1.91 |
| | 415402 | AA164687 | Hs.177576 | mannosyl (alpha-1,3)-glycoprotein beta- | 1.91 | 1.44 | 1.68 |
| | 430280 | AA361258 | Hs.237858 | interleukin 7 receptor | 1.90 | 1.52 | 1.14 |
| 35 | 426251 | M24283 | Hs.168383 | intercellular adhesion molecule 1 (CD54) | 1.90 | 2.16 | 1.21 |
| | 440773 | AA352702 | Hs.37747 | Homo sapiens, Similar to RIKEN cDNA 2700 | 1.90 | 1.84 | 2.07 |
| | 427923 | AW274357 | Hs.301406 | hypothetical protein PP3501 | 1.90 | 4.26 | 1.70 |
| | 426470 | AA528794 | Hs.128644 | ESTs | 1.90 | 2.69 | 2.04 |
| | 409557 | BE182896 | Hs.3686 | ESTs | 1.90 | 2.01 | 1.90 |
| 40 | 429714 | BE561801 | Hs.2484 | T-cell leukemia/lymphoma 1A | 1.90 | 2.49 | 2.52 |
| | 428125 | AA393071 | Hs.182579 | leucine aminopeptidase | 1.89 | 1.89 | 1.49 |
| | 427634 | AI399745 | Hs.18449 | hypothetical protein MGC10820 | 1.89 | 3.59 | 1.71 |
| | 452874 | AK001061 | Hs.30925 | hypothetical protein FLJ10199 | 1.89 | 1.67 | 1.45 |
| | 418883 | BE387036 | Hs.1211 | acid phosphatase 5, tartrate resistant | 1.89 | 2.55 | 1.39 |
| 45 | 448243 | AW369771 | | integrin, beta 8 | 1.89 | 1.96 | 1.89 |
| | 416114 | AI695549 | Hs.183868 | glucuronidase, beta | 1.89 | 1.70 | 1.10 |
| | 425935 | Z98200 | Hs.163724 | HSPC019 protein | 1.88 | 1.86 | 2.04 |
| | 440672 | AF083811 | Hs.7345 | MAD1 (mitotic arrest deficient, yeast, h | 1.88 | 4.16 | 1.78 |
| | 430171 | AF086289 | Hs.234766 | skin-specific protein | 1.87 | 2.70 | 0.75 |
| 50 | 407366 | AF026942 | Hs.17518 | gb.Homo sapiens cig33 mRNA, partial sequ | 1.87 | 2.25 | 1.87 |
| | 454294 | AB000734 | Hs.50640 | JAK binding protein | 1.87 | 1.98 | 1.46 |
| | 417370 | T28651 | Hs.82030 | tryptophanyl-tRNA synthetase | 1.87 | 2.73 | 1.71 |
| | 409417 | AA156247 | Hs.104879 | serine (or cysteine) proteinase inhibito | 1.87 | 1.79 | 2.72 |
| | 401781 | | | Target Exon | 1.87 | 1.88 | 1.16 |
| 55 | 440590 | AI863446 | Hs.266308 | mosaic serine protease | 1.86 | 1.79 | 1.13 |
| | 428450 | NM_014791 | Hs.184339 | KIAA0175 gene product | 1.86 | 1.72 | 4.39 |
| | 433675 | AW977653 | Hs.75319 | ribonucleotide reductase M2 polypeptide | 1.86 | 1.81 | 1.86 |
| | 429323 | NM_001649 | Hs.2391 | apical protein, Xenopus laevis-like | 1.86 | 1.57 | 1.86 |
| | 433001 | AF217513 | Hs.279905 | clone HQ0310 PRO0310p1 | 1.85 | 1.71 | 5.82 |
| 60 | 453107 | NM_016113 | Hs.279746 | vanilloid receptor-like protein 1 | 1.85 | 2.75 | 1.84 |
| | 430441 | BE398091 | | desmoplakin (DPI, DPII) | 1.85 | 1.80 | 2.79 |
| | 417512 | X76534 | Hs.82226 | glycoprotein (transmembrane) nmb | 1.85 | 1.80 | 1.86 |
| | 423673 | BE003054 | Hs.1695 | matrix metalloproteinase 12 (macrophage | 1.85 | 1.94 | 1.85 |
| | 431958 | X63629 | Hs.2877 | cadherin 3, type 1, P-cadherin (placenta | 1.85 | 1.72 | 2.52 |
| 65 | 414737 | AI160386 | Hs.125087 | ESTs | 1.84 | 1.90 | 1.84 |
| | 439979 | AW600291 | Hs.6823 | hypothetical protein FLJ10430 | 1.84 | 1.57 | 1.84 |
| | 428311 | NM_005651 | Hs.183671 | tryptophan 2,3-dioxygenase | 1.84 | 1.41 | 0.12 |
| | 412141 | AI183838 | Hs.48938 | hypothetical protein FLJ21802 | 1.84 | 1.70 | 3.15 |
| | 428515 | AF030339 | Hs.286229 | plexin C1 | 1.84 | 1.66 | 1.84 |
| | 427914 | AA417350 | Hs.20575 | ESTs | 1.84 | 2.32 | 2.17 |
| 70 | 439352 | BE614347 | Hs.169615 | hypothetical protein FLJ20989 | 1.84 | 1.55 | 1.84 |
| | 413278 | BE563085 | Hs.833 | interferon-stimulated protein, 15 kDa | 1.83 | 3.20 | 1.75 |
| | 435080 | AI831760 | Hs.155111 | hypothetical protein FLJ14428 | 1.83 | 1.62 | 1.47 |
| | 407966 | AA295052 | Hs.38516 | Homo sapiens, clone MGC:15887, mRNA, com | 1.83 | 1.58 | 2.11 |
| 75 | 421535 | AB002359 | Hs.105478 | phosphoribosylformylglycinamide syntha | 1.83 | 1.73 | 2.18 |
| | 433029 | NM_014322 | Hs.279926 | opsin 3 (encephalopsin) | 1.83 | 1.96 | 1.83 |
| | 426158 | NM_001982 | Hs.199067 | v-erb-b2 avian erythroblastic leukemia v | 1.83 | 1.61 | 2.46 |
| | 426890 | AA393167 | Hs.41294 | ESTs | 1.82 | 2.44 | 1.82 |
| | 411027 | AF072099 | Hs.67846 | leukocyte immunoglobulin-like receptor, | 1.82 | 2.24 | 2.01 |
| 80 | 441859 | AW194364 | Hs.94814 | ESTs, Weakly similar to FIG1 MOUSE FIG-1 | 1.82 | 2.72 | 2.16 |
| | 437435 | AA249439 | Hs.27027 | hypothetical protein DKFZp762H1311 | 1.82 | 1.50 | 1.82 |
| | 448357 | N20169 | Hs.108923 | RAB38, member RAS oncogene family | 1.82 | 2.52 | 1.78 |
| | 420674 | NM_000055 | Hs.1327 | butyrylcholinesterase | 1.82 | 1.43 | 0.68 |
| | 439219 | N33883 | Hs.41322 | ESTs | 1.82 | 1.88 | 2.43 |

| | | | | | | | |
|----|--------|-----------|-----------|--|------|------|------|
| 5 | 432810 | AA863400 | | ESTs | 1.82 | 1.43 | 1.82 |
| | 417404 | NM_007350 | Hs.82101 | pleckstrin homology-like domain, family | 1.82 | 1.98 | 1.82 |
| | 447484 | AA464839 | Hs.292566 | hypothetical protein FLJ14697 | 1.82 | 1.63 | 1.82 |
| | 436456 | AW292677 | Hs.248122 | G protein-coupled receptor 24 | 1.82 | 2.80 | 2.18 |
| | 418918 | X07871 | Hs.89476 | CD2 antigen (p50), sheep red blood cell | 1.82 | 2.28 | 2.00 |
| | 424755 | AB033094 | Hs.152925 | KIAA1268 protein | 1.82 | 1.85 | 1.62 |
| | 436315 | BE390513 | Hs.27935 | hypothetical protein MGC4837 | 1.82 | 1.74 | 5.18 |
| | 420783 | AI659838 | Hs.99923 | lectin, galactoside-binding, soluble, 7 | 1.81 | 1.87 | 0.80 |
| 10 | 417105 | X60992 | Hs.81226 | CD6 antigen | 1.81 | 1.88 | 2.03 |
| | 423961 | D13666 | Hs.136348 | periostin (OSF-2os) | 1.81 | 1.73 | 2.45 |
| | 446019 | AI362520 | | histone deacetylase 3 | 1.81 | 1.39 | 2.24 |
| | 412580 | AA113262 | Hs.17901 | Homo sapiens, clone IMAGE:3937015, mRNA, | 1.81 | 3.05 | 1.58 |
| | 409415 | AA579258 | Hs.6083 | Homo sapiens cDNA: FLJ21028 fs, clone C | 1.80 | 2.00 | 1.78 |
| 15 | 453684 | AK001922 | Hs.34578 | alpha2,3-sialyltransferase | 1.80 | 1.98 | 1.22 |
| | 446921 | AB012113 | Hs.16530 | small inducible cytokine subfamily A (Cy | 1.80 | 1.56 | 1.71 |
| | 453779 | N35187 | Hs.43388 | 28kD interferon responsive protein | 1.80 | 2.42 | 2.04 |
| | 434706 | AI656291 | Hs.116394 | ESTs | 1.80 | 1.58 | 1.80 |
| | 416065 | BE267931 | Hs.78996 | proliferating cell nuclear antigen | 1.80 | 1.79 | 2.51 |
| 20 | 453331 | AI240665 | | ESTs | 1.79 | 1.43 | 2.33 |
| | 429412 | NM_006235 | Hs.2407 | POU domain, class 2, associating factor | 1.79 | 1.46 | 4.46 |
| | 428784 | Y12851 | Hs.193470 | purinergic receptor P2X, ligand-gated io | 1.79 | 2.30 | 1.79 |
| | 453507 | AF083217 | Hs.33085 | WD repeat domain 3 | 1.79 | 1.49 | 1.51 |
| | 452826 | BE245286 | Hs.301636 | peroxisomal biogenesis factor 6 | 1.79 | 1.57 | 2.00 |
| 25 | 439237 | AW408158 | Hs.318893 | ESTs, Weakly similar to A47582 B-cell gr | 1.79 | 2.26 | 2.22 |
| | 406672 | M26041 | Hs.198253 | major histocompatibility complex, class | 1.79 | 1.76 | 1.78 |
| | 431009 | BE149762 | Hs.48956 | gap junction protein, beta 6 (connexin 3 | 1.79 | 1.43 | 3.32 |
| | 452698 | NM_001295 | Hs.301921 | chemokine (C-C motif) receptor 1 | 1.78 | 1.66 | 1.29 |
| | 424954 | NM_000546 | Hs.1846 | tumor protein p53 (Li-Fraumeni syndrome) | 1.78 | 1.73 | 2.35 |
| 30 | 436378 | AJ227874 | Hs.99244 | ESTs | 1.78 | 1.84 | 1.78 |
| | 421778 | AA428000 | Hs.283072 | actin related protein 2/3 complex, subun | 1.78 | 1.66 | 3.67 |
| | 421948 | L42583 | Hs.334309 | keratin 6A | 1.78 | 1.74 | 3.00 |
| | 414915 | NM_002462 | Hs.76391 | myxovirus (influenza) resistance 1, homo | 1.77 | 2.27 | 2.13 |
| | 437317 | AA748613 | Hs.311977 | ESTs, Highly similar to SWI/SNF related, | 1.77 | 1.98 | 2.32 |
| 35 | 427318 | AF186081 | Hs.175783 | zinc transporter | 1.77 | 1.61 | 0.92 |
| | 418403 | D66978 | Hs.84790 | KIAA0225 protein | 1.76 | 1.49 | 2.24 |
| | 421433 | AI829192 | Hs.22380 | ESTs | 1.76 | 1.49 | 2.52 |
| | 450728 | AW162923 | Hs.25363 | presenilin 2 (Alzheimer disease 4) | 1.76 | 1.74 | 1.76 |
| 40 | 428655 | H05769 | Hs.188757 | Homo sapiens, clone MGC:5564, mRNA, comp | 1.76 | 1.43 | 1.76 |
| | 427536 | BE277141 | Hs.115803 | gb:601178666F1 NIH_MGC_20 Homo sapiens c | 1.76 | 2.12 | 1.76 |
| | 433364 | AI075407 | Hs.296083 | ESTs, Moderately similar to IS4374 gene | 1.76 | 1.86 | 1.48 |
| | 401994 | | | Target Exon | 1.75 | 1.44 | 1.75 |
| | 418299 | AA279530 | Hs.83968 | integrin, beta 2 (antigen CD18 (p95), ty | 1.75 | 1.69 | 1.79 |
| 45 | 408633 | AW963372 | Hs.46677 | PRO2000 protein | 1.75 | 1.46 | 1.88 |
| | 429978 | AA249027 | | ribosomal protein S6 | 1.75 | 1.60 | 1.92 |
| | 450690 | AA296696 | Hs.333418 | FXYD domain-containing ion transport reg | 1.75 | 2.13 | 2.03 |
| | 456967 | AW004056 | Hs.168357 | T-box 2 | 1.74 | 1.95 | 1.42 |
| | 417866 | AW067903 | Hs.82772 | collagen, type XI, alpha 1 | 1.74 | 2.64 | 2.01 |
| 50 | 428746 | AW503820 | Hs.192861 | Spi-B transcription factor (Spi-1/PU.1 r | 1.74 | 2.82 | 2.31 |
| | 432642 | BE297635 | Hs.3069 | heat shock 70kD protein 9B (mortalin-2) | 1.74 | 1.51 | 1.62 |
| | 429505 | AW820035 | Hs.278679 | a disintegrin and metalloproteinase doma | 1.73 | 1.54 | 3.15 |
| | 412851 | AI826502 | Hs.97269 | ESTs | 1.73 | 1.67 | 1.05 |
| | 453953 | AW408337 | Hs.36972 | CD7 antigen (p41) | 1.73 | 2.22 | 2.28 |
| 55 | 430413 | AW842182 | Hs.241392 | small inducible cytokine AS (RANTES) | 1.73 | 2.05 | 1.47 |
| | 419485 | AA489023 | Hs.99807 | ESTs, Weakly similar to unnamed protein | 1.73 | 1.71 | 1.73 |
| | 447217 | BE465754 | Hs.17778 | neuropilin 2 | 1.73 | 1.62 | 4.70 |
| | 437673 | AW665665 | Hs.153034 | ESTs | 1.72 | 1.55 | 2.10 |
| | 437879 | BE262082 | Hs.5894 | hypothetical protein FLJ10305 | 1.72 | 2.50 | 1.80 |
| 60 | 448410 | AK000227 | Hs.21126 | hypothetical protein FLJ20220 | 1.72 | 1.48 | 3.98 |
| | 413313 | NM_002047 | Hs.283108 | glycyl-tRNA synthetase | 1.72 | 2.19 | 1.82 |
| | 452203 | X57522 | | transporter 1, ATP-binding cassette, sub | 1.72 | 2.68 | 1.68 |
| | 443950 | NM_001425 | Hs.9999 | epithelial membrane protein 3 | 1.71 | 2.17 | 2.24 |
| | 403969 | | | ENSP00000034663: Zinc finger protein 131 | 1.71 | 1.31 | 1.71 |
| 65 | 450832 | AW970602 | Hs.105421 | ESTs | 1.71 | 1.33 | 2.38 |
| | 453005 | AW055308 | Hs.31803 | ESTs, Weakly similar to N-WASP [H.sapien | 1.71 | 1.67 | 1.95 |
| | 439783 | AI125760 | Hs.24835 | hypothetical protein FLJ14594 | 1.71 | 2.10 | 2.20 |
| | 418678 | NM_001327 | Hs.167379 | cancer/testis antigen (NY-ESO-1) | 1.71 | 3.86 | 1.76 |
| | 432259 | BE269103 | Hs.274201 | 60S acidic ribosomal protein PO | 1.71 | 1.85 | 1.94 |
| | 420340 | NM_000734 | Hs.97087 | CD32 antigen, zeta polypeptide (TIT3 com | 1.71 | 2.12 | 1.98 |
| 70 | 428289 | M26301 | Hs.2253 | complement component 2 | 1.71 | 2.46 | 0.76 |
| | 424006 | AF054815 | Hs.137548 | CD84 antigen (leukocyte antigen) | 1.70 | 1.70 | 2.78 |
| | 440039 | Z46188 | Hs.6874 | KIAA0472 protein | 1.70 | 2.24 | 1.60 |
| | 406646 | M33600 | Hs.308026 | major histocompatibility complex, class | 1.70 | 2.27 | 1.33 |
| 75 | 425367 | BE271188 | Hs.155975 | protein tyrosine phosphatase, receptor I | 1.70 | 2.77 | 2.07 |
| | 420286 | AI796395 | Hs.111377 | ESTs | 1.70 | 1.50 | 3.21 |
| | 430255 | AK000703 | Hs.323822 | Homo sapiens mRNA for KIAA1551 protein, | 1.69 | 1.44 | 1.69 |
| | 445247 | AW274290 | Hs.153997 | ESTs | 1.69 | 2.57 | 1.65 |
| | 436965 | Z11894 | Hs.156110 | gb:H.sapiens rearranged mRNA for immunog | 1.69 | 1.52 | 3.13 |
| | 410257 | BE244044 | Hs.61469 | hypothetical protein | 1.69 | 1.99 | 1.97 |
| 80 | 424663 | NM_002351 | Hs.151544 | SH2 domain protein 1A, Duncan's disease | 1.69 | 1.76 | 1.69 |
| | 427792 | M63928 | Hs.180841 | tumor necrosis factor receptor superfam | 1.69 | 1.98 | 2.48 |
| | 458098 | BE550224 | | metallothionein 1E (functional) | 1.68 | 1.83 | 1.68 |
| | 425397 | J04088 | Hs.156346 | topoisomerase (DNA) II alpha (170kD) | 1.68 | 1.57 | 4.09 |
| | 421485 | AA243499 | Hs.104800 | hypothetical protein FLJ10134 | 1.68 | 1.64 | 0.68 |

| | | | | | | | |
|----|--------|-----------|-----------|--|------|------|------|
| 5 | 421563 | NM_006433 | Hs.105806 | granulysin | 1.68 | 2.24 | 1.55 |
| | 448775 | AB025237 | Hs.388 | nudix (nucleoside diphosphate linked moi | 1.68 | 1.98 | 2.05 |
| | 451418 | BE387790 | Hs.26369 | hypothetical protein FLJ20287 | 1.68 | 1.35 | 1.68 |
| | 440457 | BE387593 | Hs.21321 | Homo sapiens clone FLB9213 PRO2474 mRNA, | 1.68 | 1.88 | 1.63 |
| | 438866 | U44385 | Hs.325495 | tissue inhibitor of metalloproteinase 2 | 1.67 | 2.54 | 1.90 |
| 10 | 401760 | | | Target Exon | 1.67 | 1.93 | 1.61 |
| | 422158 | L10343 | Hs.112341 | protease inhibitor 3, skin-derived (SKAL | 1.67 | 1.85 | 4.25 |
| | 446644 | NM_003272 | Hs.15791 | transmembrane 7 superfamily member 1 (up | 1.67 | 1.94 | 1.48 |
| | 415701 | NM_003878 | Hs.78619 | gamma-glutamyl hydrolase (conjugase, fol | 1.67 | 1.65 | 0.90 |
| | 450293 | N36754 | Hs.171118 | hypothetical protein FLJ00026 | 1.67 | 1.54 | 1.95 |
| 15 | 412856 | BE386745 | Hs.74631 | basigin (OK blood group) | 1.67 | 2.71 | 1.47 |
| | 439318 | AW837046 | Hs.6527 | G protein-coupled receptor 56 | 1.66 | 1.82 | 1.19 |
| | 424399 | AJ905687 | | AJ905687:IL-BT095-190199-019 BT095 Homo | 1.66 | 3.65 | 0.44 |
| | 432355 | AA534416 | Hs.162185 | ESTs, Weakly similar to S42799 gap prec | 1.66 | 1.98 | 1.45 |
| | 427239 | BE270447 | | ubiquitin carrier protein | 1.66 | 2.94 | 1.92 |
| 20 | 425262 | D87119 | Hs.155418 | GS3955 protein | 1.66 | 2.36 | 1.66 |
| | 413869 | NM_000878 | Hs.75596 | interleukin 2 receptor, beta | 1.66 | 1.86 | 1.90 |
| | 406698 | X03068 | Hs.73931 | major histocompatibility complex, class | 1.65 | 2.05 | 1.31 |
| | 446217 | AI651594 | Hs.99709 | ESTs | 1.65 | 1.98 | 1.77 |
| | 400222 | | | NM_002082: Homo sapiens G protein-couple | 1.65 | 1.74 | 1.81 |
| 25 | 432468 | AW402155 | Hs.3003 | CD3E antigen, epsilon polypeptide (TIT3 | 1.65 | 2.50 | 1.77 |
| | 417237 | H86385 | Hs.81737 | palmitoyl-protein thioesterase 2 | 1.65 | 2.89 | 1.57 |
| | 433012 | NM_004045 | Hs.279910 | ATX1 (antioxidant protein 1, yeast) homo | 1.64 | 2.76 | 1.26 |
| | 446291 | BE397753 | Hs.14623 | interferon, gamma-inducible protein 30 | 1.64 | 1.96 | 1.24 |
| | 433867 | AK000596 | Hs.3618 | hippocampin-like 1 | 1.64 | 1.47 | 1.00 |
| 30 | 433671 | AW138797 | Hs.132906 | 19A24 protein | 1.64 | 2.17 | 1.96 |
| | 418371 | M13560 | Hs.84298 | CD74 antigen (invariant polypeptide of m | 1.64 | 2.18 | 1.43 |
| | 432336 | NM_002759 | Hs.274382 | protein kinase, interferon-inducible dou | 1.64 | 1.47 | 1.64 |
| | 409264 | NM_014937 | Hs.52463 | KIAA0966 protein | 1.64 | 1.46 | 4.89 |
| | 431836 | AF178532 | Hs.271411 | beta-site APP-cleaving enzyme 2 | 1.64 | 2.58 | 1.79 |
| 35 | 414586 | AA306160 | Hs.16488 | lymphocyte cytosolic protein 1 (L-plasti | 1.63 | 1.72 | 1.88 |
| | 418117 | AJ922013 | Hs.83496 | linker for activation of T cells | 1.63 | 1.98 | 1.99 |
| | 448304 | BE622768 | Hs.290356 | mesoderm development candidate 1 | 1.63 | 1.67 | 1.86 |
| | 425535 | AB007937 | Hs.158287 | KIAA0468 gene product | 1.63 | 2.56 | 1.97 |
| | 453258 | AW293134 | Hs.32597 | ring finger protein (C3H2C3 type) 6 | 1.63 | 1.46 | 2.43 |
| 40 | 420000 | AB036063 | Hs.94262 | p53-inducible ribonucleotide reductase s | 1.63 | 1.34 | 1.94 |
| | 447321 | AW271217 | Hs.281434 | Homo sapiens cDNA FLJ14028 fs, clone HE | 1.63 | 1.96 | 1.77 |
| | 422192 | AA305159 | Hs.113019 | fts485 | 1.62 | 1.45 | 1.62 |
| | 450701 | H39960 | Hs.288467 | hypothetical protein XP_098151 (leucine- | 1.62 | 2.23 | 1.53 |
| | 419381 | AB023420 | Hs.90093 | heat shock 70kD protein 4 | 1.62 | 1.57 | 2.38 |
| 45 | 424779 | AL046851 | Hs.153053 | CD37 antigen | 1.62 | 1.92 | 2.10 |
| | 413283 | R78669 | Hs.23756 | hypothetical protein similar to swine ac | 1.62 | 1.41 | 1.12 |
| | 414907 | X90725 | Hs.77597 | polo (Drosophila)-like kinase | 1.62 | 2.03 | 2.13 |
| | 414159 | AW511414 | Hs.257352 | apolipoprotein L 6 | 1.62 | 1.89 | 1.32 |
| | 410055 | AJ250839 | Hs.58241 | gene for serine/threonine protein kinase | 1.62 | 1.81 | 1.27 |
| 50 | 428179 | AI127772 | Hs.279696 | serum/glucocorticoid regulated kinase-II | 1.62 | 1.50 | 2.13 |
| | 436251 | BE515065 | Hs.296585 | nucleolar protein (KKE/D repeat) | 1.61 | 1.71 | 2.02 |
| | 451708 | AI306536 | Hs.60975 | ESTs | 1.61 | 2.31 | 1.70 |
| | 418113 | AI272141 | Hs.83484 | SRY (sex determining region Y)-box 4 | 1.61 | 1.53 | 2.50 |
| | 410600 | AW575742 | | ESTs, Moderately similar to S65657 alpha | 1.61 | 1.83 | 1.69 |
| 55 | 436873 | N23874 | Hs.50477 | RAB27A, member RAS oncogene family | 1.61 | 1.56 | 1.61 |
| | 440201 | AL359588 | Hs.7041 | hypothetical protein DKFZp762B226 | 1.61 | 1.58 | 1.85 |
| | 414368 | W70171 | Hs.75939 | uridine monophosphate kinase | 1.61 | 1.59 | 2.75 |
| | 454429 | BE273437 | Hs.301406 | hypothetical protein PP3501 | 1.61 | 3.54 | 1.52 |
| | 422257 | NM_001716 | Hs.113916 | Burkitt lymphoma receptor 1, GTP-binding | 1.61 | 2.15 | 1.54 |
| 60 | 426437 | BE076537 | Hs.165895 | ubiquitin-conjugating enzyme E2L 6 | 1.60 | 2.01 | 1.36 |
| | 408826 | AF216077 | Hs.48376 | Homo sapiens clone HB-2 mRNA sequence | 1.60 | 2.00 | 1.60 |
| | 414761 | AU077228 | Hs.77256 | enhancer of zeste (Drosophila) homolog 2 | 1.60 | 1.38 | 2.23 |
| | 429612 | AF062649 | Hs.252587 | pituitary tumor-transforming 1 | 1.60 | 1.78 | 2.59 |
| | 411263 | BE297802 | Hs.69360 | kinesin-like 6 (mitotic centromere-assoc | 1.60 | 1.78 | 2.07 |
| 65 | 417324 | AW265494 | | ESTs | 1.60 | 2.48 | 1.91 |
| | 430325 | AF004562 | Hs.239356 | syntaxin binding protein 1 | 1.60 | 1.74 | 2.53 |
| | 431797 | BE169641 | Hs.270134 | hypothetical protein FLJ20280 | 1.60 | 1.46 | 2.46 |
| | 434449 | AW953484 | Hs.3849 | hypothetical protein FLJ22041 similar to | 1.60 | 1.81 | 3.00 |
| | 443378 | AW392550 | Hs.9280 | proteasome (prosome, macropain) subunit, | 1.59 | 1.88 | 1.68 |
| 70 | 417437 | U52682 | Hs.82132 | interferon regulatory factor 4 | 1.59 | 1.90 | 2.26 |
| | 437949 | U78519 | Hs.41654 | ESTs, Weakly similar to A46010 X-linked | 1.59 | 2.14 | 1.59 |
| | 401797 | | | Target Exon | 1.59 | 1.82 | 1.78 |
| | 449720 | AA311152 | Hs.288708 | hypothetical protein FLJ21562 | 1.59 | 1.45 | 4.69 |
| | 424971 | AA479005 | Hs.154036 | tumor suppressing subtransferable candid | 1.59 | 1.82 | 1.68 |
| 75 | 415474 | NM_014252 | Hs.78457 | solute carrier family 25 (mitochondrial | 1.58 | 1.51 | 0.30 |
| | 430017 | AA263172 | Hs.35 | protein tyrosine phosphatase, non-recept | 1.58 | 1.72 | 2.46 |
| | 422515 | AW500470 | Hs.117950 | multifunctional polypeptide similar to S | 1.58 | 1.85 | 1.94 |
| | 434094 | AA305599 | Hs.238205 | hypothetical protein PRO2013 | 1.58 | 1.25 | 2.09 |
| | 428844 | AW972635 | Hs.301904 | hypothetical protein FLJ12671 | 1.58 | 1.72 | 1.80 |
| 80 | 440942 | AW246547 | Hs.17901 | Homo sapiens, clone IMAGE:3937015, mRNA, | 1.58 | 2.60 | 1.58 |
| | 419596 | BE379320 | Hs.91448 | MKP-1 like protein tyrosine phosphatase | 1.58 | 1.84 | 1.22 |
| | 401151 | | | Target Exon | 1.58 | 2.43 | 1.60 |
| | 441590 | AI623207 | Hs.190537 | ESTs | 1.58 | 1.40 | 1.58 |
| | 418677 | S83308 | Hs.87224 | SRY (sex determining region Y)-box 5 | 1.58 | 1.68 | 1.58 |
| | 416448 | L13210 | Hs.79339 | lectin, galactoside-binding, soluble, 3 | 1.58 | 2.28 | 1.60 |
| | 418739 | AA310964 | Hs.88012 | SHP2 interacting transmembrane adaptor | 1.58 | 2.14 | 2.10 |
| | 418216 | AA662240 | Hs.283099 | AF15q14 protein | 1.57 | 1.46 | 1.57 |

| | | | | | | | |
|----|--------|-----------|-----------|--|------|------|------|
| | 427700 | AA262294 | Hs.180383 | dual specificity phosphatase 6 | 1.57 | 1.42 | 0.88 |
| | 436485 | X59135 | Hs.156110 | immunoglobulin kappa constant | 1.57 | 1.49 | 2.69 |
| | 404872 | | | ENSP00000243173*:DJ1109J22.1 (novel home | 1.57 | 1.46 | 1.36 |
| 5 | 408212 | AA297567 | Hs.43728 | hypothetical protein | 1.57 | 1.55 | 2.73 |
| | 414699 | AJ815523 | Hs.76930 | synuclein, alpha (non A4 component of am | 1.57 | 1.36 | 1.57 |
| | 444006 | BE395085 | Hs.10086 | type I transmembrane protein Fn14 | 1.57 | 1.70 | 1.13 |
| | 432946 | U60899 | Hs.279854 | mannosidase, alpha, class 2B, member 1 | 1.57 | 1.75 | 1.57 |
| | 417929 | R27219 | Hs.74647 | Human T-cell receptor active alpha-chain | 1.57 | 2.26 | 2.10 |
| 10 | 431629 | AU077025 | Hs.265827 | interferon, alpha-inducible protein (clo | 1.57 | 2.09 | 1.57 |
| | 402876 | | | NM_022161*:Homo sapiens livin inhibitor- | 1.56 | 2.28 | 1.45 |
| | 439627 | BE621702 | Hs.29076 | hypothetical protein FLJ21841 | 1.56 | 2.97 | 1.54 |
| | 414839 | X63692 | Hs.77462 | DNA (cytosine-5)-methyltransferase 1 | 1.56 | 1.75 | 1.88 |
| | 450663 | H43540 | Hs.25292 | ribonuclease H1, large subunit | 1.56 | 2.76 | 1.67 |
| 15 | 425818 | AB021225 | Hs.159581 | matrix metalloproteinase 17 (membrane-in | 1.56 | 2.36 | 1.83 |
| | 422765 | AW409701 | Hs.1578 | baculoviral IAP repeat-containing 5 (sur | 1.56 | 1.78 | 2.06 |
| | 456508 | AA502764 | Hs.123469 | ESTs, Weakly similar to AF208855 1 BM-01 | 1.56 | 1.32 | 2.70 |
| | 453613 | F06838 | | ESTs | 1.56 | 1.76 | 1.84 |
| | 428379 | X06026 | Hs.2259 | CD3G antigen, gamma polypeptide (TIT3 co | 1.56 | 1.43 | 1.56 |
| 20 | 429500 | X78565 | Hs.289114 | hexabrachion (tenascin C, cytactin) | 1.56 | 1.47 | 3.15 |
| | 444652 | BE513613 | Hs.11538 | actin related protein 2/3 complex, subun | 1.56 | 2.01 | 1.56 |
| | 420842 | AJ083668 | Hs.50601 | hypothetical protein MGC10986 | 1.55 | 2.24 | 1.90 |
| | 447513 | AW955776 | Hs.313500 | ESTs, Moderately similar to ALU7_HUMAN A | 1.55 | 1.24 | 3.07 |
| | 408901 | AK001330 | Hs.48855 | hypothetical protein FLJ10468 | 1.55 | 1.79 | 2.17 |
| 25 | 437669 | AJ358105 | Hs.123164 | ESTs, Weakly similar to match to ESTs AA | 1.55 | 1.83 | 1.96 |
| | 439437 | AJ207788 | Hs.343628 | sialyltransferase 4B (beta-galactosidase | 1.55 | 1.63 | 2.20 |
| | 418835 | AL023694 | Hs.88977 | hypothetical protein dJ511E16.2 | 1.55 | 1.73 | 1.50 |
| | 448633 | AA311426 | Hs.21635 | tubulin, gamma 1 | 1.54 | 2.02 | 1.67 |
| | 447763 | BE199111 | Hs.115803 | hypothetical protein | 1.54 | 2.52 | 1.52 |
| 30 | 430223 | NM_002514 | Hs.235935 | nephroblastoma overexpressed gene | 1.54 | 1.54 | 3.03 |
| | 448258 | BE386983 | Hs.343214 | hypothetical protein FLJ20396 | 1.54 | 1.97 | 1.53 |
| | 440165 | AW014718 | Hs.7753 | calumenin | 1.54 | 1.53 | 2.55 |
| | 433376 | AJ249361 | Hs.74122 | caspase 4, apoptosis-related cysteine pr | 1.54 | 1.34 | 1.69 |
| | 445982 | BE410233 | Hs.13501 | pescadillo (zebrafish) homolog 1, contai | 1.54 | 2.21 | 1.54 |
| 35 | 419741 | NM_007019 | Hs.93002 | ubiquitin carrier protein E2-C | 1.54 | 2.50 | 1.94 |
| | 416926 | H03109 | Hs.263395 | HT018 protein | 1.54 | 1.41 | 2.01 |
| | 431630 | NM_002204 | Hs.265829 | integrin, alpha 3 (antigen CD49C, alpha | 1.54 | 1.89 | 1.23 |
| | 442159 | AW163390 | Hs.278554 | heterochromatin-like protein 1 | 1.54 | 1.93 | 1.79 |
| | 420421 | AF281133 | Hs.343589 | exosome component Rrp41 | 1.53 | 2.47 | 1.61 |
| 40 | 406973 | M34996 | Hs.198253 | major histocompatibility complex, class | 1.53 | 1.62 | 1.19 |
| | 422530 | AW972300 | Hs.118110 | bone marrow stromal cell antigen 2 | 1.53 | 1.74 | 1.37 |
| | 423420 | AJ571364 | Hs.128382 | Homo sapiens mRNA; cDNA DKFZp76111224 (f | 1.53 | 2.49 | 1.59 |
| | 429359 | W00482 | Hs.2399 | matrix metalloproteinase 14 (membrane-in | 1.53 | 2.72 | 1.54 |
| | 429837 | NM_003896 | Hs.225939 | sialyltransferase 9 (CMP-NeuAc: lactosyl | 1.53 | 1.64 | 2.40 |
| 45 | 412939 | AW411491 | Hs.75069 | eukaryotic translation elongation factor | 1.52 | 1.98 | 0.98 |
| | 410678 | BE540516 | Hs.293732 | hypothetical protein MGC3195 | 1.52 | 1.39 | 2.17 |
| | 431186 | NM_012249 | Hs.250597 | ras-like protein | 1.52 | 1.91 | 1.82 |
| | 406868 | AA505445 | Hs.300697 | immunoglobulin heavy constant gamma 3 (G | 1.52 | 1.57 | 1.82 |
| | 422532 | AL008726 | Hs.118126 | protective protein for beta-galactosidas | 1.51 | 2.08 | 1.19 |
| 50 | 413063 | AL035737 | Hs.75184 | chitinase 3-like 1 (cartilage glycoprote | 1.51 | 1.50 | 0.67 |
| | 417308 | H60720 | Hs.81892 | KIAA0101 gene product | 1.51 | 1.42 | 7.41 |
| | 424902 | NM_003866 | Hs.153687 | inositol polyphosphate-4-phosphatase, ty | 1.51 | 2.75 | 1.51 |
| | 405204 | | | NM_002086*:Homo sapiens growth factor re | 1.51 | 1.44 | 1.53 |
| 55 | 424481 | R19453 | Hs.1787 | proteolipid protein 1 (Pelizaeus-Merzbac | 1.51 | 1.92 | 2.32 |
| | 422516 | BE258862 | Hs.117950 | multifunctional polypeptide similar to S | 1.50 | 1.61 | 1.47 |
| | 418827 | BE327311 | Hs.47166 | HT021 | 1.50 | 1.35 | 3.53 |
| | 427550 | BE242818 | Hs.311609 | nuclear RNA helicase, DECD variant of DE | 1.50 | 1.55 | 2.09 |
| | 432992 | BE270472 | Hs.279900 | HSPC015 protein | 1.50 | 1.82 | 0.82 |
| 60 | 442432 | BE093589 | Hs.38178 | hypothetical protein FLJ23468 | 1.50 | 1.34 | 4.87 |
| | 413566 | AW604451 | Hs.285814 | sprouty (Drosophila) homolog 4 | 1.50 | 3.05 | 1.51 |
| | 422616 | BE300330 | Hs.118725 | selenophosphate synthetase 2 | 1.50 | 1.36 | 0.46 |
| | 431222 | X56777 | Hs.273790 | zona pellucida glycoprotein 3A (sperm re | 1.50 | 2.05 | 1.78 |
| | 421861 | S78798 | Hs.108966 | phosphatidylinositol-4-phosphate 5-kinas | 1.49 | 1.52 | 2.62 |
| | 422684 | BE561617 | Hs.119192 | H2A histone family, member Z | 1.49 | 1.53 | 2.02 |
| 65 | 452363 | AJ582743 | Hs.94953 | Homo sapiens, Similar to complement comp | 1.49 | 2.02 | 1.41 |
| | 411825 | AK000334 | | hypothetical protein FLJ20327 | 1.49 | 2.55 | 1.38 |
| | 409425 | U40462 | Hs.54452 | zinc finger protein, subfamily 1A, 1 (lk | 1.49 | 1.77 | 1.49 |
| | 431070 | AW408164 | Hs.249184 | transcription factor 19 (SC1) | 1.49 | 1.79 | 1.75 |
| 70 | 427080 | AW068287 | Hs.301175 | ras-related C3 botulinum toxin substrate | 1.49 | 1.57 | 2.14 |
| | 440676 | NM_004987 | Hs.112378 | LM and senescent cell antigen-like doma | 1.49 | 1.42 | 1.46 |
| | 411296 | BE207307 | Hs.10114 | growth suppressor 1 | 1.49 | 1.74 | 1.50 |
| | 442894 | W02112 | Hs.8836 | parvin, beta | 1.49 | 2.25 | 1.51 |
| | 416361 | AW204907 | Hs.6872 | ESTs, Weakly similar to CA13_HUMAN COLLA | 1.49 | 2.06 | 1.89 |
| | 424162 | AA336229 | Hs.93135 | ESTs, Weakly similar to ALU2_HUMAN ALU S | 1.49 | 1.59 | 1.65 |
| 75 | 447131 | NM_004585 | Hs.17466 | retinoic acid receptor responder (tazaro | 1.49 | 2.00 | 1.22 |
| | 427759 | BE245578 | Hs.2200 | perforin 1 (pore forming protein) | 1.49 | 2.12 | 1.41 |
| | 422846 | BE513934 | Hs.1583 | neutrophil cytosolic factor 1 (47kD, chr | 1.49 | 1.61 | 1.67 |
| | 417007 | AF224741 | Hs.80768 | chloride channel 7 | 1.48 | 1.94 | 1.71 |
| | 421924 | BE514514 | Hs.109606 | coronin, actin-binding protein, 1A | 1.48 | 1.68 | 1.67 |
| 80 | 422241 | Y00062 | Hs.170121 | protein tyrosine phosphatase, receptor t | 1.48 | 1.43 | 2.25 |
| | 410741 | Z11695 | Hs.324473 | mitogen-activated protein kinase 1 | 1.48 | 1.37 | 3.17 |
| | 447471 | AF039843 | Hs.18676 | sprouty (Drosophila) homolog 2 | 1.48 | 1.35 | 1.46 |
| | 427247 | AW504221 | Hs.174103 | integrin, alpha L (antigen CD11A (p180), | 1.47 | 1.58 | 1.48 |
| | 442945 | AJ024849 | Hs.131853 | ESTs | 1.47 | 1.73 | 1.38 |

| | | | | | | |
|--------|-----------|-----------|--|------|------|------|
| 447200 | BE543146 | Hs.281434 | Homo sapiens cDNA FLJ14028 fis, clone HE | 1.47 | 1.89 | 1.60 |
| 424085 | NM_002914 | Hs.139226 | replication factor C (activator 1) 2 (40 | 1.47 | 2.03 | 1.47 |
| 422867 | L32137 | Hs.1584 | cartilage oligomeric matrix protein (pse | 1.47 | 1.86 | 1.93 |
| 416350 | AF188625 | Hs.189507 | phospholipase A2, group IID | 1.47 | 2.92 | 1.49 |
| 458207 | T28472 | Hs.7655 | U2 small nuclear ribonucleoprotein auxil | 1.47 | 1.61 | 1.73 |
| 447940 | D86982 | Hs.20060 | KIAA0229 protein | 1.47 | 1.93 | 1.72 |
| 446106 | AA377165 | Hs.44633 | ESTs | 1.47 | 1.56 | 1.63 |
| 425811 | AL039104 | Hs.159557 | karyopherin alpha 2 (RAG cohort 1, impor | 1.47 | 1.78 | 1.84 |
| 432615 | AA557191 | Hs.55028 | ESTs, Weakly similar to I54374 gene NF2 | 1.47 | 2.04 | 1.47 |
| 435099 | AC004770 | Hs.4756 | flap structure-specific endonuclease 1 | 1.47 | 1.76 | 1.83 |
| 402294 | | | Target Exon | 1.47 | 1.27 | 1.46 |
| 430147 | R60704 | Hs.234434 | hairly/enhancer-of-split related with YRP | 1.46 | 2.00 | 1.59 |
| 414324 | Y14768 | Hs.890 | lymphotoxin beta (TNF superfamily, membe | 1.46 | 1.58 | 2.15 |
| 400270 | | | NM_000026: Homo sapiens adenylosuccinate | 1.46 | 1.42 | 2.32 |
| 414806 | D14694 | Hs.77329 | phosphatidylserine synthase 1 | 1.46 | 2.07 | 1.40 |
| 419625 | U91616 | Hs.182885 | nuclear factor of kappa light polypeptid | 1.45 | 1.78 | 1.53 |
| 430594 | AK000790 | Hs.246885 | hypothetical protein FLJ20783 | 1.45 | 1.31 | 0.90 |
| 419556 | U29615 | Hs.91093 | chitinase 1 (chitotriosidase) | 1.45 | 2.13 | 1.46 |
| 453350 | AJ917771 | Hs.61790 | hypothetical protein FLJ23338 | 1.45 | 2.00 | 1.39 |
| 448412 | AJ219083 | Hs.42532 | ESTs, Moderately similar to ALU8_HUMAN A | 1.45 | 1.37 | 3.17 |
| 411619 | AJ418609 | Hs.71040 | hypothetical protein FLJ20425 | 1.45 | 1.39 | 3.01 |
| 424218 | AF031824 | Hs.143212 | cystatin F (leukocystatin) | 1.45 | 1.82 | 1.44 |
| 450395 | BE048545 | Hs.161757 | ESTs | 1.45 | 2.40 | 1.33 |
| 438555 | AJ222089 | Hs.143878 | Homo sapiens mRNA for FLJ00024 protein, | 1.45 | 1.91 | 1.65 |
| 422497 | D29642 | Hs.1528 | KIAA0053 gene product | 1.45 | 1.94 | 1.49 |
| 400991 | | | Target Exon | 1.45 | 2.10 | 1.42 |
| 431779 | AW971178 | Hs.268571 | apolipoprotein C-I | 1.45 | 1.53 | 0.42 |
| 424618 | L29472 | Hs.1802 | major histocompatibility complex, class | 1.44 | 1.96 | 1.86 |
| 423032 | AJ684746 | Hs.119274 | RAS p21 protein activator (GTPase activa | 1.44 | 1.34 | 3.36 |
| 424232 | AB015982 | Hs.143460 | protein kinase C, nu | 1.44 | 1.28 | 2.94 |
| 436291 | BE514605 | Hs.289092 | Homo sapiens cDNA: FLJ22380 fis, clone H | 1.44 | 1.63 | 1.45 |
| 445745 | AB007924 | Hs.13245 | KIAA0455 gene product | 1.44 | 1.17 | 1.52 |
| 449209 | BE616830 | Hs.294145 | ESTs | 1.44 | 1.35 | 2.48 |
| 410129 | BE244074 | Hs.58831 | regulator of Fas-induced apoptosis | 1.44 | 2.10 | 1.79 |
| 401284 | | | Target Exon | 1.44 | 1.71 | 1.44 |
| 422675 | BE018517 | Hs.119140 | eukaryotic translation initiation factor | 1.44 | 1.68 | 1.45 |
| 433020 | AJ375726 | Hs.279918 | hypothetical protein | 1.44 | 1.37 | 2.02 |
| 420042 | AW015140 | Hs.161723 | ESTs | 1.44 | 2.02 | 1.29 |
| 453878 | AW964440 | Hs.19025 | DC32 | 1.44 | 1.69 | 1.44 |
| 427268 | X78520 | Hs.174139 | chloride channel 3 | 1.44 | 1.45 | 1.96 |
| 417386 | AL037228 | Hs.82043 | D123 gene product | 1.43 | 1.32 | 2.81 |
| 409197 | N54706 | Hs.303025 | chromosome 11 open reading frame 24 | 1.43 | 1.80 | 1.17 |
| 411009 | W37572 | Hs.285864 | ESTs | 1.43 | 1.57 | 1.72 |
| 433160 | AW207002 | Hs.134342 | TASP for testis-specific adriamycin sens | 1.43 | 1.36 | 1.49 |
| 416084 | L16991 | Hs.79006 | deoxythymidylate kinase (thymidylate kin | 1.43 | 2.15 | 1.57 |
| 407826 | AA128423 | Hs.40300 | calpain 3, (p94) | 1.43 | 1.61 | 1.69 |
| 439070 | AJ733278 | Hs.7621 | ESTs | 1.43 | 2.10 | 1.40 |
| 444090 | S69115 | Hs.10306 | natural killer cell group 7 sequence | 1.43 | 2.09 | 1.24 |
| 420162 | BE378432 | Hs.95577 | cyclin-dependent kinase 4 | 1.43 | 2.13 | 1.54 |
| 442591 | AW292797 | | hypothetical protein MGC10772 | 1.43 | 2.11 | 1.61 |
| 451668 | Z43948 | Hs.326444 | cartilage acidic protein 1 | 1.43 | 1.49 | 1.16 |
| 423639 | AB037826 | Hs.130411 | KIAA1405 protein | 1.42 | 2.08 | 1.51 |
| 426234 | BE314534 | Hs.168159 | apoptosis regulator | 1.42 | 1.57 | 1.31 |
| 424263 | M77640 | Hs.1757 | L1 cell adhesion molecule (hydrocephalus | 1.42 | 1.88 | 1.63 |
| 430294 | AJ538226 | Hs.32976 | guanine nucleotide binding protein 4 | 1.42 | 1.46 | 3.18 |
| 447126 | AW150632 | Hs.170307 | Raf guanine nucleotide exchange factor R | 1.42 | 1.36 | 1.38 |
| 432241 | AJ937060 | Hs.6298 | KIAA1151 protein | 1.42 | 1.58 | 1.98 |
| 412471 | M63193 | Hs.73946 | endothelial cell growth factor 1 (platelet | 1.41 | 2.09 | 1.29 |
| 434262 | AF121858 | Hs.12169 | sorting nexin 8 | 1.41 | 3.07 | 1.41 |
| 432238 | AL133057 | Hs.274135 | Homo sapiens mRNA; cDNA DKFZp434K1815 (f | 1.41 | 1.82 | 1.43 |
| 402474 | | | NM_004079: Homo sapiens cathepsin S (CTSS | 1.41 | 1.32 | 1.24 |
| 419897 | X90826 | Hs.93649 | upstream transcription factor 2, c-fos i | 1.41 | 1.69 | 1.80 |
| 417621 | AV654694 | Hs.82316 | interferon-induced, hepatitis C-associat | 1.41 | 1.22 | 1.74 |
| 424441 | X14850 | Hs.147097 | H2A histone family, member X | 1.41 | 1.74 | 2.15 |
| 406663 | U24683 | | immunoglobulin heavy constant mu | 1.41 | 1.51 | 2.03 |
| 409614 | BE297412 | Hs.55189 | hypothetical protein | 1.41 | 1.54 | 2.20 |
| 443885 | H91806 | Hs.15284 | ESTs | 1.41 | 1.19 | 1.41 |
| 412276 | BE262621 | Hs.73798 | macrophage migration inhibitory factor (| 1.40 | 1.88 | 1.24 |
| 425179 | AJ224442 | Hs.155020 | putative methyltransferase | 1.40 | 1.84 | 1.47 |
| 418699 | BE539639 | Hs.173030 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 1.40 | 1.27 | 2.79 |
| 432403 | AA550815 | Hs.124840 | ESTs | 1.40 | 1.83 | 1.44 |
| 417389 | BE260964 | Hs.82045 | midkine (neurite growth-promoting factor | 1.40 | 1.65 | 2.51 |
| 422596 | AF063611 | Hs.118633 | Z'-S'-oligoadenylate synthetase-like | 1.40 | 2.57 | 1.44 |
| 435292 | N20514 | Hs.172965 | ESTs | 1.40 | 1.91 | 1.43 |
| 419424 | BE041820 | Hs.38516 | Homo sapiens, clone MGC:15887, mRNA, com | 1.39 | 1.57 | 1.37 |
| 425068 | AL048716 | Hs.154387 | KIAA0103 gene product | 1.39 | 1.27 | 3.18 |
| 426020 | AL110195 | Hs.166017 | microphthalmia-associated transcription | 1.39 | 2.26 | 1.40 |
| 427740 | BE242604 | Hs.180616 | CD35 antigen (collagen type I receptor, | 1.39 | 1.76 | 0.99 |
| 403022 | | | C21000178: gi 7341207 gb AA651215.1 JAF22 | 1.39 | 1.74 | 1.36 |
| 416111 | AA033813 | Hs.79018 | chromatin assembly factor 1, subunit A (| 1.39 | 1.72 | 1.39 |
| 410103 | AW903666 | | gb:CM4-NN1032-280300-122-b02 NN1032 Homo | 1.39 | 1.46 | 1.34 |
| 439180 | AJ393742 | Hs.199067 | v-erb-b2 avian erythroblastic leukemia v | 1.39 | 1.35 | 1.79 |
| 414057 | AI815559 | Hs.75730 | signal recognition particle receptor (d | 1.39 | 1.49 | 1.17 |

| | | | | | | | |
|----|--------|-----------|-----------|---|------|------|------|
| 5 | 416511 | NM_006762 | Hs.79356 | Lysosomal-associated multispanning membr | 1.39 | 1.52 | 1.44 |
| | 423984 | AF163825 | Hs.136713 | pre-B lymphocyte gene 3 | 1.39 | 3.02 | 1.52 |
| | 448484 | BE613340 | Hs.334725 | Homo sapiens, Similar to RIKEN cDNA 9430 | 1.38 | 1.81 | 1.39 |
| | 436856 | AI469355 | Hs.127310 | ESTs | 1.38 | 1.35 | 0.99 |
| | 437179 | AA393508 | | serologically defined colon cancer antig | 1.38 | 1.26 | 4.14 |
| | 437912 | BE278594 | Hs.5912 | F-box only protein 7 | 1.38 | 2.03 | 1.40 |
| | 448664 | AI879317 | Hs.334691 | splicing factor 3a, subunit 1, 120kD | 1.38 | 1.52 | 1.38 |
| 10 | 439981 | AI348408 | Hs.124675 | ESTs, Weakly similar to T14742 hypotheri | 1.38 | 1.48 | 1.38 |
| | 432812 | AI935412 | Hs.50162 | ESTs | 1.38 | 1.43 | 2.18 |
| | 406826 | AW516005 | Hs.84298 | CD74 antigen (invariant polypeptide of m | 1.38 | 1.87 | 1.28 |
| | 446962 | AI351421 | Hs.279709 | muscle specific ring finger protein 1 | 1.38 | 1.46 | 2.23 |
| | 408787 | NM_014784 | Hs.47822 | Rho guanine exchange factor (GEF) 11 | 1.38 | 1.98 | 1.50 |
| | 428044 | AA093322 | Hs.301404 | RNA binding motif protein 3 | 1.38 | 1.29 | 2.04 |
| 15 | 412926 | AI879076 | Hs.75061 | macrophage myristoylated alanine-rich C | 1.38 | 1.52 | 2.62 |
| | 418255 | AW135405 | Hs.37251 | ESTs | 1.38 | 1.44 | 1.75 |
| | 419745 | AF042001 | Hs.93005 | slug (chicken homolog), zinc finger prot | 1.37 | 1.51 | 1.37 |
| | 448977 | X91809 | Hs.22698 | regulator of G-protein signalling 19 | 1.37 | 1.98 | 1.45 |
| | 422609 | Z46023 | Hs.118721 | sialidase 1 (lysosomal sialidase) | 1.37 | 1.75 | 1.31 |
| 20 | 435458 | F11872 | Hs.4892 | Homo sapiens clone 24841 mRNA sequence | 1.37 | 1.38 | 2.80 |
| | 429849 | X74794 | Hs.154443 | minichromosome maintenance deficient (S. | 1.37 | 1.61 | 1.62 |
| | 429849 | U33053 | Hs.2499 | protein kinase C-like 1 | 1.37 | 1.71 | 1.45 |
| | 407103 | AA424881 | Hs.256301 | hypothetical protein MGC13170 | 1.37 | 1.62 | 1.82 |
| | 452923 | BE276018 | Hs.288940 | five-span transmembrane protein M83 | 1.37 | 1.86 | 1.37 |
| 25 | 453941 | U39817 | Hs.36820 | Bloom syndrome | 1.37 | 1.59 | 1.37 |
| | 446755 | AW451473 | Hs.16134 | serine/threonine kinase 10 | 1.37 | 1.82 | 1.48 |
| | 439755 | AW748482 | Hs.77873 | B7 homolog 3 | 1.36 | 2.10 | 1.35 |
| | 447630 | AI660149 | Hs.44865 | lymphoid enhancer-binding factor 1 | 1.36 | 1.79 | 1.67 |
| | 413821 | AA844126 | Hs.55954 | ESTs, Weakly similar to C4HU complement | 1.36 | 1.91 | 1.39 |
| 30 | 445823 | AI478563 | Hs.145519 | FKSG87 protein | 1.36 | 1.29 | 0.33 |
| | 456760 | AW961251 | Hs.127828 | guanine nucleotide binding protein (G pr | 1.36 | 1.33 | 2.01 |
| | 402542 | | | Target Exon | 1.36 | 1.66 | 1.46 |
| | 451050 | AW937420 | | ESTs | 1.36 | 2.00 | 1.36 |
| | 444501 | AW247624 | Hs.11342 | ninjurin 1 | 1.36 | 1.59 | 1.14 |
| 35 | 413291 | NM_006278 | Hs.75268 | sialyltransferase 4C (beta-galactosidase | 1.36 | 2.55 | 1.42 |
| | 438129 | AA778847 | | gb:af187d03.s1 Soares_testis_NHT Homo sap | 1.36 | 1.46 | 1.32 |
| | 428398 | AI243368 | Hs.98558 | ESTs | 1.36 | 1.25 | 4.95 |
| | 439704 | AW020018 | Hs.293267 | ESTs | 1.36 | 1.84 | 1.48 |
| | 428782 | X12830 | Hs.193400 | Interleukin 6 receptor | 1.36 | 1.27 | 0.58 |
| 40 | 437316 | AI683454 | Hs.46801 | GCN5 (general control of amino-acid synt | 1.35 | 2.10 | 1.29 |
| | 439246 | AI498072 | | membrane-associated tyrosine- and threon | 1.35 | 1.81 | 1.63 |
| | 403409 | | | NM_005929:Homo sapiens antigen p97 (meta | 1.35 | 1.64 | 1.35 |
| | 446342 | BE298665 | Hs.14846 | Homo sapiens mRNA; cDNA DKFZp564D016 (tr | 1.35 | 1.37 | 2.33 |
| | 437740 | AA810265 | Hs.122915 | ESTs | 1.35 | 1.91 | 1.35 |
| 45 | 423973 | AF038461 | Hs.136574 | arachidonate 12-lipoxygenase, 12R type | 1.35 | 1.53 | 1.10 |
| | 421506 | BE302796 | Hs.105097 | thymidine kinase 1, soluble | 1.35 | 1.89 | 1.57 |
| | 457760 | AA668123 | Hs.134170 | ESTs | 1.35 | 2.03 | 1.43 |
| | 439769 | AA448828 | Hs.30596 | Homo sapiens mRNA full length insert cDN | 1.35 | 2.06 | 1.41 |
| | 406824 | AW515961 | Hs.84298 | CD74 antigen (invariant polypeptide of m | 1.35 | 1.77 | 1.27 |
| 50 | 429852 | AB010445 | Hs.225948 | small inducible cytokine subfamily A (Cy | 1.35 | 1.52 | 0.51 |
| | 421777 | BE562088 | Hs.108196 | HSPC037 protein | 1.34 | 1.65 | 1.61 |
| | 400328 | X87344 | | transporter 2, ATP-binding cassette, sub | 1.34 | 1.77 | 1.02 |
| | 421445 | AA913059 | Hs.104433 | Homo sapiens, clone IMAGE:4054868, mRNA | 1.34 | 1.77 | 1.15 |
| | 428977 | AK001404 | Hs.194698 | cyclin B2 | 1.34 | 1.53 | 1.82 |
| 55 | 418283 | S79895 | Hs.83942 | cathepsin K (pseudodysostosis) | 1.34 | 1.33 | 3.45 |
| | 425848 | BE242709 | Hs.159637 | valyl-HRNA synthetase 2 | 1.34 | 2.11 | 1.32 |
| | 431211 | M86849 | Hs.323733 | gap junction protein, beta 2, 26kD (conn | 1.34 | 1.27 | 1.97 |
| | 422758 | AF152329 | Hs.284180 | protocadherin gamma subfamily C, 3 | 1.34 | 1.61 | 1.75 |
| | 421579 | NM_002975 | Hs.105927 | stem cell growth factor; lymphocyte secr | 1.34 | 1.75 | 1.81 |
| 60 | 416374 | NM_001154 | Hs.300711 | annexin A5 | 1.34 | 1.68 | 1.55 |
| | 451092 | AI207256 | Hs.13766 | Homo sapiens mRNA for FLJ00074 protein, | 1.34 | 1.87 | 0.81 |
| | 424778 | AA251048 | Hs.153042 | lymphocyte antigen 9 | 1.34 | 1.94 | 1.42 |
| | 421703 | AI936513 | Hs.1416 | Fc fragment of IgE, low affinity II, rec | 1.33 | 2.19 | 1.48 |
| | 416700 | AW498958 | Hs.343475 | cathepsin D (lysosomal aspartyl protease | 1.33 | 1.96 | 1.18 |
| 65 | 425923 | NM_005026 | Hs.162808 | phosphoinositide-3-kinase, catalytic, de | 1.33 | 1.70 | 1.60 |
| | 418803 | U50079 | Hs.88556 | histone deacetylase 1 | 1.33 | 1.28 | 2.65 |
| | 427730 | AW250549 | Hs.180577 | granulin | 1.33 | 2.09 | 1.35 |
| | 441174 | BE312775 | Hs.294005 | Homo sapiens, clone IMAGE:3050476, mRNA, | 1.33 | 2.05 | 1.33 |
| | 412738 | N34731 | Hs.74562 | siah binding protein 1; FBP interacting | 1.33 | 1.85 | 1.35 |
| 70 | 424528 | AW073971 | Hs.238954 | ESTs, Weakly similar to KIAA1204 protein | 1.33 | 1.31 | 2.06 |
| | 422599 | BE387202 | Hs.118638 | non-metastatic cells 1, protein (NM23A) | 1.33 | 1.77 | 1.43 |
| | 422997 | BE018212 | Hs.122908 | DNA replication factor | 1.33 | 1.91 | 1.39 |
| | 415323 | BE269352 | Hs.949 | neutrophil cytosolic factor 2 (65kD, chr | 1.33 | 1.16 | 0.60 |
| | 409119 | AA531133 | Hs.4253 | hypothetical protein MGC2574 | 1.32 | 2.07 | 1.29 |
| 75 | 419652 | AL157485 | Hs.91973 | hypothetical protein | 1.32 | 2.00 | 1.33 |
| | 415697 | AI365603 | Hs.198271 | DKFZP568i1024 protein | 1.32 | 2.07 | 1.39 |
| | 434359 | AF129536 | Hs.284226 | F-box only protein 6 | 1.32 | 1.25 | 1.91 |
| | 442932 | AA457211 | Hs.8858 | bromodomain adjacent to zinc finger doma | 1.32 | 1.63 | 1.44 |
| | 444029 | AW160993 | Hs.326292 | hypothetical gene DKFZp434A1114 | 1.32 | 1.47 | 0.85 |
| 80 | 456974 | M12529 | Hs.169401 | apoptoprotein E | 1.32 | 2.51 | 1.23 |
| | 447733 | AF157482 | Hs.19400 | MAD2 (mitotic arrest deficient, yeast, h | 1.31 | 3.12 | 1.31 |
| | 448610 | NM_006157 | Hs.21602 | nel (chicken)-like 1 | 1.31 | 1.21 | 1.65 |
| | 426490 | NM_001621 | Hs.170087 | aryl hydrocarbon receptor | 1.31 | 1.68 | 1.47 |
| | 427584 | BE410293 | Hs.179718 | v-myb avian myeloblastosis viral oncogen | | | |

| | | | | | | | |
|----|--------|-----------|-----------|---|------|------|------|
| 5 | 417059 | AL037672 | Hs.81071 | extracellular matrix protein 1 | 1.31 | 1.30 | 2.14 |
| | 407777 | AA161071 | Hs.71465 | squalene epoxidase | 1.31 | 1.45 | 1.43 |
| | 408536 | AW381532 | Hs.135188 | ESTs | 1.31 | 1.38 | 0.90 |
| | 410423 | AW402432 | Hs.63489 | protein tyrosine phosphatase, non-recept | 1.31 | 1.81 | 1.49 |
| | 422486 | BE514492 | Hs.117487 | gene near HD on 4p16.3 with homology to | 1.31 | 1.63 | 1.31 |
| | 409154 | U72882 | Hs.50842 | interferon-induced protein 35 | 1.31 | 1.69 | 1.29 |
| | 425003 | AF119046 | Hs.154149 | apurinic/apyrimidinic endonuclease(APEX | 1.31 | 1.74 | 1.39 |
| | 441406 | Z45957 | Hs.7837 | phosphoprotein regulated by mitogenic pa | 1.31 | 1.43 | 0.94 |
| 10 | 421975 | AW961017 | Hs.6459 | hypothetical protein FLJ11856 | 1.30 | 2.53 | 1.34 |
| | 417361 | NM_000275 | Hs.82027 | oculocutaneous albinism II (pink-eye dil | 1.30 | 1.38 | 1.38 |
| | 425676 | AW410656 | Hs.159161 | Rho GDP dissociation inhibitor (GDI) alp | 1.30 | 2.11 | 1.36 |
| | 427289 | AI097346 | | phosphoserine aminotransferase | 1.30 | 2.27 | 1.48 |
| | 427747 | AW411425 | Hs.180655 | serine/threonine kinase 12 | 1.30 | 1.68 | 1.79 |
| 15 | 422296 | AA360231 | Hs.114416 | Homo sapiens, Similar to transducin (bet | 1.30 | 1.50 | 1.30 |
| | 436481 | AA379597 | Hs.5199 | HSPC150 protein similar to ubiquitin-con | 1.30 | 1.42 | 2.13 |
| | 423062 | NM_003655 | Hs.5637 | ESTs | 1.30 | 1.58 | 1.30 |
| | 439740 | AL365512 | Hs.6657 | hypothetical protein bK1048E9.5 | 1.30 | 1.77 | 1.35 |
| | 409340 | BE174629 | Hs.321130 | hypothetical protein MGC2771 | 1.30 | 1.57 | 1.51 |
| 20 | 416920 | AA176455 | Hs.80475 | polymerase (RNA) II (DNA directed) polyp | 1.30 | 1.67 | 1.44 |
| | 430451 | AA836472 | Hs.297939 | cathepsin B | 1.30 | 1.49 | 1.16 |
| | 457400 | AF032906 | Hs.252549 | cathepsin Z | 1.30 | 1.40 | 1.21 |
| | 403506 | | | C3001912:gi5677647[ref]NP_033602.1] zin | 1.29 | 1.88 | 1.26 |
| | 424867 | AI024860 | Hs.153591 | Not56 (D. melanogaster)-like protein | 1.29 | 2.64 | 1.31 |
| 25 | 408815 | AW957974 | Hs.25485 | hypothetical protein FLJ22341 | 1.29 | 1.79 | 1.36 |
| | 416322 | BE019494 | Hs.79217 | pyroline-5-carboxylate reductase 1 | 1.29 | 1.59 | 1.80 |
| | 440795 | AA262133 | Hs.99741 | ESTs, Weakly similar to PNL1_HUMAN PEANU | 1.29 | 2.01 | 1.43 |
| | 421846 | AA017707 | Hs.1432 | protein kinase C substrate 80K-H | 1.29 | 1.70 | 1.34 |
| | 425966 | NM_001761 | Hs.1973 | cyclin F | 1.29 | 1.63 | 1.50 |
| 30 | 446766 | AF083208 | Hs.16178 | apoptosis antagonizing transcription fac | 1.29 | 1.71 | 1.40 |
| | 406827 | AA971409 | | gb:op92cd4.s1 NCI_CGAP_Lu5 Homo sapiens | 1.29 | 2.04 | 1.35 |
| | 418613 | AA744529 | Hs.86575 | mitogen-activated protein kinase kinase | 1.29 | 1.41 | 1.94 |
| | 443086 | AW977125 | | sine oculis homeobox (Drosophila) homolo | 1.29 | 1.24 | 1.29 |
| | 439146 | AW138909 | Hs.156110 | immunoglobulin kappa constant | 1.29 | 1.99 | 1.36 |
| | 434398 | AA121098 | Hs.3838 | serum-inducible kinase (SNK) | 1.29 | 1.18 | 1.32 |
| 35 | 418322 | AA284166 | Hs.84113 | cyclin-dependent kinase inhibitor 3 (CDK | 1.29 | 1.31 | 2.19 |
| | 400261 | | | Eos Control | 1.29 | 1.59 | 1.36 |
| | 413781 | J05272 | Hs.850 | IMP (inosine monophosphate) dehydrogenas | 1.29 | 1.67 | 1.53 |
| | 412315 | AW936678 | | gb:PM2-DT0023-080300-004-a04 DT0023 Homo | 1.28 | 1.26 | 1.07 |
| 40 | 420372 | AW960049 | Hs.293660 | Homo sapiens, clone IMAGE:3535476, mRNA, | 1.28 | 1.85 | 1.40 |
| | 425449 | X52056 | Hs.157441 | spleen focus forming virus (SFFV) provir | 1.28 | 1.45 | 1.14 |
| | 454478 | AW805749 | | superoxide dismutase 2, mitochondrial | 1.28 | 2.29 | 1.07 |
| | 410275 | U85658 | Hs.61796 | transcription factor AP-2 gamma (activat | 1.28 | 1.20 | 0.93 |
| | 406016 | | | Target Exon | 1.28 | 1.47 | 1.31 |
| 45 | 449609 | BE246434 | Hs.289026 | guanine nucleotide binding protein (G pr | 1.28 | 1.26 | 3.02 |
| | 426059 | BE292842 | Hs.166120 | interferon regulatory factor 7 | 1.28 | 1.76 | 1.23 |
| | 412773 | H15785 | Hs.74573 | similar to vaccinia virus HindIII K4L OR | 1.28 | 1.60 | 1.30 |
| | 452700 | AI859390 | Hs.288940 | five-span transmembrane protein M83 | 1.28 | 1.51 | 1.22 |
| | 408543 | N78098 | Hs.44289 | ESTs | 1.28 | 2.02 | 1.08 |
| 50 | 408822 | AW500715 | Hs.57079 | Homo sapiens cDNA FLJ13267 fis, clone OV | 1.27 | 1.28 | 3.51 |
| | 425069 | AA687465 | Hs.298184 | potassium voltage-gated channel, shaker- | 1.27 | 1.66 | 1.39 |
| | 444681 | AJ243937 | Hs.288316 | chromosome 6 open reading frame 9 | 1.27 | 1.47 | 1.55 |
| | 430794 | NM_000166 | Hs.333303 | gap junction protein, beta 2, 26kD (conn | 1.27 | 1.81 | 0.89 |
| | 430637 | BE160081 | Hs.256290 | S100 calcium-binding protein A11 (calgiz | 1.27 | 1.35 | 1.68 |
| 55 | 440502 | AI824113 | Hs.78281 | regulator of G-protein signalling 12 | 1.27 | 1.67 | 1.31 |
| | 441598 | AI733219 | Hs.58262 | ESTs | 1.27 | 1.30 | 1.30 |
| | 431921 | N46466 | Hs.58879 | ESTs | 1.27 | 2.00 | 1.16 |
| | 459345 | AW503672 | | gb:U1-HF-BN0-ald-h-11-0-U1.r1 NIH_MGC_50 | 1.26 | 1.44 | 1.33 |
| | 452436 | BE077546 | Hs.31447 | ESTs, Moderately similar to A46010 X-fin | 1.26 | 1.20 | 1.45 |
| 60 | 426334 | BE305081 | Hs.169358 | hypothetical protein | 1.26 | 1.22 | 1.89 |
| | 414044 | BE614194 | Hs.75721 | profilin 1 | 1.26 | 1.48 | 1.51 |
| | 405268 | | | ENSP00000223174::KIAA0783 PROTEIN. | 1.26 | 1.19 | 2.25 |
| | 416602 | NM_006159 | Hs.79389 | Protein kinase C-binding protein NELL2 | 1.26 | 1.19 | 4.03 |
| | 439529 | BE293492 | Hs.293984 | hypothetical protein MGC13102 | 1.26 | 1.83 | 1.19 |
| 65 | 421254 | AK001724 | Hs.102950 | coat protein gamma-cop | 1.26 | 1.61 | 1.23 |
| | 417785 | X59812 | Hs.82568 | cytochrome P450, subfamily XXVIA (stero | 1.26 | 1.84 | 0.68 |
| | 419395 | BE268326 | Hs.90280 | 5-aminoimidazole-4-carboxamide ribonucle | 1.26 | 1.66 | 1.34 |
| | 418968 | NM_000078 | Hs.89538 | cholesteryl ester transfer protein, plas | 1.26 | 1.42 | 1.19 |
| | 441553 | AA281219 | Hs.121296 | ESTs | 1.26 | 1.29 | 1.28 |
| 70 | 446619 | AU076643 | Hs.313 | secreted phosphoprotein 1 (osteopontin, | 1.25 | 1.22 | 0.65 |
| | 424624 | AB032947 | Hs.151301 | Ca2+-dependent activator protein for secr | 1.25 | 1.17 | 2.95 |
| | 450087 | BE293180 | Hs.24379 | MUM2 protein | 1.25 | 1.78 | 1.28 |
| | 429604 | AK001851 | Hs.210778 | hypothetical protein FLJ10989 | 1.25 | 1.18 | 1.25 |
| | 429380 | AF023268 | Hs.200600 | secretory carrier membrane protein 3 | 1.25 | 2.22 | 1.25 |
| 75 | 440251 | AW796016 | Hs.332012 | Homo sapiens, clone IMAGE:3687782, mRNA, | 1.25 | 1.90 | 1.39 |
| | 416759 | AK000978 | Hs.79741 | hypothetical protein FLJ10116 | 1.24 | 1.32 | 1.53 |
| | 435466 | BE619165 | Hs.29203 | G protein beta subunit-like | 1.24 | 1.96 | 1.32 |
| | 450621 | AW297288 | Hs.55918 | hypothetical protein FLJ11354 | 1.24 | 1.61 | 1.27 |
| | 400214 | | | NM_007002:Homo sapiens cell membrane gly | 1.24 | 1.88 | 1.32 |
| 80 | 435013 | H91923 | Hs.110024 | NM_020142:Homo sapiens NADH:ubiquinone o | 1.24 | 1.76 | 1.25 |
| | 414733 | BE514535 | Hs.77171 | minichromosome maintenance deficient (S. | 1.24 | 1.82 | 1.42 |
| | 406851 | AA609784 | | major histocompatibility complex, class | 1.24 | 1.68 | 1.19 |
| | 448498 | AA418276 | | ESTs | 1.24 | 1.73 | 1.29 |
| | 440087 | W28969 | Hs.7718 | hypothetical protein FLJ22678 | 1.24 | 1.70 | 1.38 |

| | | | | | | | |
|----|--------|-----------|-----------|--|------|------|------|
| 5 | 411365 | M76477 | Hs.289082 | GM2 ganglioside activator protein | 1.24 | 1.61 | 1.16 |
| | 426502 | Y07759 | Hs.170157 | myosin VA (heavy polypeptide 12, myosin) | 1.24 | 2.65 | 1.24 |
| | 452056 | AW955065 | Hs.101150 | Homo sapiens, clone IMAGE:4054156, mRNA | 1.24 | 1.49 | 1.50 |
| | 427390 | AA32163 | Hs.268231 | Homo sapiens cDNA: FLJ23111 fs, clone L | 1.24 | 1.17 | 2.10 |
| | 429954 | AI918130 | Hs.21374 | ESTs | 1.23 | 1.19 | 4.77 |
| | 421178 | BE267994 | Hs.102419 | zinc finger protein | 1.23 | 1.62 | 1.28 |
| | 442609 | AL020996 | Hs.8518 | selenoprotein N | 1.23 | 2.30 | 1.24 |
| 10 | 416188 | BE157260 | Hs.79070 | v-myc avian myelocytomatosis viral oncog | 1.23 | 1.18 | 0.90 |
| | 410127 | AA354313 | Hs.58685 | CD5 antigen (p56-62) | 1.23 | 1.68 | 1.23 |
| | 452244 | N33530 | Hs.176674 | ESTs | 1.23 | 2.93 | 1.23 |
| | 406718 | AA505525 | Hs.169476 | glyceraldehyde-3-phosphate dehydrogenase | 1.23 | 1.56 | 1.29 |
| | 436939 | AA853680 | Hs.5345 | arginyl aminopeptidase (aminopeptidase B | 1.23 | 1.68 | 1.23 |
| | 414457 | AW514320 | Hs.76159 | ATPase, H transporting, lysosomal (vacuo | 1.23 | 1.58 | 1.20 |
| 15 | 416929 | N20535 | | melastatin 1 | 1.23 | 1.92 | 1.20 |
| | 401106 | | | Target Exon | 1.23 | 1.82 | 1.29 |
| | 408981 | AW500797 | Hs.49427 | Gem-interacting protein | 1.23 | 1.40 | 1.59 |
| | 413317 | U53225 | Hs.75283 | sorting nexin 1 | 1.23 | 1.43 | 1.44 |
| 20 | 422481 | AL050163 | Hs.117339 | DNAX-activation protein 10 | 1.23 | 1.71 | 1.24 |
| | 425455 | AL137522 | Hs.157777 | casein kinase 1, gamma 1 | 1.23 | 1.95 | 1.29 |
| | 451524 | AK001466 | Hs.26516 | hypothetical protein FLJ10604 | 1.23 | 2.07 | 1.27 |
| | 414399 | L47345 | Hs.155202 | transcription elongation factor B (SII) | 1.22 | 1.87 | 1.19 |
| | 422034 | AC006486 | Hs.333069 | Ets2 repressor factor | 1.22 | 1.55 | 1.21 |
| 25 | 434224 | AA380731 | Hs.84 | interleukin 2 receptor, gamma (severe co | 1.22 | 1.55 | 1.51 |
| | 429574 | BE268321 | Hs.208912 | hypothetical protein MGC861 | 1.22 | 1.49 | 1.46 |
| | 411742 | AW247593 | Hs.71819 | eukaryotic translation initiation factor | 1.22 | 1.64 | 1.40 |
| | 449027 | AJ271216 | Hs.22880 | dipeptidylpeptidase III | 1.22 | 1.63 | 1.30 |
| | 418004 | U37519 | Hs.87539 | aldehyde dehydrogenase 3 family, member | 1.22 | 1.24 | 0.71 |
| 30 | 451481 | AA300228 | Hs.295866 | hypothetical protein DKFZp434N1923 | 1.22 | 2.20 | 1.26 |
| | 422739 | H20106 | Hs.119591 | adaptor-related protein complex 2, sigma | 1.21 | 1.55 | 1.21 |
| | 424326 | NM_014479 | Hs.145296 | ADAM-like disintegrin protease, decysin | 1.21 | 1.13 | 3.29 |
| | 404186 | | | NM_019602:Homo sapiens butyrophilin-like | 1.21 | 1.59 | 1.21 |
| | 447604 | AW089933 | Hs.301342 | hypothetical protein MGC4342 | 1.21 | 1.25 | 2.00 |
| 35 | 427979 | BE379776 | Hs.181309 | proteasome (prosome, macropain) subunit, | 1.21 | 1.14 | 1.25 |
| | 414509 | AW161311 | Hs.76294 | CD63 antigen (melanoma 1 antigen) | 1.21 | 1.39 | 1.25 |
| | 428468 | AA171388 | Hs.184482 | DKFZP586D0624 protein | 1.21 | 1.66 | 1.22 |
| | 419700 | AF084935 | Hs.92357 | galactokinase 1 | 1.21 | 1.63 | 0.74 |
| | 430948 | AI347578 | Hs.124015 | hypothetical protein MGC2605 | 1.21 | 1.48 | 1.21 |
| 40 | 448143 | AF039704 | Hs.20478 | ceroid-lipofuscinosis, neuronal 2, late | 1.20 | 1.75 | 1.23 |
| | 448499 | BE613280 | Hs.77550 | hypothetical protein MGC1780 | 1.20 | 1.54 | 1.29 |
| | 442173 | N76101 | Hs.8127 | KIAA0144 gene product | 1.20 | 1.54 | 1.31 |
| | 409632 | W74001 | Hs.55279 | serine (or cysteine) proteinase inhibito | 1.20 | 1.18 | 1.11 |
| | 448230 | BE395949 | Hs.94814 | hypothetical protein MGC2865 | 1.20 | 1.83 | 1.19 |
| 45 | 403817 | | | NM_015271:Homo sapiens tripartite motif, | 1.20 | 1.22 | 1.61 |
| | 411678 | AI907114 | Hs.71465 | squalene epoxidase | 1.20 | 1.15 | 2.01 |
| | 452423 | AA991724 | Hs.180535 | hypothetical protein MGC10966 | 1.20 | 1.79 | 1.20 |
| | 424045 | AF027866 | Hs.138202 | serine (or cysteine) proteinase inhibito | 1.20 | 2.34 | 1.20 |
| | 447233 | AW246333 | Hs.17901 | Homo sapiens, clone IMAGE:3937015, mRNA, | 1.20 | 1.93 | 1.20 |
| 50 | 422565 | BE259035 | Hs.118400 | Singed (Drosophila)-like (sea urchin fas | 1.20 | 1.32 | 1.52 |
| | 446159 | NM_013379 | Hs.14089 | dipeptidyl peptidase 7 | 1.19 | 1.64 | 1.22 |
| | 434563 | AW083994 | Hs.9469 | pleckstrin homology domain-containing, 1 | 1.19 | 1.53 | 1.45 |
| | 421541 | NM_003942 | Hs.105584 | ribosomal protein S6 kinase, 90kD, polyp | 1.19 | 1.75 | 1.27 |
| | 450706 | AW167578 | Hs.14691 | ESTs, Moderately similar to I38022 hypot | 1.19 | 1.71 | 1.22 |
| 55 | 430381 | NM_006411 | Hs.240534 | 1-acylglycerol-3-phosphate O-acyltransfe | 1.19 | 1.66 | 1.21 |
| | 426329 | AL389951 | Hs.271623 | nucleoporin 50kD | 1.19 | 1.17 | 1.55 |
| | 421612 | AF161254 | Hs.106196 | BD6 antigen | 1.19 | 1.73 | 1.30 |
| | 410182 | NM_001983 | Hs.59544 | excision repair cross-complementing rode | 1.19 | 1.75 | 1.18 |
| | 434171 | BE247688 | Hs.347349 | KIAA0948 protein | 1.18 | 1.73 | 1.09 |
| 60 | 424837 | BE276113 | Hs.333034 | N-acetyltransferase, homolog of S. cerev | 1.18 | 2.13 | 1.22 |
| | 428293 | BE250944 | Hs.183556 | solute carrier family 1 (neutral amino a | 1.18 | 1.45 | 1.30 |
| | 453754 | AW972580 | Hs.172753 | ESTs | 1.18 | 1.71 | 1.35 |
| | 439012 | BE383814 | Hs.6455 | RuvB (E coli homolog)-like 2 | 1.18 | 1.60 | 1.23 |
| | 422256 | M64673 | Hs.1499 | heat shock transcription factor 1 | 1.18 | 1.51 | 1.28 |
| 65 | 439863 | BE547830 | Hs.9408 | paired immunoglobulin-like receptor beta | 1.18 | 1.89 | 1.18 |
| | 430513 | AJ012008 | Hs.241586 | G6C protein | 1.18 | 2.07 | 0.81 |
| | 427283 | AL119796 | Hs.174185 | ectonucleotide pyrophosphatase/phosphodi | 1.18 | 1.13 | 3.25 |
| | 441648 | H05734 | Hs.30559 | ESTs | 1.18 | 1.56 | 1.23 |
| | 418219 | AA731836 | Hs.137319 | ESTs | 1.18 | 1.77 | 1.23 |
| 70 | 406422 | | | Target Exon | 1.18 | 1.43 | 1.31 |
| | 414823 | AA156531 | Hs.103902 | ESTs, Weakly similar to A44851 keratin, | 1.18 | 1.66 | 1.23 |
| | 425720 | AA362394 | Hs.293984 | hypothetical protein MGC13102 | 1.18 | 1.58 | 1.15 |
| | 419250 | AW770185 | | U5 snRNP-specific protein, 116 kD | 1.17 | 1.74 | 1.21 |
| | 454390 | AB020713 | Hs.56966 | KIAA0906 protein | 1.17 | 1.33 | 1.35 |
| 75 | 428471 | X57348 | Hs.184510 | stratfin | 1.17 | 1.19 | 1.24 |
| | 430200 | BE613337 | Hs.234896 | geminin | 1.17 | 1.13 | 1.96 |
| | 412965 | L06419 | Hs.75093 | procollagen-lysine, 2-oxoglutarate 5-dio | 1.17 | 1.50 | 1.22 |
| | 430122 | NM_013342 | Hs.233765 | TCF3 (E2A) fusion partner (in childhood | 1.17 | 1.69 | 1.32 |
| | 430512 | AF182294 | Hs.241578 | U6 snRNA-associated Sm-like protein LSmb | 1.17 | 1.12 | 2.44 |
| 80 | 417080 | BE392846 | Hs.1063 | small nuclear ribonucleoprotein polypept | 1.17 | 1.93 | 1.18 |
| | 423102 | AW067812 | Hs.303025 | chromosome 11 open reading frame 24 | 1.17 | 1.89 | 1.17 |
| | 408393 | AW015318 | Hs.23165 | ESTs | 1.16 | 1.10 | 1.91 |
| | 424292 | AA338432 | | gb:EST43554 Fetal brain I Homo sapiens c | 1.16 | 1.61 | 1.21 |
| | 446759 | R61463 | Hs.16165 | expressed in activated T/LAK lymphocytes | 1.16 | 1.45 | 1.23 |
| | 427324 | AA159587 | Hs.285932 | hypothetical protein FLJ23322 | 1.16 | 1.50 | 1.23 |

| | | | | | | |
|--------|-----------|-----------|--|------|------|------|
| 446055 | AI815981 | Hs.12909 | muco1ipin 1 | 1.16 | 1.49 | 1.10 |
| 414432 | BE378174 | Hs.26506 | Homo sapiens clone CDABP0005 mRNA sequen | 1.16 | 1.67 | 1.20 |
| 417900 | BE250127 | Hs.82906 | CDC20 (cell division cycle 20, S. cerevi | 1.16 | 1.66 | 1.32 |
| 411305 | BE241596 | Hs.69547 | myelin basic protein | 1.16 | 1.15 | 4.29 |
| 438930 | AW843633 | Hs.343261 | hypothetical protein AL110115 | 1.16 | 1.37 | 1.34 |
| 407239 | AA076350 | Hs.67846 | leukocyte immunoglobulin-like receptor, | 1.15 | 1.82 | 1.17 |
| 427458 | BE208364 | Hs.29283 | ESTs, Weakly similar to LKHU proteoglyca | 1.15 | 1.46 | 1.32 |
| 402160 | | | Target Exon | 1.14 | 1.23 | 1.12 |
| 416881 | N32520 | Hs.141358 | ESTs | 1.14 | 2.42 | 1.14 |
| 420223 | N27807 | | ribosomal protein L4 | 1.14 | 1.23 | 1.14 |
| 450778 | U81375 | Hs.25450 | solute carrier family 29 (nucleoside tra | 1.14 | 1.38 | 1.27 |
| 429538 | BE182592 | Hs.139322 | small proline-rich protein 2A | 1.14 | 1.16 | 3.52 |
| 428342 | AI739168 | | Homo sapiens cDNA FLJ13458 fs, clone PL | 1.13 | 1.13 | 1.13 |
| 436696 | AA725678 | Hs.120487 | ESTs | 1.13 | 1.22 | 1.13 |
| 448950 | AF288687 | Hs.9275 | CGI-152 protein | 1.12 | 1.52 | 1.19 |
| 437696 | Z83844 | Hs.5790 | hypothetical protein dJ37E16.5 | 1.12 | 1.31 | 1.08 |
| 425009 | X58288 | Hs.154151 | protein tyrosine phosphatase, receptor t | 1.12 | 1.08 | 1.20 |
| 412099 | U64198 | Hs.73165 | interleukin 12 receptor, beta 2 | 1.12 | 2.93 | 1.12 |
| 407951 | W77762 | Hs.79015 | antigen identified by monoclonal antibod | 1.12 | 1.11 | 3.43 |
| 408116 | AA251393 | Hs.289052 | Homo sapiens, Similar to RIKEN cDNA 5430 | 1.12 | 1.50 | 1.12 |
| 450296 | AL041949 | Hs.24756 | hepatocyte growth factor-regulated tyros | 1.11 | 1.48 | 1.12 |
| 420697 | AA827705 | Hs.26605 | ESTs | 1.11 | 2.19 | 1.11 |
| 438915 | AA280174 | Hs.285681 | Williams-Beuren syndrome chromosome regi | 1.11 | 2.73 | 1.11 |
| 418399 | AF131781 | Hs.84753 | hypothetical protein FLJ12442 | 1.10 | 1.43 | 1.14 |
| 450358 | AB010098 | Hs.24907 | coronin, actin-binding protein, 2B | 1.10 | 1.35 | 1.19 |
| 444783 | AK001468 | Hs.62180 | anillin (Drosophila Scraps homolog), act | 1.10 | 1.43 | 1.10 |
| 408801 | AI866590 | Hs.63405 | Homo sapiens, clone IMAGE:3609337, mRNA, | 1.10 | 1.53 | 1.14 |
| 402622 | | | C1003392::gij12314272jamb CAC00591.1 (A | 1.10 | 1.59 | 1.06 |
| 418661 | NM_001949 | Hs.1189 | E2F transcription factor 3 | 1.09 | 1.82 | 1.09 |
| 442680 | BE270707 | Hs.8583 | similar to APOBEC1 | 1.09 | 1.49 | 1.24 |
| 439702 | AW085525 | Hs.55964 | ESTs | 1.09 | 1.68 | 1.09 |
| 423858 | AL137326 | Hs.133483 | Homo sapiens mRNA: cDNA DKFZp434B0650 (f | 1.09 | 1.10 | 1.73 |
| 443759 | BE390832 | Hs.134729 | FXYD domain-containing ion transport reg | 1.09 | 1.23 | 1.25 |
| 414396 | BE548266 | Hs.76057 | galactose-4-epimerase, UOP. | 1.09 | 1.07 | 1.23 |
| 401558 | | | ENSP00000220478::SECRETAGRANIN III. | 1.08 | 1.54 | 1.08 |
| 428411 | AW291464 | Hs.10338 | ESTs | 1.08 | 1.07 | 6.19 |
| 422051 | AW327546 | Hs.111024 | solute carrier family 25 (mitochondrial | 1.08 | 1.25 | 0.93 |
| 414694 | NM_015362 | Hs.76907 | HSPC002 protein | 1.08 | 1.18 | 1.12 |
| 453883 | AI638516 | Hs.347524 | cofactor required for Sp1 transcriptiona | 1.07 | 1.15 | 1.31 |
| 420856 | BE513294 | Hs.205736 | HLA class II region expressed gene KE2 | 1.06 | 1.47 | 1.08 |
| 412265 | AA101325 | Hs.86154 | hypothetical protein FLJ12457 | 1.06 | 1.17 | 1.22 |
| 429259 | AA420450 | Hs.292911 | Plakophilin | 1.06 | 1.08 | 0.73 |
| 417381 | AF164142 | Hs.82042 | solute carrier family 23 (nucleobase tra | 1.05 | 1.04 | 0.84 |
| 415825 | Y18024 | Hs.78877 | inositol 1,4,5-trisphosphate 3-kinase B | 1.05 | 1.09 | 1.37 |
| 444438 | N32755 | Hs.322489 | ESTs | 1.04 | 1.13 | 1.05 |
| 407394 | AF005081 | | gb:Homo sapiens skin-specific protein (x | 1.04 | 1.22 | 0.78 |
| 404960 | | | eyes absent (Drosophila) homolog 3 | 1.04 | 1.06 | 1.04 |
| 408972 | AL050100 | Hs.49378 | DKFZP586D0919 protein | 1.04 | 1.09 | 1.13 |
| 414477 | U41635 | Hs.76228 | amplified in osteosarcoma | 1.03 | 1.11 | 1.03 |
| 409327 | L41162 | Hs.53563 | collagen, type IX, alpha 3 | 1.03 | 1.02 | 2.33 |
| 435056 | AW023337 | Hs.5422 | glycoprotein M6B | 1.03 | 1.02 | 3.56 |
| 415314 | N88802 | Hs.5422 | glycoprotein M6B | 1.02 | 1.02 | 4.02 |
| 408591 | AF015224 | Hs.46452 | mannanaglobin 1 | 1.00 | 1.41 | 0.05 |
| 401203 | | | Target Exon | 1.00 | 1.02 | 0.98 |
| 400304 | AF005082 | Hs.113261 | Homo sapiens skin-specific protein (xp33 | 1.00 | 1.49 | 0.56 |
| 407395 | AF005082 | | gb:Homo sapiens skin-specific protein (x | 1.00 | 1.69 | 0.91 |
| 411388 | X72925 | Hs.69752 | desmocollin 1 | 1.00 | 3.12 | 1.00 |
| 428618 | AA885360 | | Target CAT | 1.00 | 1.77 | 1.00 |
| 402860 | | | ENSP00000239210:DJ50O24.4 (novel protein | 1.00 | 1.53 | 1.00 |
| 437211 | AA382207 | Hs.5509 | ecotropic viral integration site 2B | 1.00 | 1.39 | 1.00 |
| 409269 | AA576953 | Hs.22972 | steroid 5 alpha-reductase 2-like; HSAR g | 1.00 | 1.46 | 1.00 |
| 409190 | AU076536 | Hs.50984 | sarcoma amplified sequence | 1.00 | 0.80 | 1.00 |
| 416143 | AI955650 | | glutamyl-peptide cyclotransferase (glu | 1.00 | 1.96 | 1.00 |
| 401588 | | | C15000180::gij544344 sp Q05859 FOR4_MOUS | 1.00 | 2.04 | 1.00 |
| 419519 | AI198719 | Hs.176376 | ESTs | 1.00 | 1.91 | 1.00 |
| 448816 | AB033052 | Hs.22151 | KIAA1226 protein | 1.00 | 1.82 | 1.00 |
| 440270 | NM_015986 | Hs.7120 | cytokine receptor-like molecule 9 | 1.00 | 1.15 | 1.00 |
| 418618 | U66097 | Hs.86724 | GTP cyclohydrolase 1 (dopa-responsive dy | 1.00 | 1.66 | 0.74 |
| 422836 | AL037365 | Hs.194093 | AKAP-binding sperm protein ropporin | 1.00 | 2.21 | 1.00 |
| 452461 | N78223 | Hs.108106 | transcription factor | 1.00 | 1.61 | 1.00 |
| 428479 | Y00272 | Hs.334562 | cell division cycle 2, G1 to S and G2 to | 1.00 | 1.42 | 1.00 |
| 422420 | U03398 | Hs.1524 | tumor necrosis factor (ligand) superfam | 1.00 | 1.81 | 1.00 |
| 429477 | AI275514 | Hs.6658 | ESTs | 1.00 | 1.67 | 1.00 |
| 454027 | R40192 | Hs.21527 | Human DNA sequence from clone GS1-115M3 | 1.00 | 1.05 | 1.00 |
| 416209 | AA236776 | Hs.79078 | MAD2 (mitotic arrest deficient, yeast, h | 1.00 | 1.79 | 1.00 |
| 451993 | AA765776 | Hs.122983 | ESTs | 1.00 | 2.15 | 1.00 |
| 416947 | N23282 | Hs.184341 | ESTs, Weakly similar to B34087 hypothei | 1.00 | 1.67 | 1.00 |
| 441606 | R37263 | Hs.21065 | ESTs, Moderately similar to PC4259 ferri | 1.00 | 1.87 | 1.00 |
| 442590 | AI002686 | Hs.130313 | ESTs | 1.00 | 2.59 | 1.00 |
| 404831 | | | C1002937::gij7499208 pit T20993 hypothe | 1.00 | 1.44 | 1.00 |
| 428454 | U55936 | Hs.184376 | synaptosomal-associated protein, 23kD | 1.00 | 1.47 | 1.00 |
| 419717 | H07970 | Hs.92458 | G protein-coupled receptor 19 | 1.00 | 1.78 | 1.00 |
| 408611 | NM_004367 | Hs.46458 | chemokine (C-C motif) receptor 6 | 1.00 | 1.64 | 1.00 |

| | | | | | | | |
|----|--------|-----------|-----------|--|------|------|------|
| 5 | 421666 | AL035250 | Hs.1408 | endothelin 3 | 1.00 | 0.63 | 1.00 |
| | 446155 | AI553695 | Hs.159422 | Homo sapiens cDNA FLJ13997 fis, clone Y7 | 1.00 | 1.60 | 1.00 |
| | 423899 | NM_001427 | Hs.134989 | engrailed homolog 2 | 1.00 | 2.91 | 1.00 |
| | 423130 | AW897586 | Hs.21213 | ESTs | 1.00 | 1.65 | 1.00 |
| | 433843 | AW021423 | Hs.112819 | ESTs | 1.00 | 2.08 | 1.00 |
| | 458574 | AW384436 | Hs.135265 | Homo sapiens clone FLB8436 PRO2277 mRNA, | 1.00 | 1.41 | 1.00 |
| | 430205 | AB025904 | Hs.235168 | carbonic anhydrase XIV | 1.00 | 1.15 | 1.00 |
| | 427335 | AA448542 | Hs.251677 | G antigen 7B | 1.00 | 1.80 | 1.00 |
| 10 | 439951 | AJ347067 | Hs.124636 | ESTs | 1.00 | 2.15 | 1.00 |
| | 420248 | AJ377191 | Hs.44714 | ESTs | 1.00 | 2.35 | 1.00 |
| | 446259 | AA425204 | Hs.334721 | hypothetical protein FLJ13391 | 1.00 | 1.53 | 1.00 |
| | 447164 | AF026941 | Hs.17518 | vipirin, similar to inflammatory respon | 1.00 | 1.73 | 1.00 |
| | 447289 | AW247017 | Hs.36978 | melanoma antigen, family A, 3 | 1.00 | 1.59 | 1.00 |
| 15 | 408758 | NM_003686 | Hs.47504 | exonuclease 1 | 1.00 | 1.73 | 1.00 |
| | 453745 | AA952989 | Hs.63908 | hypothetical protein MGC14726 | 1.00 | 1.96 | 1.00 |
| | 436609 | AI022514 | Hs.131380 | ESTs | 1.00 | 2.28 | 1.00 |
| | 419308 | N40321 | | gb:yx80g07.r1 Soares melanocyte 2NbHM Ho | 1.00 | 1.74 | 1.00 |
| | 421650 | AA781795 | Hs.122587 | ESTs | 1.00 | 2.16 | 1.00 |
| 20 | 459578 | AW612538 | Hs.304491 | EST | 1.00 | 1.66 | 1.00 |
| | 446152 | AI292036 | | ESTs | 1.00 | 2.04 | 1.00 |
| | 449579 | AW207260 | Hs.134014 | ESTs, Weakly similar to T46425 hypothesi | 1.00 | 1.75 | 1.00 |
| | 418673 | NM_005582 | Hs.87205 | lymphocyte antigen 64 (mouse) homolog (| 1.00 | 1.85 | 1.00 |
| | 415004 | AA158925 | Hs.240849 | ESTs, Weakly similar to GBP1_HUMAN INTER | 1.00 | 1.92 | 1.00 |
| 25 | 426274 | D38122 | Hs.2007 | tumor necrosis factor (ligand) superfam | 1.00 | 1.72 | 1.00 |
| | 453922 | AF053306 | Hs.36708 | budding uninhibited by benzimidazoles 1 | 1.00 | 1.52 | 1.00 |
| | 417791 | AW965339 | Hs.44269 | ESTs | 1.00 | 2.02 | 1.00 |
| | 424905 | NM_002497 | Hs.153704 | NIMA (never in mitosis gene a)-related k | 1.00 | 1.28 | 1.00 |
| | 416445 | AL043004 | Hs.79337 | KIAA0135 protein | 1.00 | 1.92 | 1.00 |
| 30 | 408375 | AI224520 | Hs.40930 | ESTs | 1.00 | 0.46 | 1.00 |
| | 406964 | M21305 | | FGENES predicted novel secreted protein | 1.00 | 1.00 | 2.48 |
| | 408522 | AI541214 | Hs.46320 | Small proline-rich protein SPRK (human, | 0.98 | 0.98 | 3.24 |
| | 412828 | AL133396 | Hs.74621 | prion protein (p27-30) (Creutzfeld-Jakob | 0.95 | 0.96 | 3.06 |
| | 422270 | AF114494 | Hs.114062 | protein tyrosine phosphatase-like (proti | 0.94 | 0.96 | 1.61 |
| 35 | 446488 | AB037782 | Hs.15119 | KIAA1361 protein | 0.94 | 0.94 | 0.76 |
| | 433435 | BE545277 | Hs.340959 | Ts translation elongation factor, mitoch | 0.93 | 0.91 | 1.55 |
| | 409402 | AF208234 | Hs.695 | cystatin B (stefin B) | 0.92 | 0.93 | 2.09 |
| | 423942 | AF209704 | Hs.169407 | glycolipid transfer protein | 0.91 | 0.91 | 4.08 |
| 40 | 414219 | W20010 | Hs.75823 | ALL1-fused gene from chromosome 1q | 0.90 | 0.81 | 0.73 |
| | 429211 | AF052693 | Hs.198249 | gap junction protein, beta 5 (connexin 3 | 0.90 | 0.92 | 3.89 |
| | 417632 | R20855 | Hs.5422 | glycoprotein M6B | 0.89 | 0.79 | 0.84 |
| | 449092 | U91641 | | alpha2,8-sialyltransferase | 0.89 | 0.92 | 3.70 |
| | 426716 | NM_006379 | Hs.171921 | sema domain, immunoglobulin domain (Ig), | 0.88 | 0.90 | 2.02 |
| | 445033 | AV652402 | Hs.72901 | cyclin-dependent kinase inhibitor 2B (p1 | 0.88 | 0.87 | 0.73 |
| 45 | 408349 | BE546947 | Hs.44276 | homeo box C10 | 0.85 | 0.84 | 0.69 |
| | 429345 | R11141 | Hs.199695 | hypothetical protein | 0.84 | 0.85 | 1.32 |
| | 451621 | AI879148 | Hs.26770 | fatty acid binding protein 7, brain | 0.84 | 0.88 | 3.37 |
| | 417022 | NM_014737 | Hs.80905 | Ras association (RalGDS/AF-6) domain fam | 0.81 | 0.71 | 1.00 |
| 50 | 405885 | | | Target Exon | 0.78 | 0.78 | 0.90 |
| | 407788 | BE514982 | Hs.38991 | S100 calcium-binding protein A2 | 0.77 | 0.73 | 0.71 |
| | 417515 | L24203 | Hs.82237 | ataxia-telangiectasia group D-associated | 0.75 | 0.78 | 4.69 |
| | 421100 | AW351839 | Hs.124660 | Homo sapiens cDNA: FLJ21763 fis, clone C | 0.74 | 0.78 | 5.42 |
| | 440274 | R24595 | Hs.7122 | scrapie responsive protein 1 | 0.70 | 0.75 | 4.29 |
| 55 | 425071 | NM_013989 | Hs.154424 | deiodinase, iodothyronine, type II | 0.70 | 0.77 | 3.99 |
| | 412719 | AW016610 | Hs.816 | ESTs | 0.69 | 0.73 | 3.79 |
| | 432467 | T03667 | Hs.239388 | Human DNA sequence from clone RP1-304B14 | 0.65 | 0.64 | 1.11 |
| | 437191 | NM_006846 | Hs.331555 | serine protease inhibitor, Kazal type, 5 | 0.61 | 0.65 | 3.20 |
| | 452487 | AW207659 | Hs.6630 | Homo sapiens cDNA FLJ13329 fis, clone OV | 0.61 | 0.22 | 0.49 |
| | 448133 | AA723157 | Hs.73769 | folate receptor 1 (adult) | 0.49 | 0.30 | 0.67 |
| 60 | 439659 | AW970780 | Hs.59482 | Homo sapiens cDNA FLJ14471 fis, clone MA | 0.41 | 0.11 | 0.34 |
| | 419092 | J05581 | Hs.89603 | mucin 1, transmembrane | 0.23 | 0.30 | 0.35 |
| | 417079 | U65590 | Hs.81134 | interleukin 1 receptor antagonist | | | |

TABLE 49B:

| | | |
|----|-------------|---------------------------------------|
| 65 | Pkey: | Unique Eos probeset identifier number |
| | CAT number: | Gene cluster number |
| | Accession: | Genbank accession numbers |

| | | | |
|----|--------|------------|---|
| 70 | Pkey | CAT Number | Accession |
| | 430540 | 713_2 | BC012171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 |
| | | | BM045810 AU120387 BG770238 BG686740 BG913323 B1759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 |
| | | | AI770171 BF196861 BE856897 AA463876 AI375927 AA648810 AA948193 AA409916 AA59893 AI458188 AI240408 AI191843 AI131029 AW768399 |
| | | | AI325196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903567 |
| | | | BE73715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610 |
| 75 | | | BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BF391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 |
| | | | BE298109 AW245422 AJ423847 AI914618 H80534 BE301004 AL531791 AJ435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296 |
| | | | AJ359493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AI421728 BG767231 BM462953 |
| | | | BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512 |
| | | | W58732 W85690 BG958989 AI205206 H19721 W17051 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 |
| 80 | | | F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114 |
| | | | AI243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103 |
| | | | AW008188 R07703 AA989120 AA746235 AW028983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809 |
| | | | BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591 |
| | 431317 | 997174_1 | AW970601 AW613399 AA503435 AA502682 N91138 |

| | | | |
|----|--------|----------|--|
| | 453912 | 32562_3 | BM472224 BI966849 BI966735 AW973032 BI962894 BI963048 AA548765 AJ926504 AA041551 AW043754 AJ086702 AW008105 AA974849 AW614893 AA553737 AA916996 AW262982 AI580991 BF726843 AV693312 W35325 AA039927 BG460936 AW388482 AW388420 BF374777 W01360 N94710 H87967 |
| 5 | 420218 | 191547_1 | AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756 AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI527952 AA303734 BE349457 AW196765 AA256527 BE089727 |
| | 458997 | 11847_4 | BM453041 AA760783 BE218582 AI340046 AW166131 BF515854 AI630296 AA461307 AI090881 AW023059 AA155797 AA115486 AL597396 |
| | 430015 | 713_2 | AW889004 AW937420 AA137082 AA013374 BG619478 BG401839 |
| 10 | | | BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 BM045810 AU120387 BG770238 BG686740 BG913323 BI759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 |
| | | | AI770171 BF196861 BE856897 AA463876 AI375927 AA648810 AA948193 AA490916 AI459893 AI458188 AI240408 AI91843 AI131029 AW768399 |
| | | | AI365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI551927 AW151143 BI198825 BG819083 BM458764 BE903567 |
| | | | BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610 |
| | | | BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 |
| | | | BE298109 AW245422 AI423847 AI914618 HM0534 BE301004 AL531791 AI435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296 |
| 15 | | | AJ359493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG652159 AA421728 BG767231 BM462953 |
| | | | BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 W72512 |
| | | | W58732 W85690 BG958989 AI205206 H19721 W10751 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 |
| | | | F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114 |
| | | | AI243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103 |
| 20 | | | AW008188 R07703 AA899120 AA746235 AW028983 AA789102 AI185751 AW971465 AA489681 AW971893 AW612086 BE079336 BI860809 |
| | 425231 | 235504_1 | BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 HM0591 |
| | 417282 | 2142_2 | AA527161 BG211784 AA527065 AA505489 AW512550 |
| | | | AK025474 U11293 AF141304 BM424202 AL539879 AL554793 AL543707 AL549509 BI753328 BG756797 BI856494 BE901116 AL556989 AU133347 |
| 25 | | | BK38505 AW949559 BM012604 BG773980 BG661309 BI260149 BF436764 BG983060 BF822225 BI059728 BF917866 BF917609 BF914374 D31003 |
| | | | AA234218 AJ420466 BM083921 BE856788 BE669957 BF430992 AW614978 AW205958 BF110763 BF227758 AA195232 AI341353 AI698676 |
| | | | AI093230 AI123522 AI656594 AI208758 AA975916 AI089224 AI264922 AA256604 AA659637 BE218707 AA195203 AW999239 AW139706 N31717 |
| | | | AW205941 R95955 N39147 BM015411 AL576975 BF689524 AL563130 BI858155 AA417889 AL513995 AL568815 AU160693 AA836028 H843699 |
| | | | AL517078 AL546480 AL530507 AL561042 AA024435 W47314 AI680513 AA456116 BF836679 AW975173 H24039 AW105059 BE548113 AW370257 |
| 30 | | | BM011139 AW675130 BE276045 BF933396 AL517903 AA886367 BI030596 BG477193 BF973867 |
| | 406687 | 0_0 | M31126 |
| | 452194 | 90339_1 | AI694413 AW994700 AI912946 N73548 AI802035 AW271652 W24189 W24182 AI719718 AA024658 AW810120 AW015394 T79755 AA988043 |
| | | | AI709339 |
| | 442643 | 2736_1 | BC001588 BC007424 AF016369 NM_004697 BI756186 BE257019 BG500792 BI862776 AL121371 BG574833 AA703250 AA179511 AW052006 |
| 35 | | | AI280150 AI914000 AI358319 AI081204 AI082594 AA992449 AI470821 AI655744 AW237529 AA678858 AI984430 BF433055 BE467594 BE467573 |
| | | | AA035630 AI289987 AI184802 AI681391 AW592416 AI138377 AI139266 AA961714 AI800163 AA418751 AW451928 AA668676 AI273444 AI494387 |
| | | | BE046912 AI276555 BF196021 AA700055 AA609305 AA727596 AI635758 AI635749 H95459 AW610290 BE464994 AA527136 BF374802 AI800175 |
| | | | AW195227 AI189676 BF802049 AL513532 AL554911 AL538845 BE297273 AA315321 BM451920 BE269268 BE292835 BE018128 BG755713 |
| | | | BM041095 BG677009 AL039691 BF995709 BE735586 BE296453 BG393609 BG824453 AI567522 AI745257 AW388641 AW301265 AI141144 |
| 40 | | | AW029280 AU149362 AU152328 AA418960 AI121009 AI890398 AI528748 H13050 T47086 BI000575 BF334914 BF109661 R44450 H13259 T47087 |
| | | | AW388645 BF305834 AL577515 BM041600 BE889299 BF239768 |
| | 448243 | 13061_2 | BG166513 AA479726 BE622314 AL134913 BE006305 BE006312 BE006298 AA044582 AW994956 AA234175 AA043906 BE006303 BF327669 |
| | | | BE006317 BF326759 BF541959 |
| | 430441 | 1438_6 | BG108218 BE560548 AW380115 BE269629 AI911518 AW380113 AA902964 AA455001 AI276529 AI685597 AA970496 D61084 AW380068 AW380080 |
| | | | R00283 C15236 AW327776 D80759 |
| 45 | 432810 | 101919_1 | BG292389 C06094 AI668930 AW104534 AA310513 AA830127 AW134897 AA046953 AW965490 AI810530 BF092924 AA334151 AA334725 D31302 |
| | | | R20723 AA263003 BI824635 AI276287 AI684428 AI524234 AI335035 AW014704 AI911443 AA972102 AI367512 AI126670 AW016017 AI286003 |
| | | | AI147163 AA626033 AI539156 AA565542 AI094253 AW512612 BE889628 AA744752 BE646306 AW471324 AA999975 AA863400 H17550 AI991439 |
| | | | R46187 BE929954 AA333976 D63102 BF744491 |
| 50 | 446019 | 658727_1 | AI362520 D25917 AI670784 AI742347 AW269789 AI270700 AW610541 AW793036 AW793035 AW610540 AW362220 AW362166 AW362214 |
| | | | AW362225 AW362228 AL119827 |
| | 453331 | 16559_1 | BG571303 AA410586 AA035018 BG572117 BG620022 AA147247 BG005785 BG014448 R31981 H02668 H12498 R36203 BF992089 R73999 T49904 |
| | | | R75732 BI057974 T53681 AA147933 N50695 R68588 R25671 R31935 R25110 R36105 AK055628 BE157467 AW663674 AA190993 H01642 BF510304 |
| | | | AA626915 AA746952 AI161014 AA099554 BG572534 AI033929 AI809932 AI808765 AA411449 AI378760 AA976829 AI378620 AA096884 R75632 |
| | | | AI360919 AI350463 AW069127 AA411621 AA742532 H12451 BE208298 H03612 H12839 N58781 R75957 BF996484 AI240665 BF989591 BI056086 |
| 55 | | | BG001590 BF107035 |
| | 429978 | 35194_2 | BE738425 BE738323 BM126944 AW629678 AW265195 AI916735 AI394255 AI573090 AI354442 AW612857 AI339558 AI919424 AI377532 AI354441 |
| | | | AI308821 AA772275 AW055215 AI589705 AI336532 AA806547 AV682125 H93575 AW071172 AW769904 AI863985 AW265018 AW196655 D79662 |
| | | | BE042393 N75017 AW014741 C75509 BE748621 H92431 AW079261 AW901780 AA329482 AW960115 BI260621 AI767525 R31663 BI918664 |
| | | | AW963196 C06195 AI678018 |
| 60 | 452203 | 2630_1 | BC014081 NM_000593 X57522 L21208 L21207 L21206 L21205 L21204 AL561404 AL564623 AL560492 AL556882 AL541576 AL550654 BI823519 |
| | | | BI770023 AL554969 BI489906 AI304693 AW295947 BM146642 X57521 BG820143 BE898390 F06770 F12630 BM423610 AL561518 BM009470 |
| | | | BG742981 AA279685 AA847441 AA313737 BF172639 BF897216 BF914190 BF903647 S70277 AI569694 AW073296 AI361433 AA564644 AA487429 |
| | | | BE858232 AA838610 AI539114 AI719375 AI829129 BG057675 AI423422 AU158860 BE300655 AW170777 AA586956 AL571889 AI556850 AI576404 |
| 65 | | | AL582800 BI256544 BF342301 BG875994 AA054458 AA353161 AI940434 BE816522 AL577636 AI479650 AW150377 AU154395 AW951271 AI032220 |
| | | | AI819778 AI346733 AW771150 AW512525 AI249904 AA279809 AI352549 AW512517 BG056280 AA521222 BE271141 AL581932 AL541575 BI819184 |
| | | | AV660190 AL556475 AI620020 AW089888 AW079179 Z21518 AA687601 F04651 AI783961 T57198 AI433367 T78652 AL554968 AA365648 AL582619 |
| | | | BE874601 BF804669 AI574458 BM145502 AI266514 AI538823 AI475626 AA948210 AA884054 AA487637 AA031844 AA535221 AW794256 |
| | | | AW361447 BE788505 AI682892 AA830989 AA862356 AA653084 BM009154 AA135727 H05927 H23433 R42244 W79997 AW366665 AW366601 |
| 70 | | | AA678742 AL556474 AA135770 BE774050 BF914200 H88457 AA627746 BI560216 BI753586 |
| | 458098 | 23945_1 | AJ082245 BE467534 AI797130 BE467063 BE467767 BE218421 AI694996 BE327781 BE327407 BE833829 AA989054 AA459718 BE833855 BE550224 |
| | | | AA832519 AF086393 AV733386 BE465409 N29245 W07677 AA482971 BE503548 H18151 AA461301 W792217 W74510 AI90689 AL600773 AL600781 |
| | | | H46003 R28075 R34182 BE071550 AW885857 AI276145 AI276696 H97808 N20540 AI468553 |
| | 424399 | 2196_1 | NM_058173 AF414087 W72837 BF742809 AW070916 BE092421 AI905687 AA340069 BE074512 AI905623 AI905633 BG202312 W72838 AI139456 |
| | | | BG218084 BE926938 BE186013 AW176044 AW291950 BG185269 BG197186 BG192597 BG183176 BG207535 AI127172 BE815819 AI905624 |
| 75 | | | R75793 BG202313 AI905837 BE815853 |
| | 427239 | 20459_2 | AL532360 BE794750 AA582905 AI015067 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE138953 BE049086 AI334881 |
| | | | AW075006 AW075181 AA464019 AW302733 AW075100 AW073433 AI802854 AI334909 AI802853 AI345036 AI348921 AI340734 AI307478 AI251289 |
| | | | AW302327 AW072520 AI312145 AW073656 AW072513 AW071289 AI307559 AA876186 T29587 AI307493 AI255068 AI252868 AI252839 AW074809 |
| | | | AI252926 AI252160 AI251662 AI251262 AI610913 AI270787 AI270156 AI252075 AW073469 AW072901 AW072496 AW071420 AI305762 AI254764 |
| | | | AI802837 AI251264 AW073049 AW071311 AI340643 BE138965 BE138502 AW073456 AI334733 AI054335 BE139260 AI054302 AI054060 AI054057 |
| | | | AI053722 AI289711 BE139228 AW470478 AW271039 AW302085 BE041872 AI254494 AI271496 AI252427 BF718773 BF718645 AW074866 BE857822 |
| 80 | 400222 | 9287_3 | NM_002082 L16862 BG828886 BE795217 BE904064 BE294526 BE297283 BE394617 BE935127 BE935106 F12351 BG823182 H16710 |
| | 410600 | 497855_1 | BF347859 AW499616 AA191322 AW499617 AL601010 AW575742 AA729043 BE463447 AA086179 BE549623 AI335824 AW408712 BM149172 |

| | | |
|--------|-----------|--|
| 417324 | 292720_1 | BG775668 BG680336 AW991605 AA455904 AW265494 AW265432 BF911380 AA456370 BF911379 AA195677 BF914311 BF913866 BG775059 |
| 453613 | 10943_2 | BG951874 A1572169 |
| 411825 | 7891_1 | BG121705 BF514513 BE812196 AW173164 A1911266 A161253 AA906295 AA724987 AA972070 AW085313 B1062611 BG119864 W02997 H80902 |
| 400270 | 32329_1 | T91294 H09335 H09332 Z40007 F10399 F02595 F03100 H38987 A1801190 H80903 AW130044 F10391 T80640 H24461 R46234 R51914 |
| 442591 | 58995_1 | AK000695 AK000489 BC001688 BG235988 AW006329 A1887644 A1207230 A1148213 A1304333 A1634653 AW652636 A1281247 AA946921 AA424487 |
| 410103 | 366775_1 | BE272330 A1830588 AA159183 AA977141 BG231801 AA631793 AA975194 BF817537 AA477798 B1906631 AW083424 AA625199 NM_017767 |
| 437179 | 12239_1 | AK000334 BF984048 AW815634 AL573992 AA430612 AA928390 AA464447 AW340827 AA424290 A1927759 BG951502 AW881353 B1765535 |
| 451050 | 11847_4 | AF067853 NM_000026 X65867 BC018881 S60710 BG686218 BG707897 B1767531 BE742167 BG747544 BG768400 BG323811 AU119991 BG763638 |
| 438129 | 497522_1 | BG393097 BG761706 B1766890 B1457560 BG122629 BF972974 B1194649 BE909022 BG488681 AW328441 AW248366 BG118034 B1598504 |
| 439246 | 388_5 | BE264146 AW248440 BE410942 BE256756 A1480227 A1758918 BE251966 A1684330 AW518872 AW264087 AA631137 A1742831 A1990690 A192994 |
| 427289 | 1820_2 | AA417231 AA455931 AA416541 A1652537 A1803674 AA631209 A1923786 AW205704 A1354260 A1198865 BF593386 AW821194 A1693442 AW9797594 |
| 406827 | 0_0 | BE893700 BF242879 BE251315 AA534659 AA494551 B1047923 BG949898 BF246869 B1085069 BM007035 AA665981 A1375483 BG221393 A1867580 |
| 443086 | 25669_4 | AA128025 AW612345 R12769 W92325 R40084 AA191625 D51044 AA599257 BE878335 AA121664 A1146666 B1026299 A1872956 AA788642 |
| 400261 | 23110_1 | AA128068 BF819623 A1277591 A1435105 A1354905 AV747031 |
| 412315 | 1163860_1 | BC021240 BF430978 BG056212 AW874052 B1856040 A1572156 A1914600 A1002736 BM023413 H91902 A1563177 A1529967 BM023140 BE391587 |
| 454478 | 4273_16 | BG761312 BE277571 B1195388 BE389566 H91851 BE391930 BE391441 |
| 459345 | 191706_1 | BG003993 AW589921 AW892489 AW903666 |
| 400214 | 9255_1 | AK055109 BC019085 AA187684 BG656226 BM023227 A1932311 AW264381 AA398371 BM021483 A1432433 A1375777 A1129580 AW262782 |
| 416929 | 14596_3 | AA134107 BM023515 AA977504 A1859222 A1348454 B59725 AA975268 BM021207 AL080074 AA129218 AW207842 N90581 AA771919 A1092259 |
| 419250 | 249447_1 | A1028416 A1074114 BG656536 BE501677 AW193419 AA917040 W90430 A1342984 A1378957 AL036486 AW020068 B1491093 BF476021 R41226 |
| 424292 | 892193_1 | R59631 F04125 C02343 AA115589 R56480 A1400988 R54266 R31422 |
| 420223 | 191648_1 | BM453041 AA760783 BE218582 A1340046 AW166131 BF515854 A1630295 AA461307 A1090881 AW023059 AA155797 AA115486 A1597396 |
| 428342 | 6712_1 | AW889004 AW937420 AA137082 AA013374 BG619478 BG401839 |
| 407394 | 27110_2 | BE904404 AA778647 BF431869 AW070999 BG170122 BG191943 BG999184 R42302 |
| 428618 | 2668_1 | AK054564 AF086057 A1869310 BG393141 BE220500 AA79459 A1866575 A1361301 A1674602 BF001506 AW004996 A1446292 A1890883 A1608681 |
| 416143 | 40539_2 | AW131794 A1356096 A1433040 BG057018 A1696166 AW081428 A1392809 AA985226 AW190187 BE896007 BG171443 AW516382 AA731186 N50847 |
| 419308 | 249928_1 | AA417728 F27148 A1003145 AL520675 AL577680 A1578955 AA316669 BF804796 AA768324 A1285396 BG745142 BG325246 BG475289 A1580501 |
| 446152 | 2857941_1 | AA832445 AA832168 BF063242 AW251083 BF345614 BE871009 BG698638 BG978245 BG978247 |
| 449092 | 4406_1 | BC007350 BG766159 BG769338 BG761999 BG744385 BG770572 AW370610 AW370581 AA978353 AW327973 AW402425 A1889380 AA868504 |
| | | AW612968 AA630644 A1751211 N26980 A1394506 AA747849 BF154926 BF477185 AA649647 R39135 A1750216 T35363 W36278 AW079375 |
| | | AW612240 AA505495 AA515380 BG760793 AW370651 BG766029 AW370595 BF229885 BG762422 BG764907 T50662 AA025671 AW815715 |
| | | AV703420 H65047 AA485582 R56186 H90385 R55913 B1261497 B1018403 BF376945 T75578 BF933325 BF932853 BG502266 AW868934 AV683504 |
| | | B1018121 N41953 BF933343 BF932871 H08334 R14012 BF897622 T50816 BG698603 BF340083 Z20199 |
| | | AA971409 |
| | | BE896316 BG819393 AA187888 AW753122 |
| | | BC006097 X03066 NM_002120 M26040 AW469119 AW469127 A1299772 AW518149 A1144456 AW628070 A1629032 A1358810 A1880433 A1440472 |
| | | A1357070 A1865365 AW014799 A1767973 A1518041 AA909398 AW768606 |
| | | AW936678 AW936821 AW936683 AW936822 AW936781 AW936817 AW936811 AW936653 AW936823 AW936685 AW936815 AW936637 AW936812 |
| | | AW936730 AW936762 AW936682 AW936732 |
| | | AW796921 AW798102 AW805749 AW805872 BF985060 AW794380 BF380449 AW794466 AW794538 |
| | | AW853325 AW503672 |
| | | A1659839 BE897640 BE907077 BC003059 BC017245 BC010733 BM423383 A1537826 AL580324 BG749884 BE910412 B1085225 BG830374 |
| | | BG765711 BE513420 BE513706 AW249005 BE378229 BE250756 BG389441 BF998736 H61321 BF869238 BG979991 H49658 AA353290 D64154 |
| | | BM468130 AL549088 B1765497 AL556922 B1833272 BM009270 B1546248 BG750170 BG480128 AL561553 B1559389 BG762029 BG741197 B1561200 |
| | | B1259044 AL523216 BG333073 B1838073 BE790691 A1762878 BF972560 B1260209 B1330558 B1090606 BG468683 B1598273 B1826098 BE622086 |
| | | B1758061 BG751116 BE905428 BG764482 AL522174 BG761428 B1836634 BG749048 BG774512 BE280653 BG480630 BG716728 B1766635 |
| | | BG573991 BG389305 BF971754 BG680599 BE795075 BG324709 AA984290 BE304564 BG238313 BE252914 BF872431 BE407696 BE264894 |
| | | AL552517 BF872428 BF724779 BE279635 BF804329 BE764960 BF811388 D31335 AW951318 BF992435 BF811453 NM_007002 AL518634 |
| | | AL574934 AL523534 AL520445 AL521785 AL547001 AL558522 BE289145 B1862487 B1753281 BE258642 AL039594 BG015181 BE925165 BF872433 |
| | | A1904540 A1904495 AA776741 AA317533 BG476828 R13328 BG4489456 BF102495 BF693420 AL526597 BG104181 BG740214 BE393189 A1966312 |
| | | H61596 AW051180 B1668762 AW938619 B1086232 AA053472 BE264345 |
| | | AA609784 R97304 |
| | | BG167206 AA677283 AA677217 A1703389 A1051577 A1912137 H39571 AA650047 A1399798 H24807 AA341614 BG945259 A1074162 AW969020 |
| | | AA528934 AA659498 AA699617 H14450 H21758 H39576 AA095608 A1049973 BG054505 BG319545 A1742408 AA421324 A1580138 A1375883 |
| | | A1374848 A1367657 A1374762 A1304678 AA007357 BF477168 A1373751 A1779885 A1801494 BE349021 A1220937 AW338397 AA253409 AA418327 |
| | | AA872682 A1572030 A1521517 A1572944 A1418670 A1266089 W72413 W76492 A1809207 A1915747 H22230 H21951 H08513 H25154 |
| | | BC017849 BC005892 N42983 BF691239 N42991 N29240 N40292 N33322 N33330 N20535 |
| | | BG755078 B1226909 N41827 AW404060 B1058921 H11253 AA461274 R05714 H00515 B1086965 A1032786 B1089613 BM171783 A1127382 A1660953 |
| | | AW296271 A1582209 AA460965 A1376115 A1016900 BG055846 A1023644 AA767046 AA815039 AW403510 A1868663 A1815462 AA235654 AW292253 |
| | | AW959582 AV725205 AW959578 AA300091 W24933 R05715 AW770185 H00465 N93714 H11254 T49555 |
| | | AW966308 AA339512 AA338432 |
| | | NZ7807 AA256634 BE276324 |
| | | AK056315 A1015524 AA724079 B1713619 A1377728 AW293682 A1928140 A1092404 A1085630 AA731340 BM469629 AW968804 AA425658 AA769094 |
| | | BF446026 AW118719 A1332765 AW500888 AW576556 A1859571 AW499664 AW614573 AW629495 AW505314 W74704 A1356361 A1923640 |
| | | AW070509 A1521500 AL042095 AA609309 AA761319 A1381489 H45700 AA761333 AW265424 AA909524 AA635311 AA649040 A1392620 Z40708 |
| | | A1985564 AW263513 AA913892 A1693486 AW263502 A1806164 AW291137 B1061872 B1059498 AA134476 AW084888 AA036967 AW370823 T55263 |
| | | B1002756 AA489664 BF827261 W74741 BF963166 |
| | | AF005081 BG193848 |
| | | BC017998 B1826643 BG715794 BG722697 B1460787 BG773459 H52859 A1652853 A1990773 AW665193 AW340601 AA913806 A1337099 BE045942 |
| | | AW572790 AW515652 H15004 AA909115 B1465310 B1462024 B1561578 B1463075 BG722527 R86003 BG623286 H15003 B1562131 BG435272 |
| | | BG218868 AV705271 N34158 AL538368 BG186620 BG188697 BG181900 A1200440 BG033721 BF968528 BF792647 AW204668 AA922311 F02735 |
| | | AW342041 BG217293 BE619664 BE465887 AA745605 A1278924 A1278545 A1280994 AA809678 AA282134 T08599 AA732436 T05478 F04402 |
| | | AA262267 A1969523 N25559 A1760218 BG217318 BF893160 |
| | | N40321 AA236322 AA236215 |
| | | A1292036 A1858546 A1277390 |
| | | AK056270 AV706896 A1692935 A1681140 AW162481 AW087114 AW157019 A1689795 AW251085 AW206911 BF438207 AW134945 BE041668 |
| | | BF111425 U91641 NM_013305 BF968902 U55966 AU130750 BE174853 A1929731 AW161524 R43753 BE779668 |

| | | |
|----|------------|---|
| 80 | TABLE 49C: | |
| | Key: | Unique number corresponding to an Eos probe set |
| | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. |
| | Strand: | Indicates DNA strand from which exons were predicted. |

NL_position: Indicates nucleotide positions of predicted exons.

| | Pkey | Ref | Strand | NL_position |
|----|--------|---------|--------|--|
| 5 | 402075 | 8117407 | Plus | 121907-122035,122804-122921,124019-12416 |
| | 405451 | 7622517 | Minus | 145949-146227 |
| | 401747 | 9789672 | Minus | 118596-118816,119119-119244,119609-11976 |
| | 401454 | 9186923 | Minus | 114659-114832 |
| 10 | 405545 | 1054740 | Plus | 118677-118807,119091-119296,121626-12182 |
| | 401780 | 7249190 | Minus | 28397-28617,28920-29045,29135-29296,2941 |
| | 403328 | 8469086 | Minus | 120428-120703 |
| | 405547 | 1054740 | Plus | 124361-124520,124914-125050 |
| 15 | 403532 | 8076842 | Minus | 81750-81901 |
| | 400750 | 8119067 | Plus | 198991-199168,199316-199548 |
| | 405506 | 6466489 | Plus | 80014-80401,80593-81125 |
| | 400533 | 6981826 | Minus | 277132-277595 |
| 20 | 405779 | 7280331 | Minus | 33048-33856 |
| | 402994 | 2996643 | Minus | 4727-4969 |
| | 401781 | 7249190 | Minus | 83215-83435,83531-83656,83740-83901,8423 |
| | 401994 | 4153858 | Minus | 42904-43124,43211-43336,44607-44763,4519 |
| 25 | 403969 | 8569909 | Plus | 31237-31375,32405-32506 |
| | 401760 | 9929699 | Plus | 83126-83250,85320-85540,94719-95287 |
| | 401797 | 6730720 | Plus | 6973-7118 |
| | 401151 | 9438288 | Plus | 30848-31228 |
| 30 | 404872 | 9650523 | Minus | 18540-18718 |
| | 402876 | 9864669 | Plus | 5679-6027,7485-7584 |
| | 405204 | 7230116 | Plus | 126569-126754 |
| | 402294 | 2282012 | Minus | 2575-3000 |
| 35 | 400991 | 8096825 | Plus | 159197-159320 |
| | 401284 | 9800819 | Minus | 101307-101421 |
| | 402474 | 7547175 | Minus | 53526-53628,55755-55920,57530-57757 |
| | 403022 | 3132351 | Plus | 92097-92864 |
| 40 | 402542 | 9801558 | Minus | 67076-67594 |
| | 403409 | 9438598 | Plus | 6860-7054,12573-12771 |
| | 403506 | 7596863 | Plus | 105008-105650 |
| | 406016 | 8272661 | Plus | 41341-41940 |
| 45 | 405268 | 4156151 | Minus | 24404-24521 |
| | 401106 | 8568931 | Plus | 122694-122893 |
| | 404186 | 4481839 | Plus | 829-1110 |
| | 403817 | 8962065 | Plus | 110297-111052 |
| 50 | 406422 | 9256411 | Plus | 163003-163311 |
| | 402160 | 8516165 | Plus | 166063-166354 |
| | 402622 | 9930984 | Minus | 129861-130099 |
| | 401558 | 7139678 | Plus | 103510-104090 |
| | 404960 | 7408010 | Minus | 146186-146377,147747-147943 |
| | 401203 | 9743387 | Minus | 172961-173056,173868-173928 |
| | 402860 | 9588237 | Minus | 76423-76560 |
| | 401588 | 7230871 | Plus | 46412-46561 |
| | 404831 | 6624702 | Minus | 16833-17020,20007-20120,21605-21799,2333 |
| | 405885 | 7677703 | Minus | 42574-42998 |

TABLE 50A: ABOUT 398 GENES UPREGULATED IN PRIMARY MELANOMAS OR MELANOMA METASTASES RELATIVE TO BENIGN NEVI

Table 50A lists about 398 genes upregulated in primary melanoma or melanoma metastases relative to benign nevi. Genes were selected from 59680 probesets on the Eos/Alfymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

| | | |
|----|----------------|---|
| 55 | Pkey: | Unique Eos probeset identifier number |
| | ExAccn: | Exemplar Accession number, Genbank accession number |
| | UnigenelD: | Unigene number |
| | Unigene Title: | Unigene gene title |
| 60 | R1: | 70th percentile of primary melanoma and melanoma metastasis AIs divided by the maximum AI of benign nevi. |
| | R2: | 70th percentile of primary melanoma and melanoma metastasis AIs divided by the maximum AI of benign nevi, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator |

| | Pkey | ExAccn | UnigenelD | Unigene Title | R1 | R2 |
|----|--------|-----------|-----------|--|-------|-------|
| 65 | 422424 | AI186431 | Hs.296638 | prostate differentiation factor | 13.73 | 16.82 |
| | 446619 | AU076643 | Hs.313 | secreted phosphoprotein 1 (osteopontin) | 11.67 | 11.84 |
| | 407846 | AA426202 | Hs.40403 | Cbp/p300-interacting transactivator, wit | 9.35 | 7.59 |
| | 444381 | BE387335 | Hs.283713 | ESTs, Weakly similar to S64054 hypothesi | 8.63 | 7.90 |
| 70 | 417880 | BE241595 | Hs.82848 | selectin L (lymphocyte adhesion molecule | 8.21 | 4.09 |
| | 424321 | W74048 | Hs.1765 | lymphocyte-specific protein tyrosine kin | 7.13 | 6.10 |
| | 447210 | AF035269 | Hs.17752 | phosphatidylserine-specific phospholipas | 6.79 | 6.26 |
| | 417693 | AW959741 | Hs.40368 | adaptor-related protein complex 1, sigma | 6.55 | 6.36 |
| 75 | 429500 | X78565 | Hs.289114 | hexabrachion (tenascin C, cytactin) | 6.43 | 7.11 |
| | 414812 | X72755 | Hs.77367 | monokine induced by gamma interferon | 6.43 | 7.51 |
| | 451736 | AW080356 | Hs.23889 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 6.31 | 4.28 |
| | 418870 | AF147204 | Hs.89414 | chemokine (C-X-C motif), receptor 4 (fus | 6.20 | 4.32 |
| 80 | 428291 | AAS34009 | Hs.183487 | interferon stimulated gene (20kD) | 6.03 | 4.52 |
| | 417308 | H60720 | Hs.81892 | KIAA0101 gene product | 6.01 | 6.78 |
| | 448569 | BE382657 | Hs.21486 | signal transducer and activator of trans | 5.99 | 7.51 |
| | 439310 | AF086120 | Hs.102793 | ESTs | 5.95 | 4.79 |
| | 452838 | U65011 | Hs.30743 | preferentially expressed antigen in mela | 5.95 | 5.55 |
| | 422241 | Y00062 | Hs.170121 | protein tyrosine phosphatase, receptor t | 5.76 | 4.82 |
| | 442379 | NM_004613 | Hs.8265 | transglutaminase 2 (C polypeptide, prote | 5.76 | 2.19 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|-------|
| 5 | 409274 | NM_003930 | Hs.52644 | SKAP55 homologue | 5.65 | 4.63 |
| | 442739 | NM_007274 | Hs.8679 | cytosolic acyl coenzyme A thioester hydr | 5.58 | 3.41 |
| | 442711 | AF151073 | Hs.8645 | hypothetical protein | 5.45 | 5.79 |
| | 425118 | AU076611 | Hs.154672 | methylene tetrahydrofolate dehydrogenase | 5.42 | 5.56 |
| | 412918 | BE563957 | | activated RNA polymerase II transcriptio | 5.35 | 4.31 |
| | 428125 | AA393071 | Hs.182579 | leucine aminopeptidase | 5.33 | 4.83 |
| | 446921 | A8012113 | Hs.16530 | small inducible cytokine subfamily A (Cy | 5.33 | 5.13 |
| | 431183 | NM_006855 | Hs.250696 | KDEL (Lys-Asp-Glu-Leu) endoplasmic retic | 5.30 | 6.27 |
| 10 | 414219 | W20010 | Hs.75823 | ALL1-fused gene from chromosome 1q | 5.16 | 5.13 |
| | 426600 | NM_003378 | Hs.171014 | VEGF nerve growth factor inducible | 5.05 | 13.72 |
| | 415444 | BE247295 | Hs.78452 | solute carrier family 20 (phosphate tran | 5.03 | 4.93 |
| | 436701 | AW959032 | | ESTs, Moderately similar to I78885 serin | 5.03 | 3.42 |
| | 406648 | AA563730 | Hs.277477 | major histocompatibility complex, class | 4.99 | 3.36 |
| 15 | 410850 | AW362867 | Hs.302738 | Homo sapiens cDNA: FLJ21425 fs, clone C | 4.98 | 5.30 |
| | 418299 | AA279530 | Hs.83968 | integrin, beta 2 (antigen CD18 (p95), ly | 4.98 | 4.85 |
| | 432469 | AL080084 | | CGT-100 protein | 4.97 | 4.46 |
| | 404854 | | | Target Exon | 4.85 | 3.49 |
| | 415701 | NM_003878 | Hs.78619 | gamma-glutamyl hydrolase (conjugase, fol | 4.82 | 4.90 |
| 20 | 425397 | J04088 | Hs.156346 | topoisomerase (DNA) II alpha (170kD) | 4.81 | 5.26 |
| | 408958 | T99607 | Hs.49346 | signal recognition particle 54kD | 4.78 | 2.34 |
| | 453949 | AU077146 | Hs.36927 | heat shock 105kD | 4.78 | 5.18 |
| | 458079 | AU796870 | Hs.54277 | DNA segment on chromosome X (unique) 992 | 4.77 | 4.13 |
| | 440245 | AK001913 | Hs.7100 | hypothetical protein | 4.74 | 3.32 |
| 25 | 412228 | AW503785 | Hs.73792 | complement component (3d/Epstein Barr vi | 4.74 | 1.55 |
| | 417834 | BE172058 | Hs.82689 | tumor rejection antigen (gp96) 1 | 4.73 | 4.25 |
| | 451003 | AF058696 | Hs.25812 | Nijmegen breakage syndrome 1 (nibrin) | 4.67 | 4.69 |
| | 424571 | BE379766 | | polymerase (RNA) II (DNA directed) polyp | 4.62 | 3.02 |
| | 434203 | BE262677 | Hs.283558 | hypothetical protein PRO1855 | 4.61 | 5.45 |
| 30 | 452268 | NM_003512 | Hs.28777 | H2A histone family, member L | 4.60 | 2.88 |
| | 421311 | N71848 | Hs.283609 | hypothetical protein PRO2032 | 4.60 | 3.24 |
| | 410491 | AA465131 | Hs.64001 | Homo sapiens clone 25218 mRNA sequence | 4.60 | 4.34 |
| | 425706 | AW406678 | Hs.122559 | hypothetical protein FLJ22570 | 4.59 | 3.58 |
| | 450293 | N36754 | Hs.171118 | hypothetical protein FLJ00026 | 4.57 | 3.82 |
| 35 | 406836 | AW514501 | Hs.156110 | immunoglobulin kappa constant | 4.57 | 9.27 |
| | 413441 | AJ929374 | Hs.75367 | Src-like-adaptor | 4.53 | 3.60 |
| | 431129 | AL137751 | Hs.263671 | Homo sapiens mRNA; cDNA DKFZp434i0812 (f | 4.48 | 4.89 |
| | 418506 | AA084248 | Hs.85339 | G protein-coupled receptor 39 | 4.47 | 3.72 |
| 40 | 411060 | NM_006074 | Hs.318501 | Homo sapiens mRNA full length insert cDN | 4.47 | 3.96 |
| | 417501 | AL041219 | Hs.82222 | sema domain, immunoglobulin domain (fg) | 4.45 | 2.40 |
| | 437763 | AA469369 | Hs.5831 | tissue inhibitor of metalloproteinase 1 | 4.43 | 4.27 |
| | 448883 | BE614989 | Hs.7503 | hypothetical protein FLJ14153 | 4.42 | 3.91 |
| | 417274 | N92036 | Hs.81848 | RAD21 (S. pombe) homolog | 4.41 | 3.80 |
| 45 | 419285 | D31887 | Hs.89868 | KIAA0062 protein | 4.40 | 3.20 |
| | 418321 | D63477 | Hs.84087 | KIAA0143 protein | 4.38 | 2.79 |
| | 430154 | AW583058 | Hs.234726 | serine (or cysteine) proteinase inhibito | 4.37 | 3.86 |
| | 428450 | NM_014791 | Hs.184339 | KIAA0175 gene product | 4.36 | 4.65 |
| | 428297 | AA236291 | Hs.183583 | serine (or cysteine) proteinase inhibito | 4.36 | 3.42 |
| 50 | 447232 | AW499834 | Hs.327 | interleukin 10 receptor, alpha | 4.36 | 3.31 |
| | 409598 | NM_014018 | Hs.55097 | mitochondrial ribosomal protein S28 | 4.35 | 3.10 |
| | 442432 | BE093589 | Hs.38178 | hypothetical protein FLJ23468 | 4.34 | 5.61 |
| | 407047 | X65965 | | gb:H.sapiens SOD-2 gene for manganese su | 4.33 | 3.31 |
| | 443991 | NM_002250 | Hs.10082 | potassium intermediate/small conductance | 4.33 | 3.57 |
| 55 | 452322 | BE566343 | Hs.28988 | glutaredoxin (thioltransferase) | 4.32 | 2.20 |
| | 420991 | AW504814 | Hs.287379 | Homo sapiens mRNA for FLJ001111 protein, | 4.32 | 3.60 |
| | 449722 | BE280074 | Hs.23960 | cyclin B1 | 4.31 | 5.79 |
| | 408380 | AF123050 | Hs.44532 | diubiquitin | 4.30 | 3.62 |
| | 427127 | AW802282 | Hs.22265 | pyruvate dehydrogenase phosphatase | 4.28 | 4.18 |
| 60 | 417933 | X02308 | Hs.82962 | thymidylate synthetase | 4.28 | 5.06 |
| | 432828 | AB042326 | Hs.287402 | chondroitin 4-sulfotransferase | 4.25 | 4.15 |
| | 450306 | AL080080 | Hs.24766 | thioredoxin domain-containing | 4.24 | 3.15 |
| | 440266 | AA088809 | Hs.19525 | hypothetical protein FLJ22794 | 4.23 | 3.65 |
| | 407951 | W77762 | Hs.79015 | antigen identified by monoclonal antibod | 4.22 | 4.21 |
| 65 | 427337 | Z46223 | Hs.176663 | Fc fragment of IgG, low affinity IIb, r | 4.20 | 4.11 |
| | 409889 | AW361666 | Hs.49500 | KIAA0746 protein | 4.20 | 4.26 |
| | 449626 | AA774247 | Hs.301637 | zinc finger protein 258 | 4.19 | 2.65 |
| | 422846 | BE513934 | Hs.1583 | neutrophil cytosolic factor 1 (47kD, chr | 4.18 | 6.80 |
| | 415726 | T89844 | Hs.78712 | aminolevulinic acid, synthase 1 | 4.16 | 4.28 |
| 70 | 444207 | AJ565004 | | cathepsin D (lysosomal aspartyl protease | 4.16 | 1.89 |
| | 416980 | AA381133 | Hs.80684 | high-mobility group (nonhistone chromoso | 4.14 | 3.32 |
| | 438718 | AL040058 | Hs.6375 | uncharacterized hypothalamus protein HT0 | 4.14 | 3.02 |
| | 437802 | AJ475995 | Hs.122910 | ESTs | 4.12 | 4.18 |
| | 446392 | AF142419 | Hs.15020 | homolog of mouse quaking QKI (KH domain | 4.12 | 3.87 |
| | 409451 | AA382169 | Hs.54483 | N-myc (and STAT) interactor | 4.11 | 3.80 |
| 75 | 427247 | AW504221 | Hs.174103 | integrin, alpha L (antigen CD11A (p180), | 4.11 | 5.71 |
| | 414359 | M62194 | Hs.75929 | cadherin 11, type 2, OB-cadherin (osteob | 4.10 | 4.25 |
| | 450071 | AA018283 | Hs.24359 | Homo sapiens cDNA FLJ11174 fs, clone PL | 4.10 | 2.91 |
| | 452882 | AW972990 | Hs.196270 | folate transporter/carrier | 4.10 | 4.25 |
| | 414522 | AW518944 | Hs.76325 | immunoglobulin J chain | 4.09 | 3.99 |
| 80 | 407756 | AA116021 | Hs.38260 | ubiquitin specific protease 18 | 4.09 | 4.60 |
| | 405506 | | | Target Exon | 4.08 | 3.64 |
| | 444677 | AL110212 | Hs.301005 | purine-rich element binding protein B | 4.07 | 2.43 |
| | 417497 | AW402482 | Hs.82212 | CD53 antigen | 4.07 | 6.55 |
| | 413715 | AW851121 | Hs.75497 | Homo sapiens cDNA: FLJ22139 fs, clone H | 4.06 | 3.27 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|------|
| | 421508 | NM_004833 | Hs.105115 | absent in melanoma 2 | 4.05 | 4.39 |
| | 408688 | AI634522 | Hs.152925 | KIAA1268 protein | 4.05 | 3.32 |
| | 439453 | BE264974 | Hs.6566 | thyroid hormone receptor interactor 13 | 4.04 | 3.53 |
| 5 | 445701 | AF055581 | Hs.13131 | lymphocyte adaptor protein | 4.02 | 4.20 |
| | 451131 | AI267586 | Hs.268012 | fatty-acid-Coenzyme A ligase, long-chain | 4.01 | 3.96 |
| | 449291 | BE176893 | Hs.23440 | KIAA1105 protein | 4.01 | 2.34 |
| | 443071 | AL080021 | Hs.8986 | complement component 1, q subcomponent | 4.00 | 6.97 |
| | 417615 | BE548641 | Hs.82314 | hypoxanthine phosphoribosyltransferase 1 | 3.99 | 4.27 |
| 10 | 408246 | N55669 | Hs.333823 | mitochondrial ribosomal protein L13 | 3.98 | 3.66 |
| | 408819 | AW163483 | Hs.48320 | double ring-finger protein, Dorfin | 3.98 | 3.76 |
| | 424058 | AL121516 | Hs.138617 | thyroid hormone receptor interactor 12 | 3.97 | 2.38 |
| | 418942 | AI566004 | Hs.141269 | Homo sapiens cDNA: FLJ21550 fis, clone C | 3.97 | 3.40 |
| | 424756 | AW504657 | Hs.152931 | tamin B receptor | 3.93 | 2.67 |
| 15 | 421958 | AA357185 | Hs.105918 | ras homolog gene family, member H | 3.89 | 2.39 |
| | 440692 | AL031591 | Hs.7370 | phosphatidylinositol transfer protein, b | 3.88 | 3.23 |
| | 433001 | AF217513 | Hs.279905 | clone HQ0310 PRO0310p1 | 3.88 | 4.24 |
| | 418255 | AW135405 | Hs.37251 | ESTs | 3.87 | 2.53 |
| | 444371 | BE540274 | Hs.239 | forkhead box M1 | 3.86 | 4.29 |
| 20 | 450515 | AW304226 | | biphenyl hydrolase-like (serine hydrolas | 3.85 | 3.73 |
| | 416114 | AI695549 | Hs.183868 | glucuronidase, beta | 3.85 | 3.74 |
| | 440596 | H13032 | Hs.103378 | hypothetical protein MGC11034 | 3.84 | 1.90 |
| | 417020 | T78413 | | heterogeneous nuclear ribonucleoprotein | 3.82 | 2.04 |
| | 448503 | BE243146 | Hs.21332 | BTB (POZ) domain containing 1 | 3.81 | 3.07 |
| 25 | 446506 | AI123118 | Hs.15159 | chemokine-like factor, alternatively spl | 3.81 | 3.69 |
| | 417059 | AL037672 | Hs.81071 | extracellular matrix protein 1 | 3.80 | 6.01 |
| | 410668 | BE379794 | Hs.159551 | hypothetical protein | 3.80 | 5.22 |
| | 420107 | AL043980 | Hs.7886 | pellino (Drosophila) homolog 1 | 3.79 | 3.93 |
| | 446071 | N51527 | Hs.13659 | hypothetical protein DKFZp586F2423 | 3.79 | 2.74 |
| | 419731 | S47242 | Hs.92909 | SON DNA binding protein | 3.77 | 1.85 |
| 30 | 443710 | AI928136 | Hs.9691 | Homo sapiens cDNA: FLJ23249 fis, clone C | 3.77 | 4.98 |
| | 406837 | R70292 | Hs.156110 | immunoglobulin kappa constant | 3.77 | 7.42 |
| | 436481 | AA379597 | Hs.5199 | HSPC150 protein similar to ubiquitin-con | 3.76 | 3.55 |
| | 419381 | AB023420 | Hs.90093 | heat shock 70kD protein 4 | 3.76 | 3.81 |
| 35 | 423979 | AF229181 | Hs.136644 | CS box-containing WD protein | 3.76 | 3.97 |
| | 402474 | | | NM_004079:Homo sapiens cathepsin S (CTSS | 3.76 | 4.01 |
| | 412828 | AL133396 | Hs.74621 | prion protein (p27-30) (Creutzfeld-Jakob | 3.75 | 3.77 |
| | 454080 | AI199711 | Hs.576 | fucosidase, alpha-L-1, tissue | 3.74 | 6.15 |
| | 408085 | N25929 | Hs.342849 | ADP-ribosylation factor-like 5 | 3.74 | 2.92 |
| 40 | 426096 | D87436 | Hs.166318 | lipin 2 | 3.72 | 2.98 |
| | 417105 | X60992 | Hs.81226 | CD6 antigen | 3.72 | 2.78 |
| | 418322 | AA284166 | Hs.84113 | cyclin-dependent kinase inhibitor 3 (CDK | 3.72 | 3.37 |
| | 447735 | AA775268 | Hs.6127 | Homo sapiens cDNA: FLJ23020 fis, clone L | 3.70 | 4.09 |
| | 409264 | NM_014937 | Hs.52463 | KIAA0966 protein | 3.69 | 4.79 |
| 45 | 429170 | NM_001394 | Hs.2359 | dual specificity phosphatase 4 | 3.69 | 2.94 |
| | 428398 | AI249368 | Hs.98558 | ESTs | 3.68 | 3.82 |
| | 423494 | AW504365 | Hs.24143 | Wiskott-Aldrich syndrome protein interac | 3.67 | 3.52 |
| | 413235 | BE243445 | Hs.75248 | topoisomerase (DNA) II beta (180kD) | 3.67 | 2.79 |
| | 423712 | W46802 | Hs.81988 | disabled (Drosophila) homolog 2 (mitogen | 3.66 | 3.42 |
| 50 | 409703 | NM_006187 | Hs.56009 | Z'-5-oligoadenylate synthetase 3 (100 k | 3.66 | 6.44 |
| | 447225 | R62676 | Hs.17820 | Rho-associated, coiled-coil containing p | 3.65 | 2.93 |
| | 414829 | AA321568 | Hs.77436 | pleckstrin | 3.65 | 2.30 |
| | 400219 | | | Eos Control | 3.64 | 2.76 |
| | 437239 | AW503395 | Hs.5541 | ATPase, Ca transporting, ubiquitous | 3.63 | 2.73 |
| 55 | 422445 | M23114 | Hs.1526 | ATPase, Ca transporting, cardiac muscle, | 3.62 | 3.60 |
| | 449971 | AA807346 | Hs.288581 | Homo sapiens cDNA FLJ14296 fis, clone PL | 3.62 | 3.62 |
| | 424460 | BE275979 | Hs.296014 | polymerase (RNA) II (DNA directed) polyp | 3.62 | 3.06 |
| | 427609 | AK000436 | Hs.179791 | hypothetical protein FLJ20429 | 3.62 | 2.31 |
| | 400750 | | | Target Exon | 3.61 | 2.74 |
| 60 | 424541 | AW392551 | Hs.180559 | ESTs, Weakly similar to A56194 thromboxa | 3.61 | 2.25 |
| | 427051 | BE178110 | Hs.173374 | Homo sapiens cDNA FLJ10500 fis, clone NT | 3.60 | 4.20 |
| | 433867 | AK000596 | Hs.3618 | hippocampin-like 1 | 3.59 | 4.19 |
| | 421986 | AL137438 | Hs.110454 | SEC15 (S. cerevisiae)-like | 3.59 | 1.58 |
| | 414841 | H55601 | Hs.77490 | glutathione S-transferase theta 1 | 3.58 | 1.00 |
| 65 | 429693 | BE254962 | Hs.211612 | SEC24 (S. cerevisiae) related gene famil | 3.57 | 3.00 |
| | 425204 | NM_002436 | Hs.1861 | membrane protein, palmitoylated 1 (55kD) | 3.56 | 3.09 |
| | 441669 | R78195 | Hs.29692 | Homo sapiens cDNA FLJ11436 fis, clone HE | 3.56 | 3.26 |
| | 442043 | BE567620 | Hs.99210 | ESTs | 3.55 | 3.56 |
| | 406636 | L12064 | | gb:Homo sapiens (clone WR4.12VL) an6-th | 3.55 | 3.83 |
| 70 | 446341 | AL040763 | Hs.310735 | ESTs, Moderately similar to ALU7_HUMAN A | 3.54 | 3.52 |
| | 432485 | N90866 | Hs.276770 | CDW52 antigen (CAMPATH-1 antigen) | 3.54 | 4.66 |
| | 422765 | AW409701 | Hs.1578 | baculoviral IAP repeat-containing 5 (sur | 3.54 | 3.25 |
| | 412630 | AA738437 | Hs.26226 | Homo sapiens cDNA: FLJ21286 fis, clone C | 3.54 | 1.87 |
| | 432841 | M93425 | Hs.62 | protein tyrosine phosphatase, non-recept | 3.53 | 3.96 |
| 75 | 425177 | AF127577 | Hs.155017 | nuclear receptor interacting protein 1 | 3.53 | 3.40 |
| | 426643 | AA857131 | Hs.171595 | HIV TAT specific factor 1 | 3.51 | 2.21 |
| | 420137 | AA306478 | Hs.95327 | CD3D antigen, delta polypeptide (TIT3 co | 3.51 | 2.51 |
| | 429248 | U96759 | Hs.198307 | von Hippel-Lindau binding protein 1 | 3.51 | 2.85 |
| | 452852 | AK001972 | Hs.30822 | hypothetical protein FLJ11110 | 3.51 | 2.71 |
| 80 | 451791 | Z78407 | Hs.27023 | vesicle transport-related protein | 3.49 | 2.91 |
| | 418310 | AA814100 | Hs.86693 | ESTs | 3.49 | 1.45 |
| | 406868 | AA505445 | Hs.300697 | immunoglobulin heavy constant gamma 3 (G | 3.48 | 6.81 |
| | 400200 | | | NM_002788:Homo sapiens proteasome (pros | 3.48 | 2.51 |
| | 438746 | AI885815 | Hs.184727 | Human melanoma-associated antigen p97 (m | 3.47 | 6.94 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|-------|
| 5 | 441646 | AB023169 | Hs.7935 | KIAA0952 protein | 3.47 | 3.38 |
| | 427968 | A1857607 | Hs.181301 | cathepsin S | 3.45 | 2.71 |
| | 440201 | AL359588 | Hs.7041 | hypothetical protein DKFZp762B226 | 3.45 | 3.45 |
| | 434608 | AA805443 | Hs.179909 | hypothetical protein FLJ22995 | 3.44 | 3.68 |
| | 427527 | A1809057 | Hs.153261 | immunoglobulin heavy constant mu | 3.44 | 6.70 |
| | 413385 | M34455 | Hs.840 | indoleamine-pyrrole 2,3 dioxygenase | 3.44 | 2.72 |
| | 435550 | A1224456 | Hs.324507 | H.sapiens polyA site DNA | 3.43 | 2.76 |
| | 453857 | AL080235 | Hs.35861 | DKFZP586E1621 protein | 3.43 | 3.64 |
| 10 | 423392 | AA195037 | Hs.169341 | HTPAP protein | 3.43 | 2.29 |
| | 418460 | M26315 | Hs.85258 | CD8 antigen, alpha polypeptide (p32) | 3.43 | 2.78 |
| | 453915 | AA588721 | Hs.286218 | ribosomal protein L44 | 3.41 | 3.06 |
| | 442485 | BE092285 | Hs.29724 | hypothetical protein FLJ13187 | 3.41 | 4.23 |
| | 432606 | NM_002104 | Hs.3066 | granzyme K (serine protease, granzyme 3; | 3.40 | 3.93 |
| 15 | 417410 | AF063020 | Hs.82110 | PC4 and SFRS1 interacting protein 1 | 3.40 | 2.12 |
| | 436810 | AA353044 | Hs.5321 | ARP3 (actin-related protein 3, yeast) ho | 3.40 | 4.70 |
| | 422545 | X02761 | Hs.287820 | fibronectin 1 | 3.39 | 7.58 |
| | 409142 | AL136877 | Hs.50758 | SMC4 (structural maintenance of chromoso | 3.36 | 4.12 |
| | 434826 | AF155661 | Hs.22265 | pyruvate dehydrogenase phosphatase | 3.34 | 5.05 |
| 20 | 448410 | AK000227 | Hs.21126 | hypothetical protein FLJ20220 | 3.33 | 4.31 |
| | 416065 | BE267931 | Hs.78996 | proliferating cell nuclear antigen | 3.33 | 4.60 |
| | 432642 | BE297635 | Hs.3069 | heat shock 70kD protein 9B (mortalin-2) | 3.32 | 4.49 |
| | 425234 | AW152225 | Hs.165909 | ESTs, Weakly similar to I38022 hypotheri | 3.24 | 4.22 |
| | 43623 | AA345519 | Hs.9641 | complement component 1, q subcomponent, | 3.23 | 12.31 |
| 25 | 426490 | NM_001621 | Hs.170087 | aryl hydrocarbon receptor | 3.23 | 5.07 |
| | 443958 | BE241880 | Hs.10029 | cathepsin C | 3.16 | 4.97 |
| | 412577 | Z22968 | Hs.74076 | CD163 antigen | 3.14 | 4.75 |
| | 414050 | NM_004766 | Hs.75724 | coatomer protein complex, subunit beta 2 | 3.13 | 4.00 |
| | 421633 | AF121860 | Hs.106260 | sorting nexin 10 | 3.12 | 4.45 |
| 30 | 413936 | AF113676 | Hs.297681 | serine (or cysteine) proteinase inhibito | 3.11 | 4.00 |
| | 428797 | AA496205 | Hs.193700 | Homo sapiens mRNA; cDNA DKFZp586I0324 (f | 3.10 | 4.03 |
| | 430314 | AA369601 | Hs.239138 | pre-B-cell colony-enhancing factor | 3.06 | 4.49 |
| | 430413 | AW842182 | Hs.241392 | small inducible cytokine A5 (RANTES) | 3.04 | 4.98 |
| | 418526 | BE019020 | Hs.85838 | solute carrier family 16 (monocarboxylic | 3.03 | 4.49 |
| 35 | 452139 | AA099969 | Hs.16331 | Homo sapiens cDNA: FLJ21482 fis, clone C | 3.01 | 4.75 |
| | 439237 | AW408158 | Hs.318893 | ESTs, Weakly similar to A47582 B-cell gr | 2.95 | 5.55 |
| | 422684 | BE561617 | Hs.119192 | H2A histone family, member Z | 2.94 | 4.64 |
| | 406782 | AA430373 | | gb:zw20f11.s1 Soares ovary tumor NbHOT H | 2.93 | 10.28 |
| 40 | 438549 | BE386801 | Hs.21858 | trinucleotide repeat containing 3 | 2.91 | 5.40 |
| | 450455 | AL117424 | Hs.25035 | chloride intracellular channel 4 | 2.90 | 4.86 |
| | 427528 | AU077143 | Hs.179565 | minichromosome maintenance deficient (S. | 2.89 | 4.04 |
| | 422530 | AW972300 | Hs.118110 | bone marrow stromal cell antigen 2 | 2.87 | 9.61 |
| | 423605 | AF047826 | Hs.129887 | cadherin 19, type 2 | 2.83 | 4.86 |
| | 410231 | AA314163 | Hs.61153 | proteasome (prosome, macropain) 26S subu | 2.82 | 5.02 |
| 45 | 419956 | AL137939 | Hs.40096 | cadherin 19, type 2 | 2.80 | 4.30 |
| | 416511 | NM_006762 | Hs.79356 | Lysosomal-associated multispanning membr | 2.79 | 5.80 |
| | 429732 | U20158 | Hs.2488 | lymphocyte cytosolic protein 2 (SH2 doma | 2.78 | 4.21 |
| | 448517 | AA082750 | Hs.42194 | hypothetical protein FLJ22649 similar to | 2.78 | 4.23 |
| | 416784 | AA334592 | Hs.79914 | tumican | 2.78 | 4.40 |
| 50 | 427792 | M63928 | Hs.180841 | tumor necrosis factor receptor superfam | 2.77 | 4.23 |
| | 412140 | AA219691 | Hs.73625 | RAB6 interacting, kinesin-like (rabkines | 2.77 | 4.17 |
| | 427080 | AW068287 | Hs.301175 | ras-related C3 botulinum toxin substrate | 2.76 | 4.43 |
| | 446272 | BE268912 | Hs.14601 | hematopoietic cell-specific Lyn substrat | 2.75 | 4.20 |
| | 437179 | AA393508 | | serologically defined colon cancer antig | 2.74 | 4.07 |
| 55 | 429402 | AF116571 | Hs.201671 | SRY (sex determining region Y)-box 13 | 2.72 | 4.63 |
| | 421360 | AA297012 | Hs.103839 | erythrocyte membrane protein band 4.1-i | 2.71 | 4.93 |
| | 409202 | AA236881 | Hs.51043 | hexosaminidase B (beta polypeptide) | 2.68 | 4.15 |
| | 426124 | A1268389 | Hs.250697 | phosphatidylinositol glycan, class F | 2.68 | 4.00 |
| | 422672 | X12784 | Hs.119129 | collagen, type IV, alpha 1 | 2.67 | 4.72 |
| 60 | 417389 | BE260964 | Hs.82045 | midkine (neurite growth-promoting factor | 2.65 | 7.77 |
| | 409415 | AA579258 | Hs.6083 | Homo sapiens cDNA: FLJ21026 fis, clone C | 2.65 | 4.47 |
| | 410341 | AW499885 | Hs.42915 | ARP2 (actin-related protein 2, yeast) ho | 2.64 | 5.61 |
| | 433027 | AF191018 | Hs.279923 | putative nucleotide binding protein, est | 2.63 | 4.34 |
| | 424687 | J05070 | Hs.151738 | matrix metalloproteinase 9 (gelatinase B | 2.62 | 4.95 |
| 65 | 409430 | R21945 | Hs.346735 | splicing factor, arginine/serine-rich 5 | 2.60 | 6.00 |
| | 424779 | AL046851 | Hs.153053 | CD37 antigen | 2.60 | 4.27 |
| | 409354 | N68188 | Hs.159472 | Homo sapiens cDNA: FLJ22224 fis, clone H | 2.60 | 4.64 |
| | 427550 | BE242818 | Hs.311609 | nuclear RNA helicase, DECD variant of DE | 2.57 | 4.27 |
| | 426143 | BE379836 | | proleasome (prosome, macropain) subunit, | 2.56 | 4.20 |
| 70 | 421563 | NM_006433 | Hs.105806 | granulysin | 2.56 | 4.13 |
| | 425593 | AA278921 | Hs.1908 | proteoglycan 1, secretory granule | 2.55 | 5.46 |
| | 428169 | A1928984 | Hs.182793 | golgi phosphoprotein 2 | 2.54 | 5.78 |
| | 429800 | AA333375 | Hs.223014 | antizyme inhibitor | 2.50 | 5.15 |
| | 407241 | M34516 | | gb:Human omega light chain protein 14.1 | 2.50 | 4.98 |
| 75 | 421739 | AB004550 | Hs.107526 | UDP-Gal:betaGlcNAc beta 1,4- galactosylt | 2.45 | 5.58 |
| | 412819 | T25829 | Hs.24048 | FK506 binding protein precursor | 2.45 | 7.20 |
| | 412025 | A1827451 | Hs.24143 | Wiskott-Aldrich syndrome protein interac | 2.44 | 4.11 |
| | 435523 | T62849 | Hs.11090 | membrane-spanning 4-domains, subfamily A | 2.44 | 4.67 |
| | 445350 | AF052112 | Hs.12540 | lysophospholipase I | 2.44 | 5.44 |
| 80 | 449296 | AL137257 | Hs.23458 | Homo sapiens cDNA: FLJ23015 fis, clone L | 2.41 | 4.31 |
| | 440065 | W03476 | Hs.266331 | hypothetical protein MGC4595 | 2.41 | 4.25 |
| | 400223 | | | Eos Control | 2.39 | 5.68 |
| | 422658 | AF231981 | Hs.250175 | homolog of yeast long chain polyunsatura | 2.39 | 6.62 |
| | 431629 | AU077025 | Hs.265827 | interferon, alpha-inducible protein (clo | 2.38 | 7.22 |

| | | | | | | |
|----|--------|-----------|-----------|---|------|-------|
| | 414622 | AI752666 | Hs.76669 | nicotinamide N-methyltransferase | 2.38 | 5.21 |
| | 415149 | X12451 | Hs.78056 | cathepsin L | 2.37 | 7.71 |
| | 435099 | AC004770 | Hs.4756 | flap structure-specific endonuclease 1 | 2.37 | 5.68 |
| 5 | 427407 | BE268649 | Hs.177766 | ADP-ribosyltransferase (NAD; poly (ADP-ribose) polymerase 2 | 2.31 | 4.89 |
| | 426432 | AF001601 | Hs.169857 | paraoxonase 2 | 2.29 | 4.83 |
| | 430555 | AI815486 | Hs.243901 | Homo sapiens cDNA FLJ20738 fs, clone HE | 2.27 | 5.03 |
| | 413869 | NM_000878 | Hs.75596 | interleukin 2 receptor, beta | 2.25 | 4.14 |
| | 412617 | AK001364 | Hs.808 | heterogeneous nuclear ribonucleoprotein | 2.21 | 4.31 |
| 10 | 447547 | NM_007229 | Hs.18842 | protein kinase C and casein kinase subst | 2.19 | 4.62 |
| | 416232 | AW502678 | Hs.79090 | exportin 1 (CRM1, yeast, homolog) | 2.18 | 4.84 |
| | 420842 | AI083668 | Hs.50601 | hypothetical protein MGC10986 | 2.14 | 4.22 |
| | 411358 | R47479 | Hs.94761 | KIAA1691 protein | 2.13 | 4.65 |
| | 428227 | AA321649 | Hs.2248 | small inducible cytokine subfamily B (Cy | 2.13 | 4.03 |
| 15 | 406687 | M31126 | | matrix metalloproteinase 11 (stromelysin | 2.11 | 4.16 |
| | 417331 | AW411297 | Hs.81972 | SHC (Src homology 2 domain-containing) 1 | 2.11 | 4.25 |
| | 450344 | AW994032 | Hs.8768 | hypothetical protein FLJ10849 | 2.11 | 4.09 |
| | 429642 | X68264 | Hs.211579 | melanoma cell adhesion molecule (MCAM) (| 2.11 | 5.42 |
| | 416448 | L13210 | Hs.79339 | lectin, galactoside-binding, soluble, 3 | 2.10 | 6.42 |
| 20 | 418613 | AA744529 | Hs.86575 | mitogen-activated protein kinase kinase | 2.10 | 4.00 |
| | 453352 | T10446 | | ESTs | 2.09 | 4.48 |
| | 409220 | BE243323 | Hs.51233 | tumor necrosis factor receptor superfam | 2.09 | 4.98 |
| | 414045 | NM_002951 | Hs.75722 | ribophorin II | 2.07 | 4.59 |
| | 422451 | AA310753 | Hs.42491 | ESTs, Weakly similar to S65657 alpha-1C- | 2.07 | 4.09 |
| 25 | 414085 | AA114016 | Hs.75746 | aldehyde dehydrogenase 1 family, member | 2.06 | 5.06 |
| | 452363 | AI582743 | Hs.94953 | Homo sapiens, Similar to complement comp | 2.04 | 11.17 |
| | 438393 | AA351815 | Hs.50740 | Homo sapiens cDNA: FLJ22272 fs, clone H | 2.03 | 4.36 |
| | 413313 | NM_002047 | Hs.283108 | glycyl-tRNA synthetase | 2.02 | 4.79 |
| | 412994 | D32257 | Hs.75113 | general transcription factor IIIA | 2.00 | 4.67 |
| 30 | 424415 | NM_001975 | Hs.146580 | enolase 2, (gamma, neuronal) | 1.98 | 4.79 |
| | 421897 | AW583693 | Hs.109253 | N-terminal acetyltransferase complex and | 1.98 | 4.17 |
| | 442159 | AW163390 | Hs.278554 | heterochromatin-like protein 1 | 1.95 | 7.53 |
| | 429451 | BE409861 | Hs.202833 | heme oxygenase (decycling) 1 | 1.95 | 4.63 |
| | 416967 | BE616731 | Hs.80645 | interferon regulatory factor 1 | 1.95 | 4.31 |
| 35 | 400203 | | | Eos Control | 1.94 | 5.03 |
| | 437317 | AA748613 | Hs.311977 | ESTs, Highly similar to SWI/SNF related, | 1.94 | 4.03 |
| | 414945 | BE076358 | Hs.77667 | lymphocyte antigen 6 complex, locus E | 1.93 | 4.68 |
| | 416224 | NM_002902 | Hs.79088 | reticulocalbin 2, EF-hand calcium bindin | 1.92 | 4.12 |
| | 445411 | AL137255 | Hs.12646 | hypothetical protein FLJ22693 | 1.91 | 4.23 |
| 40 | 413945 | NM_000591 | Hs.75627 | CD14 antigen | 1.90 | 5.00 |
| | 413317 | U53225 | Hs.75283 | sorting nexin 1 | 1.89 | 4.20 |
| | 448719 | AA033627 | Hs.21858 | trinucleotide repeat containing 3 | 1.89 | 4.26 |
| | 430838 | N46664 | Hs.169395 | hypothetical protein FLJ12015 | 1.88 | 4.15 |
| | 427239 | BE270447 | | ubiquitin carrier protein | 1.87 | 5.72 |
| 45 | 450440 | AB024334 | Hs.25001 | tyrosine 3-monooxygenase/tryptophan 5-mo | 1.87 | 5.81 |
| | 433671 | AW138797 | Hs.132906 | 19A24 protein | 1.85 | 4.27 |
| | 413190 | AA151802 | Hs.40368 | adaptor-related protein complex 1, sigma | 1.85 | 5.19 |
| | 414915 | NM_002462 | Hs.76391 | myxovirus (influenza) resistance 1, homo | 1.85 | 4.31 |
| | 430040 | AW503115 | Hs.227823 | pMS protein | 1.83 | 5.57 |
| 50 | 417929 | R27219 | Hs.74647 | Human T-cell receptor active alpha-chain | 1.82 | 4.29 |
| | 414570 | Y00285 | Hs.76473 | insulin-like growth factor 2 receptor | 1.81 | 4.39 |
| | 414416 | AW409985 | Hs.76084 | hypothetical protein MGC2721 | 1.80 | 4.20 |
| | 428977 | AK001404 | Hs.194698 | cyclin B2 | 1.79 | 4.17 |
| | 418707 | U97502 | Hs.87497 | butyrophilin, subfamily 3, member A2 | 1.78 | 4.30 |
| 55 | 425367 | BE271188 | Hs.155975 | protein tyrosine phosphatase, receptor t | 1.78 | 5.44 |
| | 425811 | AL039104 | Hs.159557 | karyopherin alpha 2 (RAG cohort 1, impor | 1.77 | 5.11 |
| | 422009 | AI742845 | Hs.110713 | DEK oncogene (DNA binding) | 1.77 | 4.37 |
| | 424909 | S78187 | Hs.153752 | cell division cycle 25B | 1.74 | 5.00 |
| | 409154 | U72882 | Hs.50842 | interferon-induced protein 35 | 1.74 | 4.86 |
| 60 | 413892 | AI878921 | Hs.75607 | myristoylated alanine-rich protein kinas | 1.73 | 4.37 |
| | 444954 | AW247076 | Hs.12163 | eukaryotic translation initiation factor | 1.71 | 5.02 |
| | 424263 | M77640 | Hs.1757 | L1 cell adhesion molecule (hydrocephalus | 1.70 | 4.68 |
| | 424825 | AF207069 | Hs.153357 | procollagen-lysine, 2-oxoglutarate 5-dio | 1.70 | 4.59 |
| | 427378 | BE515037 | Hs.177556 | melanoma antigen, family D, 1 | 1.67 | 5.59 |
| 65 | 413322 | AA380158 | Hs.75290 | ADP-ribosylation factor 4 | 1.67 | 4.39 |
| | 442414 | BE408758 | Hs.8297 | ribonuclease 6 precursor | 1.65 | 4.03 |
| | 410129 | BE244074 | Hs.58831 | regulator of Fas-induced apoptosis | 1.64 | 4.24 |
| | 422976 | AU076657 | Hs.1600 | chaperonin containing TCP1, subunit 5 (e | 1.64 | 4.91 |
| | 443051 | AA333660 | Hs.71331 | hypothetical protein MGC5350 | 1.64 | 4.08 |
| 70 | 452472 | AW957300 | Hs.294142 | ESTs, Weakly similar to C55663 oligodend | 1.63 | 4.41 |
| | 446143 | BE245342 | Hs.306079 | sec61 homolog | 1.62 | 4.70 |
| | 431142 | AA852596 | Hs.250641 | tropomyosin 4 | 1.62 | 4.86 |
| | 407752 | AA573581 | Hs.13328 | ESTs | 1.62 | 4.19 |
| | 416322 | BE019494 | Hs.79217 | pyrroline-5-carboxylate reductase 1 | 1.61 | 4.51 |
| 75 | 414572 | AU077174 | Hs.288181 | cathepsin H | 1.60 | 5.25 |
| | 415017 | F06434 | Hs.77805 | ATPase, H transporting, lysosomal (vacuo | 1.60 | 4.56 |
| | 452056 | AW955065 | Hs.101150 | Homo sapiens, clone IMAGE:4054156, mRNA, | 1.58 | 5.46 |
| | 413976 | BE295452 | Hs.75655 | procollagen-proline, 2-oxoglutarate 4-di | 1.58 | 4.05 |
| | 414420 | AA043424 | Hs.76095 | immediate early response 3 | 1.58 | 4.00 |
| 80 | 419638 | N46504 | Hs.91747 | profilin 2 | 1.57 | 5.57 |
| | 422624 | BE616678 | Hs.76152 | KDEL (Lys-Asp-Glu-Leu) endoplasmic retic | 1.57 | 4.44 |
| | 415819 | AU077330 | | transcription elongation factor A (SII), | 1.55 | 4.89 |
| | 439627 | BE621702 | Hs.29076 | hypothetical protein FLJ21841 | 1.55 | 6.66 |
| | 425243 | N89487 | Hs.155291 | KIAA0005 gene product | 1.54 | 4.38 |

| | | | | | | |
|----|-------------|---------------------------------------|--|--|------|------|
| 5 | 424799 | BE550723 | Hs.153179 | fatty acid binding protein 5 (psoriasis- | 1.53 | 4.22 |
| | 416971 | R34657 | Hs.80658 | uncoupling protein 2 (mitochondrial, pro | 1.53 | 7.41 |
| | 426059 | BE292842 | Hs.166120 | interferon regulatory factor 7 | 1.51 | 4.12 |
| | 418879 | AW162087 | Hs.5437 | Tax1 (human T-cell leukemia virus type I | 1.50 | 4.02 |
| | 432999 | BE294029 | Hs.279903 | Ras homolog enriched in brain 2 | 1.50 | 4.18 |
| | 415661 | AF057307 | Hs.78575 | prosaposin (variant Gaucher disease and | 1.49 | 4.19 |
| | 428098 | AU077258 | Hs.182429 | protein disulfide isomerase-related prot | 1.49 | 5.74 |
| 10 | 452264 | AU077013 | Hs.28757 | transmembrane 9 superfamily member 2 | 1.48 | 4.53 |
| | 415198 | AW009480 | Hs.943 | natural killer cell transcript 4 | 1.47 | 4.95 |
| | 411794 | AL118577 | Hs.75658 | phosphorylase, glycogen; brain | 1.45 | 4.61 |
| | 433271 | BE621697 | Hs.14317 | nucleolar protein family A, member 3 (H | 1.45 | 4.15 |
| | 421416 | BE302950 | Hs.104125 | adenylyl cyclase-associated protein | 1.42 | 4.67 |
| | 415089 | N25117 | Hs.299465 | ribosomal protein S26 | 1.41 | 5.19 |
| 15 | 421975 | AW961017 | Hs.6459 | hypothetical protein FLJ11856 | 1.41 | 4.03 |
| | 400202 | | | NM_002795*:Homo sapiens proteasome (pros | 1.41 | 4.44 |
| | 413278 | BE563085 | Hs.833 | interferon-stimulated protein, 15 kDa | 1.41 | 4.57 |
| | 412968 | AW500508 | Hs.75102 | alanyl-tRNA synthetase | 1.40 | 4.25 |
| | 440704 | M69241 | Hs.162 | insulin-like growth factor binding prote | 1.39 | 4.11 |
| 20 | 447099 | AB030656 | Hs.17377 | coronin, actin-binding protein, 1C | 1.39 | 4.51 |
| | 428511 | AA019912 | Hs.184693 | transcription elongation factor B (SIII) | 1.38 | 4.90 |
| | 413825 | BE299181 | Hs.75564 | CD151 antigen | 1.37 | 4.44 |
| | 441737 | X79449 | Hs.7957 | adenosine deaminase, RNA-specific | 1.36 | 4.29 |
| | 440087 | W28969 | Hs.7718 | hypothetical protein FLJ22678 | 1.36 | 4.10 |
| 25 | 413566 | AW604451 | Hs.285814 | sprouty (Drosophila) homolog 4 | 1.35 | 4.50 |
| | 413019 | BE281604 | Hs.75140 | low density lipoprotein-related protein- | 1.35 | 5.14 |
| | 433026 | AW160616 | Hs.279921 | HSPC035 protein | 1.35 | 4.14 |
| | 427380 | NM_005534 | Hs.177559 | interferon gamma receptor 2 (interferon | 1.34 | 4.35 |
| | 428289 | M26301 | Hs.2253 | complement component 2 | 1.33 | 4.23 |
| 30 | 419715 | AF070523 | Hs.92384 | vitamin A responsive; cytoskeleton relat | 1.32 | 4.61 |
| | 425299 | AW505214 | Hs.155560 | calnexin | 1.31 | 4.76 |
| | 422242 | AJ251760 | Hs.273385 | guanine nucleotide binding protein (G pr | 1.30 | 5.30 |
| | 448483 | AA356392 | Hs.21321 | Homo sapiens clone FLB9213 PRO2474 mRNA, | 1.29 | 6.09 |
| | 407143 | C14076 | Hs.332329 | EST | 1.29 | 4.56 |
| 35 | 413125 | BE244589 | Hs.75207 | glyoxalase I | 1.26 | 5.56 |
| | 439053 | BE244588 | Hs.6456 | chaperonin containing TCP1, subunit 2 (b | 1.26 | 4.98 |
| | 413929 | BE501689 | Hs.75617 | collagen, type IV, alpha 2 | 1.25 | 4.76 |
| | 419663 | AA394208 | Hs.92198 | calcium-regulated heat-stable protein (2 | 1.24 | 4.56 |
| | 422166 | W72424 | Hs.112405 | S100 calcium-binding protein A9 (calgran | 1.21 | 8.96 |
| 40 | 416636 | N32536 | Hs.42645 | solute carrier family 16 (monocarboxylic | 1.21 | 4.02 |
| | 425335 | BE394327 | Hs.296267 | folistatin-like 1 | 1.18 | 4.29 |
| | 446211 | AJ021993 | Hs.14331 | S100 calcium-binding protein A13 | 1.17 | 4.32 |
| | 428642 | NM_014899 | Hs.10432 | KIAA0878 protein | 1.13 | 4.17 |
| | 454117 | BE410100 | Hs.40368 | adaptor-related protein complex 1, sigma | 1.10 | 4.00 |
| 45 | 428216 | M18468 | Hs.183037 | protein kinase, cAMP-dependent, regulato | 1.09 | 4.40 |
| | 431211 | M86849 | Hs.323733 | gap junction protein, beta 2, 26kD (conn | 1.00 | 4.70 |
| | 422158 | L10343 | Hs.112341 | protease inhibitor 3, skin-derived (SKAL | 0.98 | 4.40 |
| | 408522 | AI541214 | Hs.46320 | Small proline-rich protein SPRK (human, | 0.90 | 4.78 |
| 50 | TABLE 50B: | | | | | |
| | Pkey: | Unique Eos probeset identifier number | | | | |
| | CAT number: | Gene cluster number | | | | |
| | Accession: | Genbank accession numbers | | | | |
| 55 | Pkey | CAT Number | Accession | | | |
| | 412918 | 2764_3 | BE748583 AL519009 AV755430 AV756363 AV711927 BI523434 AI521453 AA846815 AW024829 AW949702 BG218926 AA626658 AI445621 AI452815 AA946555 AA723580 AA612925 BG105326 BG532618 AW513994 AW602165 AI373448 AA907901 AW135104 BG186662 W69205 BG219754 BE774875 BG190378 AA483698 BE066066 BE066067 BE066062 AW304207 BE939361 AW795569 BG210592 AW795644 BE939358 AW102886 BE065977 BG182971 H97042 D58090 BI046351 H81248 AI750112 AW372079 C05492 D58287 D57835 AA935095 BF700910 BG215802 BG195459 AW368467 BG495535 BG533177 BI087962 BE541579 BF130753 Z69892 AA210833 BM353155 AI473754 AI147901 AI803109 AA843296 AA418925 AI478552 AI400067 AI360304 AA418828 AW301673 BE218952 AI632804 BF433234 AA394157 BF378047 BE467036 AA319724 AW290940 AJ222671 AI347724 AW001711 AI028652 AA398130 AI470582 AI915936 AA908929 C75102 N36920 H50440 AI919034 AJ004399 AI383862 AI123606 AA648518 AA516258 AI865321 N22865 AA848101 AI589792 AA758196 AA214630 AI373911 AW194733 AA213447 AI290291 BF437165 AA757592 BF086904 AW959032 AW992466 BF446888 AI936337 BE938849 AW149064 AI701629 N90021 | | | |
| 60 | 436701 | 28142_1 | BC016556 BC016365 NM_016040 AF151858 BI561037 AW966873 AW967497 BE219482 BE018650 AW770511 AW469095 AW470133 BM150181 BM193977 AI824135 AI632346 AI129838 BM147664 AI292112 BE244667 AA251084 AW503659 BM193866 BM194481 BF446862 AL597435 BF000262 AI824386 AI990100 AW087624 AA668793 AL080084 BI335866 BI820940 BG779242 BM069854 AA282620 AA256771 AW964511 AA451623 H00335 AW370399 AW954201 BM145846 BG111760 AI750065 BG655794 AA564085 BG494071 BM069606 AI675331 BE302224 AI476466 AI625980 BM144854 AI184602 AI343932 AW135586 AW029464 AI708651 AA824243 BM145917 AA662210 AA825708 AI335858 AI273704 AA662171 N48971 AA976614 AI344537 AA609603 AI873901 AI859995 AA833589 AA765811 AI150322 AI926816 BM148634 N98862 AA019347 AA897062 AA831100 N69889 BE243185 AA282179 AA831098 AA112676 AI702407 BG621752 BE006492 AA353202 BG674256 N46921 BI048774 AW300233 BF739890 AW966879 AA393405 BF115146 AA910851 AA013099 N28878 AA287713 BE348728 BG616446 AL599953 AL599952 BF381073 AW505056 AA094735 H03813 AA287714 H27168 R54718 BF792697 AV693603 AV685883 BG619956 BF541504 BF216789 AA319751 BM452652 BF335838 AA280397 BG171509 BF571997 AA490239 AW388161 BE842126 BG165309 N71903 AI955397 AI536898 BE242040 F09718 AA772421 AA450218 M78543 BE241414 AA013098 H00297 AW576477 AW150918 AW591371 AI382711 N71926 H72497 AI285602 AA745055 AI281647 BF377670 T65207 BC532880 BG721680 AA285143 H27167 AW500235 BG494497 BF668899 | | | |
| 65 | 432469 | 58644_1 | BE379766 AW152643 AI803450 AI564343 AI092711 AI140525 AW152156 AI620740 AI554689 AI161209 AI290242 AI339745 AI374611 AI347388 AI858296 AI140529 AI366124 AA493912 AA406235 AA433889 AI057160 AW022264 AI097277 AI144126 AI080051 AA983529 AA860507 NS3469 AA843767 N81163 N70628 AA424577 AA983537 BF000304 AA626688 AA235977 AI057152 AI095366 AI095356 AA458646 AW194479 AA150439 AI375272 AW571777 AI359198 AA933793 BE614394 BE738239 AA127883 AI034344 T59504 D81608 AA908704 AW051665 AA382785 AA307208 N24639 AI370715 BE244980 AA548596 AW449675 AI191008 BF223749 N70752 N22266 AI191012 AA028001 AI419106 BF215661 BF591548 BG942356 AI474968 BE858217 BF793358 AV756758 BG483603 AI093724 BF693395 BG545345 AI744294 T59549 AA811773 BG499757 | | | |
| 70 | | | | | | |
| 75 | | | | | | |
| 80 | 424571 | 9758_1 | | | | |

| | | |
|--------|--------|---|
| 444207 | 9172_3 | BE739425 AA514221 AA865491 AI828293 AA470456 AI276739 AA169357 BE932464 AA514889 AW819039 AW819083 BE843048 AI432496 AJ470335 AI247243 BG533994 AA513783 AI887309 AA528036 AW972006 AW873028 AI924914 AI818810 AW152378 AW084946 AI521413 AI669583 BE932521 AI581370 BE180238 AW089750 AW771461 AW089714 AI590949 AI819148 AA731056 BF815234 BF911506 AA235803 AA485373 AI735658 AW393133 AW073080 AI707637 BF353320 BE843111 AW819036 AW393135 BG697291 AV648670 AV654332 AV687530 BG566964 AW807430 AI676072 AA837010 AI452482 AI625817 AW241750 BE048616 AI290928 AI680714 AA485530 BE175687 AV648513 AW130312 AI000556 AA632893 BE674169 BF001208 AA948166 BE175650 AA524664 AA490345 AI244948 AA602956 AA483492 AA918178 AW802049 BG675859 AV658871 BG678060 AI565004 AW819026 BE843092 AV686437 AV723049 BG616948 AI911647 AI743490 AI091096 BE857251 AI962074 AA040027 AW769317 AA343477 AA640112 BF876213 R82948 H26425 H82876 BE843095 BE843140 BG536641 BG617830 AA235802 BE774985 BE006682 BF342375 AA903144 BF338083 BF984258 AV657996 AI749532 BE768614 BE857252 BE932516 BE768573 AV657993 AV657777 AV752631 BE774974 T55847 BF095761 BF911511 BE710793 BE180119 BG617338 H45942 T55897 AV657718 BG563497 BE299605 AI589870 AA847598 AI470122 BF939896 AI304356 BE223045 BF435800 AI394207 AI087171 AW025415 AI079409 AW008420 AW304226 N34543 AW603578 AA526961 AA983631 N99134 AA626645 R45023 AA902417 AW672925 AA449985 AA953982 AW675471 AA010062 N80194 H14620 H28475 H26247 BF333581 AW842369 H06848 H05608 H81745 H15016 R51905 AA860423 AI860904 AA876023 AK024824 BI089104 AI596792 AI880004 BF969921 BE349489 AA843097 AI475644 AW576123 AW731676 AI339951 AI128503 AW243903 BG231992 BG052368 AW889757 BE001258 AA312566 AA476446 AU089876 AA312196 BF749977 M94859 AF070646 BG564196 BG623597 AU117332 BG680963 BI667083 AU134542 AU138830 AU761759 BG679882 AA209406 AW512644 AW514813 AI570535 BE547592 BG655418 AI459204 BF725673 BE870032 BF001968 AL047245 BF724470 BF058818 H18415 BE076849 BE076857 BE076848 BE076856 AV708687 AA380923 BE076851 F08118 L18887 BF795701 AI128383 BE908383 AW673350 AW500108 BE079837 BE929419 BF686758 AW503373 AW580528 BE005524 BI917505 BI457781 BE883812 BI668159 AA213643 AA374821 BF969974 BM480200 AU136152 BE395635 AV685066 AV693355 AL040984 AA676820 BG896408 BE082272 BE082312 C05287 BE082264 AA379850 AW672902 AI625855 BF033526 AW296557 AA728815 BE077058 AW081700 AA911707 AA362640 BE707179 BG913228 BG116191 BG752367 AA074678 AL036937 BG113760 H03524 BG681802 AI564688 AU149556 BE178600 BE813488 AI452433 AI208989 AA599392 AA580385 AA486274 AA629899 AA565929 AA114046 AA094252 BM450328 BG529968 R68320 BE076792 BE090073 BE076855 BE076859 BE076829 AA361719 AA379164 AI202712 BG223315 BE122741 BG534531 AA903494 H24978 BF085150 BE739158 AA352904 C21593 BG697597 AA134969 AA374612 BE566182 BE871838 BE076911 AW579175 BF966390 BI458494 BG386452 BG913195 BM456787 N40286 T80095 N39642 H42119 BG483861 AW381621 R69347 AW128895 AI367416 AI095285 AA099344 BE568161 AA180109 BF246488 BI561938 AW579170 BG567212 L12064 L12083 L12065 L12075 L12066 L12085 L12072 L12082 L12081 L12062 L12080 BC005265 BG176720 AW006027 BM352064 AW026316 AI635822 AI880584 AI693769 AI092211 BI492387 AI400449 AW166297 BF939910 AA232282 AW021432 AI333893 AA494308 AA854899 AI436795 AW069256 AA682373 AI092748 AA993184 AI126077 AI081758 AI240686 AI261863 AI378423 AA465237 AI376096 AA035579 AI087306 AA448162 AA129977 AI090903 AI080686 AI288939 N33004 AI801240 AW021546 AI370773 AI086064 AA669528 AI250053 AI870113 AA853181 AA858014 BG055562 BG939559 AW080765 AA032283 AW467587 H40506 D00762 NM_002788 AA641134 AI582295 AI417525 AI563975 AI093566 AI070743 AI290741 AW073417 BE875418 BM264076 BG876884 AI680535 AW854219 BE774635 AW854212 BG952443 AW854221 AW854208 BE156348 BE843056 AW858991 BE937569 BG878291 BG876450 AW819099 AI908570 AA449871 AU135228 BM478404 BF126296 AA375499 AA248473 AA430373 AA968771 AK055109 BC019085 AA187684 BG656226 BM023227 AI932311 AW264381 AA398371 BM021483 AI432433 AI375777 AI129580 AW262782 AA134107 BM023515 AA977504 AI859222 AI348454 R69725 AA975268 BM021207 AL080074 AA129218 AW207842 N90581 AA4771918 AI092259 AI028416 AI074114 BG656536 BE501677 AW193419 AA917040 W90430 AI342984 AI378957 AL036486 AW020068 BI491093 BF476021 R41226 R69631 F04125 C02343 AA115589 R56480 AI400988 R54266 R31422 BC005265 BG176720 AW006027 BM352064 AW026316 AI635822 AI880584 AI693769 AI092211 BI492387 AI400449 AW166297 BF939910 AA232282 AW021432 AI333893 AA494308 AA854899 AI436795 AW069256 AA682373 AI092748 AA993184 AI126077 AI081758 AI240686 AI261863 AI378423 AA465237 AI376096 AA035579 AI087306 AA448162 AA129977 AI090903 AI080686 AI288939 N33004 AI801240 AW021546 AI370773 AI086064 AA669528 AI250053 AI870113 AA853181 AA858014 BG055562 BG939559 AW080765 AA032283 AW467587 H40506 D00762 NM_002788 AA641134 AI582295 AI417525 AI563975 AI093566 AI070743 AI290741 AW073417 BE875418 BM264076 BG876884 AI680535 AW854219 BE774635 AW854212 BG952443 AW854221 AW854208 BE156348 BE843056 AW858991 BE937569 BG878291 BG876450 AW819099 AI908570 AA449871 AU135228 BM478404 BF126296 AA375499 AA248473 NM_005648 BC013809 L34587 BF103775 BG702618 BG716553 BI667090 BG505863 BF983483 BG718195 BI857891 BG501016 BMD43599 AL521812 BG705730 BI495545 BI495546 BF112248 BM023182 BM023123 AI075173 AW051799 BF058224 BI324885 BF436008 AA398446 BG223275 BM019558 BM023382 BG164174 N56909 BI467064 BM023464 AI207475 BM311415 BG758430 BG758807 AI934826 N90351 BG422026 BE910312 AI027778 AI081950 AI360890 BM009115 AI191829 BG759697 AI138728 AA399403 AI355589 AI364277 AA868702 AA393660 AA025127 BG027630 AA962774 AA631224 BG940967 BE791087 AA573315 W81685 AA393525 BG944103 AI393125 AI149864 AA977655 N90314 BE612839 BG491847 AI129091 AA461234 AA781198 AA759256 AA888954 AA975844 AI184099 AI018025 AA398363 AI003331 AI193380 AA626020 AI244476 AI601114 AW135664 AI206607 AW263599 AA813219 AI684453 AA878626 AA772222 AI085496 AI630226 BG940966 AI022010 AA770649 AA887624 AA491739 AA974295 BG530040 AA037091 AA019912 BI160457 H64512 BG503896 M31126 BG619646 AA367158 BI850421 AW998556 BF107010 BF969630 BF185964 AA361080 AW960026 AA147486 AI807023 AW770262 BI492178 BM145577 AA829932 AW021238 AW629477 AI337862 AI457141 BI712705 BM194542 BI712465 AI380070 N27407 AI609764 AI274152 AI206228 AI076874 AI261827 AI610982 AI469158 AI406090 AI168768 AA491675 C16249 C16232 C16209 C16275 C16274 C16243 R23287 BF246254 R66736 R23212 C14593 NM_002794 D26599 BM469989 BF305151 BG821966 BI089030 AW007738 BI222910 BM049422 BG028749 AI189162 AI831230 AW131497 BM272215 BE791105 AW778828 AA479594 AA480133 AA131997 AA284572 AA453009 BF928258 AA152127 AA393918 BF765307 BE247542 BF934697 BF341798 BE253409 AA470620 AI828932 AW379902 AV762678 AV741784 AV760892 AI025755 AA878562 AA630630 AA761708 AA862518 AA855831 AA862947 N53065 AA131821 AA293499 N23342 N26856 AI147346 AW951549 AA772963 BE245986 BG208493 AI831666 BG474873 BI023168 AU149647 BG197069 BG191102 BF304178 BE536135 AA706900 AA443583 AI002710 AW276192 AU149842 BG214797 BG198193 AW197923 AW627799 T98663 BG194788 BG214656 BF345258 BG716363 AI066528 BI546220 AA339815 AA132004 AA353826 H97858 BG187823 BF841463 AI351714 AV735966 BG196439 BG216840 BG198438 BG400762 AL532360 BE794750 AA582906 AI015067 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE138953 BE049086 AI334881 AW075006 AW075181 AA464019 AW302733 AW075100 AW073433 AI802854 AI334909 AI802853 AI345036 AI348921 AI340734 AI307478 AI251289 AW302327 AW072520 AI312145 AW073658 AW072513 AW071289 AI307559 AA876186 T29587 AI307493 AI255068 AI252868 AI252839 AW074809 AI252926 AI252160 AI251662 AI251262 AI610913 AI270787 AI270156 AI252075 AW073469 AW072901 AW072496 AW071420 AI305762 AI254764 AI802837 AI251264 AW073049 AW071311 AI340643 BE138965 BE138502 AW073456 AI334733 AI054335 BE139260 AI054302 AI054060 AI054057 AI053722 AI289711 BE139228 AW407478 AW271039 AW302085 BE041872 AI254494 AI271496 AI252427 BF178773 BF178645 AW074866 BE857822 BE739429 AA660292 AL549095 BF752457 BE783002 BG035869 AW601528 AI880413 BF593762 AA974415 AW305318 AA716501 AI936239 AI809486 AI744171 AW804992 BF108747 AW804693 BE219333 AI807707 AA306963 BG012140 BF741621 BF741619 AW062543 AA155832 AU151381 AU158043 AU150410 AU145605 AU150252 AA188205 AU153035 AI147293 AA084507 AA868165 AI887120 AI468336 AW023112 H44035 F01513 AA747672 AW779630 AA757298 R77738 AI150931 R38473 AA189022 H96984 AL550490 AW949737 AU150194 AU149258 AI749453 AW172950 AW276160 AI753604 AI421762 AW575512 AI275633 AW516120 AI340167 AI567728 AI797326 AI471532 AI074080 AI633122 AW674646 AW316571 AA258187 AA102780 AA258186 AI363307 AA862862 AI206836 AA629555 AA486287 AI185097 AI872389 BE465687 |
|--------|--------|---|

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 400202 11771_2
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A1246746 A1351453 A1189679 AA594582 A1038639 AA862764 AA544332 AA912423 AA601552 AW014502 AA694605 AW068949 BF941650
 AW297886 BF941649 A1077854 A1027442 AA705602 AW020757 B1491734 AA977135 AA653973 B1522334 AA398723 A1280083 A1419671 AW009199
 AA496011 A1144081 A1538440 BF741690 BF741680 H41990 AV724108 AW955578 BE698790 T29312 BG954488 R33179 B1832621 BF742040
 BE091493 H92122 BG614879 AW993709 A1216562 H44107 AA393530 BE173154 BG285054 BF751883 AA489308 BF741676 R64496 BE183198
 H97097 AW062534 BF036430 AW192614 BF431707 N30258 AA629072 BG954496 A1401616 BG960957
 BE873890 BF745945 AA156007 AA573157 AW874610 AA916387 N75963 BM083306 AW044671 BC013008 NM_002795 D26598 BG118716 B1910891
 BF972860 BG119842 B1094093 ALS38757 BE271653 B1856538 BE909573 BG109826 BE784430 BE899255 B1833973 BM010809 BE621321 BG684956
 BE904726 B1871370 AV708990 BF971483 BE298241 B1197007 BE272092 BG120374 AW963509 BE540572 AV744947 BG943041 AW327463
 BG472870 BE393697 N28533 AA316042 N42043 AW404246 AW892094 AA379896 AW801110 AW406977 AA379791 BG941889 BE076254 AA360459
 AA379385 AA320056 BG942618 D31230 AA308300 AA360371 AA371733 AA732937 AA494241 W32225 BF745937 A1383690 BG202360

TABLE 50C:

Pkey:

Ref:

Strand:

Nt_position:

Unique number corresponding to an Eos probeset

Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.

Indicates DNA strand from which exons were predicted.

Indicates nucleotide positions of predicted exons.

| Pkey | Ref | Strand | Nt_position |
|--------|---------|--------|-------------------------------------|
| 404854 | 7143420 | Plus | 14260-14537 |
| 405506 | 6466489 | Plus | 80014-80401,80593-81125 |
| 402474 | 7547175 | Minus | 53526-53628,55755-55920,57530-57757 |
| 400750 | 8119067 | Plus | 198991-199168,199316-199548 |

TABLE 51A: ABOUT 453 GENES UPREGULATED IN PRIMARY MELANOMAS RELATIVE TO NORMAL SKIN

Table 51A lists about 453 genes upregulated in primary melanomas relative to normal skin. Genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey:

ExAccn:

UnigenID:

Unigen Title:

R1:

R2:

Unique Eos probeset identifier number

Exemplar Accession number, Genbank accession number

Unigene number

Unigene gene title

90th percentile of primary melanoma AIs divided by 90th percentile of normal skin AIs

90th percentile of primary melanoma AIs divided by 90th percentile of normal skin AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

| Pkey | ExAccn | UnigenID | Unigen Title | R1 | R2 |
|--------|-----------|-----------|--|-------|-------|
| 452838 | U65011 | Hs.30743 | preferentially expressed antigen in mela | 14.06 | 15.56 |
| 430377 | NM_001922 | Hs.301865 | dopachrome tautomerase (dopachrome delta | 13.64 | 11.62 |
| 428555 | NM_000372 | Hs.2053 | tyrosinase (oculocutaneous albinism IA) | 13.50 | 7.98 |
| 438549 | BE386801 | Hs.21858 | trinucleotide repeat containing 3 | 12.78 | 13.80 |
| 422424 | A1186431 | Hs.296638 | prostate differentiation factor | 11.88 | 15.56 |
| 426600 | NM_003378 | Hs.171014 | VEGF nerve growth factor inducible | 10.14 | 22.46 |
| 430822 | AJ005371 | Hs.248017 | glyceraldehyde-3-phosphate dehydrogenase | 9.33 | 7.25 |
| 457211 | AW972565 | Hs.32399 | ESTs, Weakly similar to S51797 vasodilat | 8.66 | 9.62 |
| 438380 | T06430 | Hs.6194 | chondroitin sulfate proteoglycan BEHAB/b | 7.87 | 9.58 |
| 417355 | D13168 | Hs.82002 | endothelin receptor type B | 7.66 | 4.63 |
| 447210 | AF035269 | Hs.17752 | phosphatidylserine-specific phospholipas | 7.38 | 9.04 |
| 413554 | AA319146 | Hs.75426 | secretogranin II (chromogranin C) | 6.64 | 7.32 |
| 415752 | BE314524 | Hs.78776 | putative transmembrane protein | 6.46 | 4.65 |
| 421508 | NM_004833 | Hs.105115 | absent in melanoma 2 | 6.44 | 7.00 |
| 449644 | AW960707 | Hs.148324 | ESTs | 6.43 | 5.92 |
| 426312 | AF026939 | Hs.181874 | interferon-induced protein with tetratri | 6.27 | 6.47 |
| 446921 | AB012113 | Hs.16530 | small inducible cytokine subfamily A (Cy | 6.17 | 3.70 |
| 429500 | X78565 | Hs.289114 | hexabrachion (tenascin C, cytactin) | 6.09 | 3.92 |
| 414812 | X72755 | Hs.77367 | monokine induced by gamma interferon | 6.04 | 7.73 |
| 452973 | H88409 | Hs.40527 | ESTs | 6.04 | 5.89 |
| 402075 | | | ENSP00000251056: Plasma membrane calcium | 5.96 | 2.50 |
| 436856 | AI469355 | Hs.127310 | ESTs | 5.72 | 5.29 |
| 425088 | AA663372 | Hs.169395 | hypothetical protein FLJ12015 | 5.68 | 5.88 |
| 439310 | AF086120 | Hs.102793 | ESTs | 5.62 | 6.30 |
| 429170 | NM_001394 | Hs.2359 | dual specificity phosphatase 4 | 5.62 | 3.30 |
| 413670 | AB000115 | Hs.75470 | hypothetical protein, expressed in osteo | 5.50 | 4.28 |
| 409512 | AW979187 | Hs.293591 | melanoma differentiation associated prot | 5.36 | 4.14 |
| 430540 | AW245422 | | Homo sapiens cDNA: FLJ22105 fis, clone H | 5.36 | 4.64 |
| 436315 | BE390513 | Hs.27935 | hypothetical protein MGC4837 | 5.35 | 4.31 |
| 442426 | AI373062 | Hs.332938 | hypothetical protein MGC5370 | 5.28 | 4.03 |
| 435056 | AW023337 | Hs.5422 | glycoprotein M6B | 5.23 | 3.25 |
| 432828 | AB042326 | Hs.287402 | chondroitin 4-sulfotransferase | 5.20 | 5.52 |
| 430294 | AJ538226 | Hs.32976 | guanine nucleotide binding protein 4 | 5.14 | 4.82 |
| 431639 | AK000680 | Hs.266175 | phosphoprotein associated with GEMs | 5.09 | 4.35 |
| 430838 | N46664 | Hs.169395 | hypothetical protein FLJ12015 | 5.06 | 3.68 |
| 414004 | AA737033 | Hs.7155 | ESTs, Moderately similar to 2115357A TYK | 5.04 | 4.23 |
| 407366 | AF026942 | Hs.17518 | gb:Homo sapiens cig33 mRNA, partial sequ | 4.94 | 6.29 |
| 422192 | AA305159 | Hs.113019 | fts485 | 4.88 | 5.62 |
| 420208 | BE276055 | Hs.95972 | silver (mouse homolog) like | 4.88 | 6.00 |
| 446006 | NM_004403 | Hs.13530 | deafness, autosomal dominant 5 | 4.77 | 4.33 |
| 440065 | W03476 | Hs.266331 | hypothetical protein MGC4595 | 4.74 | 9.85 |
| 421574 | AJ000152 | Hs.105924 | defensin, beta 2 | 4.74 | 5.75 |
| 440274 | R24595 | Hs.7122 | scrapie responsive protein 1 | 4.72 | 2.78 |
| 417166 | AA431323 | Hs.42146 | ESTs | 4.68 | 4.29 |
| 415314 | N88802 | Hs.5422 | glycoprotein M6B | 4.65 | 3.73 |
| 443983 | H04482 | Hs.163724 | ESTs | 4.64 | 3.06 |

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|----|--------|-----------|-----------|--|------|-------|
| 5 | 432642 | BE297635 | Hs.3069 | heat shock 70kD protein 98 (mortalin-2) | 4.62 | 2.87 |
| | 437179 | AA393508 | | serologically defined colon cancer anti | 4.62 | 5.08 |
| | 417933 | X02308 | Hs.82962 | thymidylate synthetase | 4.58 | 3.02 |
| | 431620 | AA126109 | Hs.264981 | Z'-5'-oligoadenylate synthetase 2 (69-71 | 4.50 | 4.37 |
| | 431629 | AU077025 | Hs.265827 | interferon, alpha-inducible protein (clo | 4.49 | 16.82 |
| 10 | 447937 | AL109716 | Hs.20034 | Homo sapiens mRNA full length insert cDN | 4.44 | 5.95 |
| | 409264 | NM_014937 | Hs.52463 | KIAA0966 protein | 4.42 | 2.94 |
| | 434203 | BE262677 | Hs.283558 | hypothetical protein PRO1855 | 4.42 | 3.54 |
| | 422309 | U79745 | Hs.114924 | solute carrier family 16 (monocarboxylic | 4.38 | 3.30 |
| | 449722 | BE280074 | Hs.23960 | cyclin B1 | 4.32 | 4.07 |
| 15 | 446619 | AU076643 | Hs.313 | secreted phosphoprotein 1 (osteopontin, | 4.30 | 3.82 |
| | 450065 | AL050107 | Hs.24341 | transcriptional co-activator with PDZ-bi | 4.28 | 4.36 |
| | 424247 | X14008 | Hs.234734 | lysosome (renal amyloidosis) | 4.27 | 3.05 |
| | 413916 | N49813 | Hs.75615 | apoptoprotein C-II | 4.25 | 4.68 |
| | 420267 | N37030 | Hs.173337 | ESTs | 4.24 | 4.24 |
| 20 | 442739 | NM_007274 | Hs.8679 | cytosolic acyl coenzyme A thioester hydr | 4.21 | 3.00 |
| | 433576 | BE080715 | Hs.161091 | ESTs | 4.20 | 6.31 |
| | 412652 | A1801777 | | ESTs | 4.20 | 2.73 |
| | 438209 | AL120659 | Hs.6111 | aryl-hydrocarbon receptor nuclear trans | 4.20 | 5.18 |
| | 441553 | AA281219 | Hs.121296 | ESTs | 4.14 | 4.94 |
| 25 | 407856 | AA045281 | Hs.266175 | phosphoprotein associated with GEMs | 4.14 | 3.14 |
| | 439926 | AW014875 | Hs.137007 | ESTs | 4.12 | 4.76 |
| | 429903 | AL134197 | Hs.93597 | cyclin-dependent kinase 5, regulatory su | 4.12 | 4.85 |
| | 400860 | | | Target Exon | 4.10 | 5.20 |
| | 409415 | AA579258 | Hs.6083 | Homo sapiens cDNA: FLJ21028 fis, clone C | 4.08 | 6.02 |
| 30 | 416636 | N32536 | Hs.42645 | solute carrier family 16 (monocarboxylic | 4.08 | 2.42 |
| | 452826 | BE245286 | Hs.301636 | peroxisomal biogenesis factor 6 | 4.06 | 2.96 |
| | 407748 | AL079409 | Hs.38176 | KIAA0606 protein; SCN Circadian Oscillat | 4.06 | 2.28 |
| | 417632 | R20855 | Hs.5422 | glycoprotein M6B | 4.01 | 2.96 |
| | 418064 | BE387287 | Hs.83384 | S100 calcium-binding protein, beta (neur | 4.00 | 4.62 |
| 35 | 448111 | AA053486 | Hs.20315 | interferon-induced protein with tetratri | 4.00 | 2.82 |
| | 420674 | NM_000055 | Hs.1327 | butyrylcholinesterase | 4.00 | 2.90 |
| | 451668 | Z43948 | Hs.326444 | cartilage acidic protein 1 | 3.99 | 5.17 |
| | 430015 | AW768399 | | ESTs | 3.96 | 3.89 |
| | 407756 | AA116021 | Hs.38260 | ubiquitin specific protease 18 | 3.94 | 2.91 |
| 40 | 430223 | NM_002514 | Hs.235935 | nephroblastoma overexpressed gene | 3.93 | 3.89 |
| | 433364 | AU075407 | Hs.296083 | ESTs, Moderately similar to I54374 gene | 3.93 | 4.70 |
| | 448719 | AA033627 | Hs.21858 | trinucleotide repeat containing 3 | 3.92 | 7.78 |
| | 419381 | AB023420 | Hs.90093 | heat shock 70kD protein 4 | 3.87 | 3.34 |
| | 402609 | | | KIAA1209 protein | 3.87 | 3.69 |
| 45 | 408083 | BE383668 | Hs.42484 | hypothetical protein FLJ10618 | 3.86 | 4.04 |
| | 409703 | NM_006187 | Hs.56009 | Z'-5'-oligoadenylate synthetase 3 (100 k | 3.85 | 3.64 |
| | 420218 | AW958037 | | ribosomal protein L4 | 3.84 | 3.20 |
| | 434826 | AF155661 | Hs.22265 | pyruvate dehydrogenase phosphatase | 3.84 | 5.19 |
| | 410600 | AW575742 | | ESTs, Moderately similar to S65657 alpha | 3.82 | 5.74 |
| 50 | 442117 | AW664964 | Hs.128899 | ESTs; hypothetical protein for IMAGE:447 | 3.82 | 2.96 |
| | 428513 | BE220806 | Hs.184697 | Homo sapiens clone 23785 mRNA sequence | 3.82 | 4.03 |
| | 417381 | AF164142 | Hs.82042 | solute carrier family 23 (nucleobase tra | 3.80 | 3.56 |
| | 432094 | AU658580 | Hs.61426 | Homo sapiens mesenchymal stem cell prote | 3.79 | 3.23 |
| | 443105 | X96753 | Hs.9004 | chondroitin sulfate proteoglycan 4 (mela | 3.77 | 3.66 |
| 55 | 423605 | AF047826 | Hs.129887 | cadherin 19, type 2 | 3.72 | 2.28 |
| | 407846 | AA426202 | Hs.40403 | Cbp/p300-interacting transactivator, wit | 3.72 | 5.34 |
| | 442578 | AK001643 | Hs.8395 | hypothetical protein FLJ10781 | 3.71 | 3.42 |
| | 448966 | AW372914 | Hs.86149 | phosphoinositol 3-phosphate-binding prot | 3.68 | 3.31 |
| | 428227 | AA321649 | Hs.2248 | small inducible cytokine subfamily B (Cy | 3.68 | 4.24 |
| 60 | 400750 | | | Target Exon | 3.68 | 2.74 |
| | 447217 | BE465754 | Hs.17778 | neuropilin 2 | 3.66 | 3.60 |
| | 459373 | BE408266 | Hs.301406 | hypothetical protein PP3501 | 3.66 | 3.48 |
| | 419628 | H67546 | Hs.49768 | ESTs | 3.62 | 4.13 |
| | 406868 | AA505445 | Hs.300697 | immunoglobulin heavy constant gamma 3 (G | 3.61 | 4.40 |
| 65 | 421866 | M24470 | Hs.1435 | guanosine monophosphate reductase | 3.59 | 3.53 |
| | 421709 | AA159394 | Hs.107056 | CED-6 protein | 3.57 | 2.63 |
| | 438501 | Z44110 | Hs.86149 | phosphoinositol 3-phosphate-binding prot | 3.56 | 3.54 |
| | 408962 | BE386436 | Hs.44317 | SRY (sex determining region Y)-box 10 | 3.55 | 2.70 |
| | 425139 | AW630488 | Hs.25338 | protease, serine, 23 | 3.50 | 2.80 |
| 70 | 428411 | AW291464 | Hs.10338 | ESTs | 3.49 | 2.58 |
| | 452744 | AJ267652 | Hs.246107 | Homo sapiens mRNA; cDNA DKFZp434E082 (tr | 3.48 | 4.61 |
| | 411305 | BE241596 | Hs.69547 | myelin basic protein | 3.48 | 3.37 |
| | 447343 | AA256641 | Hs.236894 | ESTs, Highly similar to S02392 alpha-2-m | 3.47 | 2.68 |
| | 429954 | AJ918130 | Hs.21374 | ESTs | 3.47 | 2.63 |
| 75 | 417621 | AV654694 | Hs.82316 | interferon-induced, hepatitis C-associat | 3.46 | 2.34 |
| | 435256 | AF193766 | Hs.13872 | cytokine-like protein C17 | 3.46 | 2.47 |
| | 450534 | AJ570189 | Hs.25132 | KIAA0470 gene product | 3.42 | 3.65 |
| | 421100 | AW351839 | Hs.124660 | Homo sapiens cDNA: FLJ21763 fis, clone C | 3.41 | 2.63 |
| | 418506 | AA084248 | Hs.85339 | G protein-coupled receptor 39 | 3.40 | 4.02 |
| 80 | 442711 | AF151073 | Hs.8645 | hypothetical protein | 3.39 | 2.95 |
| | 453344 | BE349075 | Hs.44571 | ESTs | 3.38 | 2.38 |
| | 436700 | AJ693690 | Hs.301406 | hypothetical protein PP3501 | 3.36 | 4.60 |
| | 418007 | M13509 | Hs.83169 | matrix metalloproteinase 1 (interstitial | 3.36 | 2.61 |
| | 433867 | AK000596 | Hs.3618 | hippocalcin-like 1 | 3.36 | 4.26 |
| | 408393 | AW015318 | Hs.23165 | ESTs | 3.36 | 2.10 |
| | 447484 | AA464839 | Hs.292566 | hypothetical protein FLJ14697 | 3.36 | 2.49 |
| | 412828 | AL133396 | Hs.74621 | prion protein (p27-30) (Creutzfeld-Jakob | 3.35 | 2.27 |

| | | | | | | |
|----|--------|-----------|-----------|---|------|------|
| 5 | 426158 | NM_001982 | Hs.199067 | v-erb-b2 avian erythroblastic leukemia v | 3.35 | 2.58 |
| | 440325 | NM_003812 | Hs.7164 | a disintegrin and metalloproteinase doma | 3.34 | 2.55 |
| | 420602 | AF060877 | Hs.99236 | regulator of G-protein signalling 20 | 3.34 | 5.96 |
| | 439963 | AW247529 | Hs.6793 | platelet-activating factor acetylhydrola | 3.34 | 2.73 |
| | 406663 | U24683 | | immunoglobulin heavy constant mu | 3.31 | 5.21 |
| | 427540 | R12014 | Hs.20976 | ESTs | 3.30 | 3.40 |
| | 412141 | AI183838 | Hs.48938 | hypothetical protein FLJ21802 | 3.29 | 2.80 |
| | 400282 | | | NM_005313:Homo sapiens glucose regulated | 3.29 | 3.46 |
| 10 | 419870 | AW403911 | Hs.266175 | phosphoprotein associated with GEMs | 3.28 | 5.20 |
| | 416539 | Y07909 | Hs.79368 | epithelial membrane protein 1 | 3.28 | 2.79 |
| | 431518 | AA743462 | Hs.165337 | ESTs | 3.27 | 2.51 |
| | 402994 | | | NM_002463*:Homo sapiens myxovirus (infl | 3.26 | 6.38 |
| | 419956 | AL137939 | Hs.40096 | cadherin 19, type 2 | 3.26 | 4.48 |
| 15 | 421379 | Y15221 | Hs.103982 | small inducible cytokine subfamily B (Cy | 3.26 | 3.71 |
| | 444371 | BE540274 | Hs.239 | forkhead box M1 | 3.25 | 3.72 |
| | 432874 | W94322 | Hs.279651 | melanoma inhibitory activity | 3.25 | 5.33 |
| | 417282 | AA195203 | | RAB3C, member RAS oncogene family | 3.24 | 3.20 |
| | 439669 | AW602166 | Hs.222399 | CEGP1 protein | 3.24 | 2.32 |
| 20 | 422530 | AW972300 | Hs.118110 | bone marrow stromal cell antigen 2 | 3.24 | 6.20 |
| | 403817 | | | NM_015271:Homo sapiens tripartite motif | 3.23 | 3.70 |
| | 407857 | AI928445 | Hs.92254 | synaptotagmin-like 2 | 3.22 | 2.49 |
| | 426334 | BE305081 | Hs.169358 | hypothetical protein | 3.21 | 2.46 |
| | 453837 | AL138387 | Hs.256126 | baculoviral IAP repeat-containing 7 (liv | 3.19 | 5.50 |
| 25 | 427283 | AL119796 | Hs.174185 | ectonucleotide pyrophosphatase/phosphodi | 3.18 | 2.04 |
| | 437379 | AL359575 | Hs.23765 | Homo sapiens mRNA; cDNA DKFZp547M123 (fr | 3.18 | 3.73 |
| | 424090 | X99699 | Hs.139262 | XIAP associated factor-1 | 3.18 | 4.44 |
| | 410491 | AA465131 | Hs.64001 | Homo sapiens clone 25218 mRNA sequence | 3.18 | 3.26 |
| | 408418 | AW963897 | Hs.44743 | KIAA1435 protein | 3.16 | 2.21 |
| 30 | 412326 | R07566 | Hs.73817 | small inducible cytokine A3 (homologous | 3.16 | 4.04 |
| | 402829 | | | C1002500.gi6754254[refl]NP_034610.1 hea | 3.15 | 4.57 |
| | 437862 | AW978107 | Hs.5884 | Homo sapiens mRNA; cDNA DKFZp586C0224 (f | 3.15 | 3.07 |
| | 425935 | Z98200 | Hs.163724 | HSPC019 protein | 3.14 | 3.08 |
| | 417124 | BE122762 | Hs.25338 | ESTs | 3.14 | 2.73 |
| 35 | 425071 | NM_013989 | Hs.154424 | deiodinase, iodothyronine, type II | 3.11 | 2.16 |
| | 412490 | AW803564 | Hs.288850 | Homo sapiens cDNA: FLJ22528 fis, clone H | 3.10 | 2.43 |
| | 442271 | AF000652 | Hs.8180 | syndecan binding protein (syntenin) | 3.10 | 2.83 |
| | 415817 | U88967 | Hs.78867 | protein tyrosine phosphatase, receptor-t | 3.10 | 1.78 |
| | 429083 | Y09397 | Hs.227817 | BCL2-related protein A1 | 3.10 | 3.17 |
| 40 | 437673 | AW565665 | Hs.153034 | ESTs | 3.10 | 3.32 |
| | 407813 | AL120247 | Hs.40109 | KIAA0872 protein | 3.10 | 3.90 |
| | 445745 | AB007924 | Hs.13245 | KIAA0455 gene product | 3.10 | 3.35 |
| | 451537 | R56631 | Hs.26550 | retinoid X receptor, gamma | 3.09 | 4.45 |
| | 408654 | BE018882 | Hs.46721 | UCC1 protein | 3.08 | 3.65 |
| 45 | 444484 | AK002126 | Hs.11260 | hypothetical protein FLJ11264 | 3.08 | 2.12 |
| | 446019 | AI362520 | | histone deacetylase 3 | 3.08 | 2.26 |
| | 434276 | AF123659 | Hs.93605 | leucine zipper, putative tumor suppresso | 3.08 | 5.29 |
| | 427871 | AW992405 | Hs.59622 | Homo sapiens, clone IMAGE:3507281, mRNA, | 3.06 | 3.36 |
| | 403532 | | | NM_024638:Homo sapiens hypothetical prot | 3.06 | 3.37 |
| 50 | 433160 | AW207002 | Hs.134342 | TASP for testis-specific adriamycin sens | 3.04 | 3.17 |
| | 446341 | AL040763 | Hs.310735 | ESTs, Moderately similar to ALU7_HUMAN A | 3.03 | 2.98 |
| | 426501 | AW043782 | Hs.293616 | ESTs | 3.03 | 2.01 |
| | 450325 | AI935962 | Hs.91973 | ESTs | 3.02 | 2.19 |
| | 418941 | AA452970 | Hs.235527 | E1B-55kDa-associated protein 5 | 3.02 | 3.29 |
| 55 | 431797 | BE169641 | Hs.270134 | hypothetical protein FLJ20280 | 3.02 | 2.54 |
| | 442064 | AI422867 | Hs.88594 | ESTs | 3.00 | 1.96 |
| | 405451 | | | dihydropyrimidinase-like 3 | 3.00 | 2.98 |
| | 414915 | NM_002462 | Hs.76391 | myxovirus (influenza) resistance 1, homo | 2.99 | 6.41 |
| 60 | 454117 | BE410100 | Hs.40368 | adaptor-related protein complex 1, sigma | 2.98 | 3.25 |
| | 452958 | AA883929 | Hs.40527 | ESTs | 2.98 | 4.14 |
| | 427647 | W19744 | Hs.180059 | Homo sapiens cDNA FLJ20653 fis, clone KA | 2.96 | 3.30 |
| | 409190 | AU076536 | Hs.50984 | sarcoma amplified sequence | 2.96 | 2.47 |
| | 428819 | AL135623 | Hs.193914 | KIAA0575 gene product | 2.96 | 4.16 |
| | 428450 | NM_014791 | Hs.184339 | KIAA0175 gene product | 2.96 | 2.41 |
| 65 | 414219 | W20010 | Hs.75823 | ALL1-fused gene from chromosome 1q | 2.95 | 2.79 |
| | 411358 | R47479 | Hs.94761 | KIAA1691 protein | 2.95 | 4.70 |
| | 432467 | T03667 | Hs.239388 | Human DNA sequence from clone RP1-304B14 | 2.94 | 2.65 |
| | 400222 | | | NM_002082*:Homo sapiens G protein-couple | 2.94 | 2.69 |
| | 405785 | | | NM_025184*:Homo sapiens hypothetical pro | 2.94 | 2.55 |
| 70 | 409760 | AA302840 | | gb. EST10534 Adipose tissue, white 1 Homo | 2.94 | 2.57 |
| | 418113 | AI272141 | Hs.83484 | SRY (sex determining region Y)-box 4 | 2.93 | 2.52 |
| | 409038 | T97490 | Hs.50002 | small inducible cytokine subfamily A (Cy | 2.93 | 2.43 |
| | 456760 | AW961251 | Hs.127828 | guanine nucleotide binding protein (G pr | 2.92 | 3.20 |
| | 459710 | AI701596 | Hs.121592 | ESTs | 2.91 | 4.45 |
| 75 | 411395 | AA889673 | Hs.7542 | KIAA1802 protein | 2.90 | 2.72 |
| | 427528 | AU077143 | Hs.179565 | minichromosome maintenance deficient (S. | 2.90 | 2.27 |
| | 406964 | M21305 | | FGENES predicted novel secreted protein | 2.90 | 2.03 |
| | 428834 | AW899713 | Hs.339315 | ESTs | 2.89 | 3.55 |
| | 413190 | AA151802 | Hs.40368 | adaptor-related protein complex 1, sigma | 2.89 | 3.87 |
| 80 | 438619 | AB032773 | | TU12B1-TY protein | 2.88 | 2.37 |
| | 442432 | BE093589 | Hs.38178 | hypothetical protein FLJ23458 | 2.87 | 2.00 |
| | 428782 | X12830 | Hs.193400 | interleukin 6 receptor | 2.86 | 2.51 |
| | 454027 | R40192 | Hs.21527 | Human DNA sequence from clone GS1-115M3 | 2.86 | 3.07 |
| | 453107 | NM_016113 | Hs.279746 | vanilloid receptor-like protein 1 | 2.86 | 5.58 |

| | | | | | | |
|----|--------|-----------|-----------|---|------|-------|
| | 414737 | AI160386 | Hs.125087 | ESTs | 2.84 | 2.79 |
| | 412140 | AA219691 | Hs.73625 | RAB6 interacting, kinesin-like (rabkines | 2.84 | 3.80 |
| | 447735 | AA775268 | Hs.6127 | Homo sapiens cDNA: FLJ23020 fis, clone L | 2.83 | 2.11 |
| | 416091 | AF295370 | Hs.283082 | defensin, beta 3 | 2.83 | 3.32 |
| 5 | 442445 | AA082665 | Hs.209561 | KIAA1715 protein | 2.81 | 2.17 |
| | 408208 | BE018717 | | ESTs | 2.81 | 2.43 |
| | 430066 | AI929659 | Hs.237825 | signal recognition particle 72kD | 2.80 | 2.25 |
| | 424755 | AB033094 | Hs.152925 | KIAA1268 protein | 2.80 | 2.74 |
| 10 | 422616 | BE300330 | Hs.118725 | selenophosphate synthetase 2 | 2.79 | 2.01 |
| | 405506 | | | Target Exon | 2.78 | 2.65 |
| | 411619 | AI418609 | Hs.71040 | hypothetical protein FLJ20425 | 2.78 | 3.10 |
| | 400236 | | | Eos Control | 2.78 | 2.21 |
| | 452698 | NM_001295 | Hs.301921 | chemokine (C-C motif) receptor 1 | 2.78 | 3.15 |
| | 446488 | AB037782 | Hs.15119 | KIAA1361 protein | 2.78 | 2.80 |
| 15 | 439778 | AL109729 | Hs.99364 | putative transmembrane protein | 2.78 | 3.78 |
| | 420005 | AW271106 | Hs.133294 | ESTs | 2.78 | 2.86 |
| | 428642 | NM_014899 | Hs.10432 | KIAA0878 protein | 2.77 | 3.07 |
| | 453779 | N35187 | Hs.43388 | 28kD interferon responsive protein | 2.76 | 4.56 |
| 20 | 425289 | AW139342 | Hs.155530 | interferon, gamma-inducible protein 16 | 2.76 | 1.83 |
| | 437723 | AI672731 | Hs.13256 | ESTs | 2.76 | 4.23 |
| | 416730 | T99937 | | gb:ye72d04.r1 Soares fetal liver spleen | 2.76 | 2.98 |
| | 426153 | AF057169 | Hs.182771 | vitelliform macular dystrophy (Best dise | 2.76 | 3.21 |
| | 444670 | H58373 | Hs.332938 | hypothetical protein MGC5370 | 2.76 | 3.97 |
| 25 | 421351 | AU076667 | Hs.103755 | receptor-interacting serine-threonine ki | 2.74 | 3.50 |
| | 406673 | M34996 | Hs.198253 | major histocompatibility complex, class | 2.74 | 3.24 |
| | 427268 | X78520 | Hs.174139 | chloride channel 3 | 2.74 | 2.82 |
| | 428403 | AI393048 | Hs.326159 | leucine rich repeat (in FLII) interactin | 2.74 | 1.95 |
| | 409417 | AA156247 | Hs.104879 | serine (or cysteine) proteinase inhibito | 2.74 | 2.99 |
| 30 | 419705 | AW368634 | Hs.154331 | ESTs | 2.74 | 2.28 |
| | 440457 | BE387593 | Hs.21321 | Homo sapiens clone FLB9213 PRO2474 mRNA, | 2.72 | 3.60 |
| | 413599 | AJ006239 | Hs.75438 | quinoid dihydropteridine reductase | 2.72 | 2.43 |
| | 447164 | AF026941 | Hs.17518 | vipirin; similar to inflammatory respon | 2.72 | 4.77 |
| | 430594 | AK000790 | Hs.246885 | hypothetical protein FLJ20783 | 2.72 | 3.67 |
| 35 | 413278 | BE563085 | Hs.833 | interferon-stimulated protein, 15 kDa | 2.71 | 12.06 |
| | 424572 | M19650 | Hs.179600 | 2',3'-cyclic nucleotide 3' phosphodiester | 2.70 | 2.40 |
| | 409142 | AL136877 | Hs.50758 | SMC4 (structural maintenance of chromoso | 2.70 | 3.81 |
| | 425996 | W67330 | | hypothetical protein AL110115 | 2.69 | 3.85 |
| | 430441 | BE398091 | | desmoplakin (DPI, DP1) | 2.68 | 2.55 |
| 40 | 442355 | AA456539 | Hs.8262 | lysosomal-associated membrane protein 2 | 2.68 | 1.67 |
| | 421362 | AK000050 | Hs.103853 | hypothetical protein FLJ20043 | 2.68 | 2.94 |
| | 437158 | AW090198 | | KIAA1150 protein | 2.68 | 1.89 |
| | 412315 | AW936678 | | gb:PM2-DT0023-080300-004-a04 DT0023 Homo | 2.68 | 2.80 |
| | 432878 | BE386490 | Hs.279663 | Pirin | 2.68 | 2.58 |
| 45 | 408822 | AW500715 | Hs.57079 | Homo sapiens cDNA FLJ13267 fis, clone OV | 2.68 | 2.74 |
| | 426759 | AI590401 | Hs.21213 | ESTs | 2.68 | 2.35 |
| | 405486 | | | Target Exon | 2.67 | 2.70 |
| | 410326 | AI368909 | Hs.47650 | ESTs | 2.67 | 3.33 |
| | 434040 | AW444613 | Hs.288809 | hypothetical protein FLJ20159 | 2.66 | 2.54 |
| 50 | 437396 | BE140396 | Hs.21621 | hypothetical protein DKFZp7620076 | 2.66 | 1.91 |
| | 412719 | AW016610 | Hs.816 | ESTs | 2.66 | 4.21 |
| | 451708 | AI306536 | Hs.60975 | ESTs | 2.66 | 5.69 |
| | 418299 | AA279530 | Hs.83968 | integrin, beta 2 (antigen CD18 (p95), ly | 2.66 | 2.31 |
| | 425017 | AL119305 | Hs.26409 | ESTs | 2.66 | 2.73 |
| 55 | 400235 | | | NM_005336:Homo sapiens high density lipo | 2.66 | 2.29 |
| | 444809 | BE207568 | Hs.208219 | oculospian | 2.64 | 2.86 |
| | 436291 | BE568452 | Hs.344037 | protein regulator of cytokinesis 1 | 2.64 | 2.33 |
| | 406382 | | | C16001275:gi12698037 dbj BAB21837.1 (| 2.64 | 2.48 |
| | 432241 | AI937060 | Hs.6298 | KIAA1151 protein | 2.63 | 3.16 |
| 60 | 417308 | H60720 | Hs.81892 | KIAA0101 gene product | 2.63 | 2.10 |
| | 429294 | AA095971 | Hs.198793 | Homo sapiens cDNA: FLJ22463 fis, clone H | 2.62 | 2.43 |
| | 453935 | AI633770 | Hs.42572 | ESTs | 2.62 | 1.99 |
| | 401454 | | | NM_014226*:Homo sapiens renal tumor anti | 2.62 | 3.01 |
| | 436456 | AW292677 | Hs.248122 | G protein-coupled receptor 24 | 2.62 | 5.94 |
| 65 | 418478 | U38945 | Hs.1174 | cyclin-dependent kinase inhibitor 2A (me | 2.61 | 3.02 |
| | 453256 | AI565587 | Hs.32556 | KIAA0379 protein | 2.60 | 2.68 |
| | 451622 | AW139587 | Hs.30579 | Homo sapiens cDNA: FLJ23070 fis, clone L | 2.60 | 2.51 |
| | 424006 | AF054815 | Hs.137548 | CD84 antigen (leukocyte antigen) | 2.60 | 2.56 |
| | 409354 | N58188 | Hs.159472 | Homo sapiens cDNA: FLJ22224 fis, clone H | 2.59 | 3.00 |
| 70 | 425392 | N39725 | Hs.15220 | zinc finger protein 106 | 2.58 | 3.52 |
| | 427286 | AW732802 | Hs.2132 | epidermal growth factor receptor pathway | 2.58 | 1.86 |
| | 418166 | AI754416 | | Cdc42 effector protein 3 | 2.58 | 2.15 |
| | 413794 | AF234532 | Hs.61638 | myosin X | 2.58 | 2.54 |
| | 445707 | AI248720 | Hs.114390 | ESTs | 2.58 | 1.95 |
| 75 | 416640 | BE262478 | Hs.79404 | neuron-specific protein | 2.57 | 2.46 |
| | 427982 | NM_016156 | Hs.181326 | KIAA1073 protein | 2.56 | 1.74 |
| | 439453 | BE264974 | Hs.6566 | thyroid hormone receptor interactor 13 | 2.56 | 2.22 |
| | 455839 | BE145814 | | gb:MR0-HT0208-101299-202-a04 HT0208 Homo | 2.55 | 2.34 |
| | 447737 | AK000643 | Hs.19404 | DKFZP564L0862 protein | 2.55 | 2.31 |
| 80 | 423799 | AW026300 | Hs.132906 | 19A24 protein | 2.54 | 2.11 |
| | 442762 | AF035119 | Hs.8700 | deleted in liver cancer 1 | 2.54 | 2.47 |
| | 432886 | BE159028 | Hs.279704 | chromatin accessibility complex 1 | 2.54 | 3.99 |
| | 440676 | NM_004987 | Hs.112378 | LIM and senescent cell antigen-like doma | 2.54 | 2.96 |
| | 424481 | R19453 | Hs.1787 | proteolipid protein 1 (Pelizaeus-Merzbac | 2.53 | 6.98 |

| | | | | | | |
|----|--------|-----------|-----------|---|------|------|
| | 422340 | AW296219 | Hs.115325 | RAB7, member RAS oncogene family-like 1 | | |
| | 428844 | AW972635 | Hs.301904 | hypothetical protein FLJ12671 | 2.53 | 3.06 |
| | 458997 | AW937420 | | ESTs | 2.53 | 3.13 |
| 5 | 419591 | AF090900 | Hs.91393 | Homo sapiens cDNA: FLJ21887 fis, clone H | 2.53 | 1.63 |
| | 414807 | AJ738616 | Hs.77348 | hydroxyprostaglandin dehydrogenase 15-(N | 2.52 | 2.30 |
| | 429238 | NM_002849 | Hs.198288 | protein tyrosine phosphatase, receptor t | 2.52 | 1.80 |
| | 432882 | NM_013257 | Hs.279696 | serum/glucocorticoid regulated kinase-li | 2.52 | 3.02 |
| | 407260 | L09095 | | gb:Homo sapiens mRNA fragment | 2.52 | 3.05 |
| 10 | 431186 | NM_012249 | Hs.250697 | ras-like protein | 2.50 | 5.00 |
| | 417542 | J04129 | Hs.82269 | progesterone-associated endometrial prote | 2.49 | 6.16 |
| | 419556 | U29615 | Hs.91093 | chitinase 1 (chito/hiosidase) | 2.49 | 4.71 |
| | 408209 | NM_004454 | Hs.43697 | ets variant gene 5 (ets-related molecule | 2.48 | 5.77 |
| | 405885 | | | Target Exon | 2.48 | 3.77 |
| 15 | 406837 | R70292 | Hs.156110 | immunoglobulin kappa constant | 2.46 | 3.11 |
| | 412609 | Z48804 | Hs.74124 | ocular albinism 1 (Nettleship-Falls) | 2.44 | 3.10 |
| | 421633 | AF121860 | Hs.106260 | sorting nexin 10 | 2.44 | 4.90 |
| | 415929 | AA724373 | Hs.49344 | hypothetical protein FLJ11006 | 2.44 | 4.31 |
| | 413171 | AA318325 | Hs.75219 | tyrosinase-related protein 1 | 2.42 | 3.19 |
| 20 | 406621 | X57809 | Hs.8997 | immunoglobulin lambda locus | 2.37 | 3.57 |
| | 414142 | AW368397 | Hs.334485 | hemocentin (fibrin G) | 2.36 | 5.87 |
| | 410700 | AA352335 | Hs.65641 | hypothetical protein FLJ20073 | 2.36 | 3.04 |
| | 414283 | AW960011 | Hs.154993 | ESTs | 2.36 | 3.66 |
| | 453931 | AL121278 | Hs.25144 | ESTs | 2.34 | 4.95 |
| 25 | 422515 | AW500470 | Hs.117950 | multifunctional polypeptide similar to S | 2.34 | 4.18 |
| | 435292 | N20514 | Hs.172965 | ESTs | 2.32 | 3.45 |
| | 412926 | AJ879076 | Hs.75061 | macrophage myristoylated alanine-rich C | 2.32 | 4.94 |
| | 440197 | AW340708 | Hs.317714 | pallid (mouse) homolog, pallidin | 2.31 | 3.78 |
| | 425262 | D87119 | Hs.155418 | GS3955 protein | 2.30 | 3.95 |
| 30 | 439979 | AW600291 | Hs.6823 | hypothetical protein FLJ10430 | 2.29 | 5.08 |
| | 403969 | | | ENSP00000034663:Zinc finger protein 131 | 2.28 | 4.05 |
| | 421686 | AB011156 | Hs.106794 | KIAA0584 protein | 2.28 | 3.64 |
| | 432800 | BE391046 | Hs.278962 | AIM-1 protein | 2.26 | 3.31 |
| | 406782 | AA430373 | | gb:zw20f11.s1 Soares ovary tumor NbHOT H | 2.24 | 4.08 |
| 35 | 415539 | AJ733881 | Hs.72472 | BMP-R1B | 2.24 | 3.47 |
| | 447523 | BE613328 | Hs.21938 | hypothetical protein FLJ12492 | 2.22 | 3.66 |
| | 433180 | AB038651 | Hs.31854 | K562 cell-derived leucine-zipper-like pr | 2.20 | 3.43 |
| | 415825 | Y18024 | Hs.78877 | inositol 1,4,5-trisphosphate 3-kinase B | 2.20 | 3.52 |
| | 407241 | M34516 | | gb:Human omega light chain protein 14.1 | 2.19 | 3.76 |
| 40 | 422243 | AW803733 | Hs.23585 | hypothetical protein MGC12250 | 2.18 | 3.17 |
| | 417324 | AW265494 | | ESTs | 2.18 | 3.28 |
| | 412819 | T25829 | Hs.24048 | FK506 binding protein precursor | 2.16 | 5.85 |
| | 432342 | AL036128 | Hs.274404 | plasminogen activator, tissue | 2.14 | 3.49 |
| | 427923 | AW274357 | Hs.301406 | hypothetical protein PP3501 | 2.13 | 4.39 |
| 45 | 417437 | U52682 | Hs.82132 | interferon regulatory factor 4 | 2.13 | 5.48 |
| | 425535 | AB007937 | Hs.158287 | KIAA0458 gene product | 2.13 | 3.08 |
| | 429638 | AJ916662 | Hs.211577 | kinectin 1 (kinesin receptor) | 2.13 | 8.66 |
| | 409154 | U72882 | Hs.50842 | interferon-induced protein 35 | 2.12 | 3.01 |
| | 429951 | AL040521 | Hs.15220 | zinc finger protein 106 | 2.12 | 4.66 |
| 50 | 418918 | X07871 | Hs.89476 | CD2 antigen (p50), sheep red blood cell | 2.12 | 3.71 |
| | 419200 | AW966405 | | EST | 2.11 | 4.27 |
| | 416448 | L13210 | Hs.79339 | lectin, galactoside-binding, soluble, 3 | 2.11 | 3.58 |
| | 425069 | AA687465 | Hs.298184 | potassium voltage-gated channel, shaker- | 2.10 | 5.34 |
| | 445133 | AW157646 | Hs.198689 | ESTs | 2.07 | 7.86 |
| 55 | 411492 | T46848 | Hs.70337 | immunoglobulin superfamily, member 4 | 2.06 | 3.68 |
| | 408015 | AW136771 | Hs.244349 | epidermal differentiation complex protei | 2.04 | 3.36 |
| | 424412 | H15512 | Hs.10043 | hypothetical protein FLJ13074 | 2.03 | 3.41 |
| | 431657 | AJ345227 | Hs.105448 | ESTs, Weakly similar to B34087 hypothe | 2.03 | 3.82 |
| | 427536 | BE277141 | Hs.115803 | gb:G01178666F1 NIH_MGC_20 Homo sapiens c | 2.02 | 3.03 |
| 60 | 400533 | | | ENSP00000209376::PREDE65 protein (Fragmen | 2.02 | 3.09 |
| | 432680 | T47364 | Hs.278613 | interferon, alpha-inducible protein 27 | 2.00 | 3.29 |
| | 410129 | BE244074 | Hs.58831 | regulator of Fas-induced apoptosis | 1.99 | 3.07 |
| | 417312 | AW888411 | Hs.250811 | leukemia-associated phosphoprotein p18 (| 1.97 | 4.52 |
| | 423952 | AW877787 | Hs.136102 | KIAA0853 protein | 1.97 | 3.26 |
| 65 | 455705 | AW161061 | | ESTs, Weakly similar to zinc finger prot | 1.94 | 3.79 |
| | 419723 | AL120193 | Hs.339810 | longevity assurance (LAG1, S. cerevisiae | 1.93 | 3.16 |
| | 438866 | U44385 | Hs.325495 | tissue inhibitor of metalloproteinase 2 | 1.93 | 3.11 |
| | 448410 | AK000227 | Hs.21126 | hypothetical protein FLJ20220 | 1.93 | 3.47 |
| | 400292 | AA250737 | Hs.72472 | BMP-R1B | 1.92 | 3.00 |
| 70 | 436797 | AA731491 | Hs.334477 | hypothetical protein MGC14879 | 1.92 | 4.07 |
| | 406851 | AA609784 | | major histocompatibility complex, class | 1.90 | 3.04 |
| | 428437 | AV656017 | Hs.184325 | CGI-76 protein | 1.90 | 6.53 |
| | 431836 | AF178532 | Hs.271411 | beta-site APP-cleaving enzyme 2 | 1.89 | 3.39 |
| | 424687 | J05070 | Hs.151738 | matrix metalloproteinase 9 (gelatinase B | 1.89 | 4.04 |
| 75 | 426322 | J05068 | Hs.2012 | transcobalamin I (vitamin B12 binding pr | 1.87 | 3.64 |
| | 425221 | AV649864 | Hs.155188 | TATA box binding protein (TBP)-associate | 1.85 | 4.21 |
| | 420162 | BE378432 | Hs.95577 | cyclin-dependent kinase 4 | 1.85 | 3.13 |
| | 443530 | BE563088 | Hs.9552 | bindin of Arl Two | 1.85 | 3.04 |
| | 433671 | AW138797 | Hs.132906 | 19A24 protein | 1.85 | 3.20 |
| 80 | 424415 | NM_001975 | Hs.146580 | enolase 2, (gamma, neuronal) | 1.84 | 3.39 |
| | 400991 | | | Target Exon | 1.82 | 3.22 |
| | 418677 | S83308 | Hs.87224 | SRY (sex determining region Y)-box 5 | 1.82 | 4.11 |
| | 424441 | X14850 | Hs.147097 | H2A histone family, member X | 1.82 | 3.43 |
| | 424825 | AF207069 | Hs.153357 | procollagen-lysine, 2-oxoglutarate 5-dio | 1.81 | 3.12 |
| | | | | | 1.79 | 5.31 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|------|
| 5 | 425818 | AB021225 | Hs.159581 | matrix metalloproteinase 17 (membrane-in | 1.79 | 3.40 |
| | 416426 | AA180256 | Hs.210473 | Homo sapiens cDNA FLJ14872 fis, clone PL | 1.78 | 3.38 |
| | 414945 | BE076358 | Hs.77667 | lymphocyte antigen 6 complex, locus E | 1.77 | 3.69 |
| | 440942 | AW246547 | Hs.17901 | Homo sapiens, clone IMAGE:3937015, mRNA, | 1.77 | 3.12 |
| | 401591 | | | Target Exon | 1.75 | 4.30 |
| | 425923 | NM_005026 | Hs.162808 | phosphoinositide-3-kinase, catalytic, de | 1.75 | 3.68 |
| | 412844 | AJ828045 | Hs.18016 | Homo sapiens mRNA; cDNA DKFZp586H0324 (f | 1.74 | 3.53 |
| | 417237 | H86385 | Hs.81737 | palmitoyl-protein thioesterase 2 | 1.73 | 3.06 |
| 10 | 419849 | BE041436 | Hs.93379 | eukaryotic translation initiation factor | 1.72 | 4.38 |
| | 454429 | BE273437 | Hs.301406 | hypothetical protein PP3501 | 1.72 | 4.38 |
| | 440672 | AF083811 | Hs.7345 | MAD1 (mitotic arrest deficient, yeast, h | 1.72 | 3.61 |
| | 408204 | AA454501 | Hs.43666 | protein tyrosine phosphatase type IVA, m | 1.72 | 3.06 |
| | 430148 | BE387620 | Hs.234489 | lactate dehydrogenase B | 1.71 | 4.38 |
| 15 | 426502 | Y07759 | Hs.170157 | myosin VA (heavy polypeptide 12, myosin) | 1.70 | 3.13 |
| | 413317 | U53225 | Hs.75283 | sorting nexin 1 | 1.70 | 3.08 |
| | 417333 | AL157545 | Hs.173179 | bromodomain and PHD finger containing, 3 | 1.68 | 3.15 |
| | 407222 | H96850 | | gb:Y03b12.s1 Soares melanocyte 2NtHM Ho | 1.68 | 4.19 |
| | 413566 | AW604451 | Hs.285814 | sprouty (Drosophila) homolog 4 | 1.67 | 5.74 |
| | 404067 | | | Target Exon | 1.67 | 4.73 |
| 20 | 447630 | AI660149 | Hs.44865 | lymphoid enhancer-binding factor 1 | 1.66 | 3.22 |
| | 443337 | Y07604 | Hs.9235 | non-metastatic cells 4, protein expresse | 1.65 | 3.17 |
| | 427747 | AW411425 | Hs.180655 | serine/threonine kinase 12 | 1.64 | 3.35 |
| | 437912 | BE278594 | Hs.5912 | F-box only protein 7 | 1.64 | 3.24 |
| | 404140 | | | NM_006510:Homo sapiens ret finger protei | 1.64 | 3.10 |
| 25 | 414214 | D49958 | Hs.75819 | glycoprotein M5A | 1.64 | 3.45 |
| | 427239 | BE270447 | | ubiquitin carrier protein | 1.62 | 3.58 |
| | 427289 | AJ097346 | | phosphoserine aminotransferase | 1.62 | 5.89 |
| | 452923 | BE276018 | Hs.288940 | five-span transmembrane protein M83 | 1.62 | 3.23 |
| 30 | 426020 | AL110195 | Hs.166017 | microphthalmia-associated transcription | 1.62 | 4.00 |
| | 439627 | BE621702 | Hs.29076 | hypothetical protein FLJ21841 | 1.61 | 5.00 |
| | 451489 | NM_005503 | Hs.26468 | amyloid beta (A4) precursor protein-bind | 1.60 | 3.06 |
| | 414699 | AJ815523 | Hs.76930 | synuclein, alpha (non A4 component of am | 1.58 | 3.34 |
| | 411825 | AK000334 | | hypothetical protein FLJ20327 | 1.56 | 3.18 |
| 35 | 438552 | AJ245820 | Hs.6314 | type I transmembrane receptor (seizure-r | 1.56 | 3.23 |
| | 428081 | AA421048 | Hs.95011 | syntrophin, beta 1 (dystrophin-associate | 1.55 | 3.10 |
| | 401914 | | | Target Exon | 1.54 | 3.33 |
| | 424902 | NM_003866 | Hs.153687 | inositol polyphosphate-4-phosphatase, ty | 1.54 | 3.15 |
| | 441648 | H05734 | Hs.30559 | ESTs | 1.52 | 3.36 |
| 40 | 439769 | AA448828 | Hs.30596 | Homo sapiens mRNA full length insert cDN | 1.52 | 3.17 |
| | 437696 | Z83844 | Hs.5790 | hypothetical protein dJ37E16.5 | 1.52 | 4.93 |
| | 413019 | BE281604 | Hs.75140 | low density lipoprotein-related protein- | 1.52 | 3.01 |
| | 419741 | NM_007019 | Hs.93002 | ubiquitin carrier protein E2-C | 1.52 | 3.83 |
| | 422596 | AF063611 | Hs.118633 | 2'-5'-oligoadenylate synthetase-like | 1.50 | 3.04 |
| 45 | 421851 | R18586 | Hs.108896 | lambda-crystallin | 1.47 | 3.10 |
| | 448499 | BE613280 | Hs.77550 | hypothetical protein MGC1780 | 1.44 | 3.07 |
| | 427378 | BE515037 | Hs.177556 | melanoma antigen, family D, 1 | 1.44 | 3.00 |
| | 412641 | M16660 | Hs.74335 | heat shock 90kD protein 1, beta | 1.42 | 3.66 |
| | 448143 | AF039704 | Hs.20478 | ceroid-lipofuscinosis, neuronal 2, late | 1.42 | 4.16 |
| 50 | 413291 | NM_006278 | Hs.75268 | sialyltransferase 4C (beta-galactosidase | 1.41 | 3.30 |
| | 435968 | AW161481 | Hs.111577 | integral membrane protein 3 | 1.41 | 3.30 |
| | 422485 | BE514492 | Hs.117487 | gene near HD on 4p16.3 with homology to | 1.40 | 3.01 |
| | 443759 | BE390832 | Hs.134729 | FXD domain-containing ion transport reg | 1.39 | 3.82 |
| | 444441 | AW613841 | Hs.301394 | hypothetical protein MGC3101 | 1.39 | 3.43 |
| 55 | 430205 | AB025904 | Hs.235168 | carbonic anhydrase XIV | 1.36 | 3.32 |
| | 406827 | AA971409 | | gb:op92c04.s1 NCL CGAP_Lu5 Homo sapiens | 1.35 | 3.03 |
| | 406906 | Z25424 | | gb:H.sapiens protein-serine/threonine ki | 1.34 | 6.25 |
| | 426890 | AA393167 | Hs.41294 | ESTs | 1.34 | 3.66 |
| | 433320 | D60647 | Hs.250879 | ESTs, Highly similar to CTXN RAT CORTEXI | 1.34 | 3.18 |
| 60 | 450358 | AB010098 | Hs.24907 | coronin, actin-binding protein, 2B | 1.33 | 3.19 |
| | 421612 | AF161254 | Hs.106196 | BDG antigen | 1.33 | 3.03 |
| | 438915 | AA280174 | Hs.285681 | Williams-Beuren syndrome chromosome regi | 1.32 | 3.68 |
| | 428342 | AI739168 | | Homo sapiens cDNA FLJ13458 fis, clone PL | 1.32 | 3.10 |
| | 449444 | AW818436 | | salute carrier family 16 (monocarboxylic | 1.30 | 3.30 |
| 65 | 404700 | | | Target Exon | 1.30 | 3.14 |
| | 403043 | | | Target Exon | 1.30 | 4.22 |
| | 409858 | NM_006586 | Hs.56828 | trinucleotide repeat containing 5 | 1.29 | 3.09 |
| | 424679 | AL117477 | Hs.119960 | DKFZP727G051 protein | 1.27 | 3.13 |
| | 406908 | Z25437 | | gb:H.sapiens protein-tyrosine kinase gen | 1.27 | 3.66 |
| 70 | 432665 | AW603880 | | ATPase, H transporting, lysosomal (vacuo | 1.26 | 3.09 |
| | 423130 | AW897586 | Hs.21213 | ESTs | 1.24 | 3.34 |
| | 453220 | AB033089 | Hs.32452 | Homo sapiens mRNA for KIAA1263 protein, | 1.24 | 3.15 |
| | 442680 | BE270707 | Hs.8583 | similar to APOBEC1 | 1.22 | 3.94 |
| | 422319 | AW403342 | Hs.115232 | splicing factor 3a, subunit 2, 66kD | 1.21 | 3.36 |
| 75 | 402408 | | | NM_030920*:Homo sapiens hypothetical pro | 1.04 | 3.37 |
| | 424905 | NM_002497 | Hs.153704 | NIMA (never in mitosis gene a)-related k | 1.00 | 3.02 |

TABLE 51B:

| | | |
|----|-------------|---------------------------------------|
| 80 | Pkey: | Unique Eos probeset identifier number |
| | CAT number: | Gene cluster number |
| | Accession: | Genbank accession numbers |

Pkey CAT Number Accession

| | | |
|--------|-----------|--|
| 430540 | 713_2 | BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 BM045810 AU120387 BG770238 BG686740 BG913323 B1759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 AI770171 BF196861 BE856897 AA463876 AJ375927 AA648810 AA948193 AA490916 AA459893 AA58188 AI240408 AI191843 AI131029 AW768399 AI365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903567 BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610 BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 BE298109 AW245422 AI423847 AI914618 H80534 BE301004 AL531791 AI435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296 AI359493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AI421728 BG767231 BM462953 BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512 W58732 W85690 BG958989 AI205206 H19721 W17051 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114 AU243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103 AW008188 R07703 AA989120 AA746235 AW028983 AA789102 AI185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809 BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591 AK055109 BC019085 AA187684 BG656226 BM023227 AI932311 AW264381 AA398371 BM021483 AI432433 AI375777 AI129580 AW262782 AI134107 BM023515 AA977504 AI859222 AI348454 R69725 AA975268 BM021207 AL080074 AA129218 AW207842 N90581 AA771919 AI092259 AI028416 AI074114 BG656536 BE501677 AW193419 AA917040 W90430 AI342984 AI378957 AL036486 AW020068 BI491093 BF476021 R41226 R69631 F04125 C02343 AA115589 R56480 AI400988 R54266 R31422 AI801777 BE677762 AW008210 AW009441 BE350994 BE207949 AI091475 AI802774 AI827533 AI075363 AI659979 AA687855 AI078125 AI090285 AA670058 AA602411 AA683472 AI436058 AA612826 AI038932 BG057726 AI167355 BF449023 AI289476 AW074381 BF972912 AI991780 AA889119 AI537472 Z39730 AI868953 AI192337 BE812978 BE812939 AA115248 H99006 AI915784 F08973 I16748 D20468 AA609899 BF081234 AA115336 BE812876 BE812972 BE812982 BE813006 BE813019 R43883 BE812981 |
| 437179 | 12239_1 | BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 BM045810 AU120387 BG770238 BG686740 BG913323 B1759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 AI770171 BF196861 BE856897 AA463876 AJ375927 AA648810 AA948193 AA490916 AA459893 AA58188 AI240408 AI191843 AI131029 AW768399 AI365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903567 BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610 BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 BE298109 AW245422 AI423847 AI914618 H80534 BE301004 AL531791 AI435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296 AI359493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AI421728 BG767231 BM462953 BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512 W58732 W85690 BG958989 AI205206 H19721 W17051 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114 AU243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103 AW008188 R07703 AA989120 AA746235 AW028983 AA789102 AI185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809 BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591 |
| 430015 | 713_2 | AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003092 AW271756 AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727 BF347859 AW499616 AA191322 AW499617 AL601010 AW575742 AA729043 BE463447 AA086179 BE459623 AI335824 AW408712 BM149172 BC014433 Z49835 D16234 U42068 D83485 NM_005313 AL535156 AL533202 AL533596 AL531770 AL542767 AL551050 AL548510 AL542531 ALS48618 BE799237 AL547374 AL560312 AL543505 AL540727 AL541255 BG765697 AI126498 BI289574 BG576125 AL519304 AL548821 AL542983 BI596431 BI829284 AL045490 BE407984 BI668702 BI713725 BE547233 BM312673 BG822625 AW239512 BM312685 BE296719 BM312059 BI712618 BF724689 AA353713 BF477104 BI838605 BG170854 BE612762 BF917301 BF332271 BI049186 BE715514 AW392181 BE768470 AI912855 AW991405 BG739837 AA287804 AW801855 AL568814 AW384099 AW384058 AW754178 AI001019 R33917 BE814037 AI576164 AK025474 U11293 AF141304 BM442402 AL539879 AL554793 AL543707 AL549509 BI753328 BG756797 BI856494 BE901116 AL556989 AU133347 BI838505 AW949559 BM012604 BG773980 BG661309 BI260149 BF436764 BG983060 BF822225 BI059728 BF917866 BF917609 BF914374 D31003 AJ234218 AJ420466 BM083921 BE856788 BE669957 BF430992 AW614978 AW205958 BF110763 BF222758 AA195232 AI341353 AI698676 AO93230 AI123522 AI656594 AI208758 AA975916 AI089224 AI264922 AA256604 AA659637 BE218707 AA195203 AW999239 AW139706 N31717 AW205941 R95955 N39147 BM015411 AL576975 BF689524 AL563130 BI858155 AA417889 AL513995 AL568815 AI160693 AA836028 H84388 AL517078 AL546480 AL530507 AL561042 AA024435 W47314 AI680513 AA456116 BF836679 AW975173 H24039 AW105059 BE548113 AW370257 BM011139 AW675130 BE276045 BF933396 AL517903 AA886367 BI030596 BG477193 BF973867 AI382520 D25917 AI670784 AI742347 AW269789 AI207700 AW610541 AW793036 AW793035 AW610540 AW362220 AW362166 AW362214 AW362225 AW362228 AL119827 NM_002082 L16862 BG828886 BE795217 BE904064 BE294526 BE297283 BE394617 BE935127 BE935106 F12351 BG823182 H16710 AA302840 T93016 T92950 AU184997 AA077551 NM_016575 AB032773 AI765521 BF593742 AI497757 AJ761233 AW467938 BF000670 AI818496 N24761 AL043306 BF476138 BF593836 AA132787 AI147248 AI086795 AA151317 T95298 AW083548 AA058371 T29751 AI769860 AI784548 AW205506 AI800679 AI041733 AI459902 BE327641 AI865829 AI254736 AI302433 AI744176 AI241825 AA027842 AL524933 AL524932 BF947764 BF340737 BF948700 BG996395 N53455 N21027 AI127616 N35901 AA682443 AA678249 AA719371 AA132582 T15981 H99958 N40717 AW959402 AI267251 BF909329 AI142035 T95379 H29420 RS9632 H17318 H17331 H29327 R40829 R43395 RS9573 AI749561 R56599 H16755 AI694500 AA027907 BI757837 AW439843 AW172765 BE018717 BE464329 BE302285 H96902 BF477981 BE674508 BE670755 H95980 T15387 M80359 NM_002376 AU132239 AU120606 AU124963 AI065116 BE900808 BF968374 AI806648 BG774205 AW250728 BE265845 AA290719 AU125196 BG428863 AA333580 AA604551 W73300 AI932646 AA082201 AA627618 BF038887 BF337051 BI021159 AW057581 AI983156 AI268004 T71931 T90093 AW194009 H93969 AI742843 AI935080 BE041751 H93970 AW797399 W05032 T87824 T82912 AW129639 AI221821 AI911810 AA703093 AA160135 AW779124 AA102559 AA969546 D29560 BI915937 AA707716 BI085679 AA700887 AA081085 H80564 T99937 T70802 BM006551 AA367152 AW953705 AI631833 AW237429 AW027804 AA729038 BE503409 AI521935 BF739953 AA702982 AA557633 AA780065 AI218139 AW194264 D20120 AI082715 AI969980 BE857686 BE326711 AW953706 AI393749 AI383821 W67199 AA431759 AI796526 AI521794 AI796380 AW117545 AI749657 AI537634 NS0122 BG108218 BE560548 AW380115 BE269629 AI911518 AW380113 AA902964 AA455001 AI276529 AI685597 AA970496 D10814 AW380068 AW380080 R00283 C15236 AW327776 D80759 AL050068 AA160485 AW173544 AW296506 AW439860 AI521563 AI702529 AI393606 AW138323 AA570109 H19504 BM021968 BF063327 BF593552 AA630766 AI597717 AI807128 AA523012 AI356250 AW451857 AA974203 AI762577 BF512552 AW007307 BE675286 AW450602 AA962057 AW516069 AI582546 BF221924 BF222543 AI801808 AW468599 AW000736 AI866625 AW223536 BM021837 AA911956 AI880606 W85516 T03370 AW611634 H41653 AI468349 H19588 AW090198 AW043993 R39847 AW936678 AW936821 AW936682 AW936781 AW936811 AW936653 AW936823 AW936685 AW936815 AW936637 AW936812 AW936730 AW936762 AW936682 AW936732 |
| 416730 | 1988296_1 | BC001179 NM_005336 M64098 BC014305 BI827845 BI918183 AU124191 AU125604 AU140930 AL043307 BG763670 BG824279 AU125959 BI518466 BE271867 BM264138 BE314823 BM090633 BE273657 BG419830 BM048338 AU134368 BE163486 BE163483 BG421980 BG768130 AW500482 AI910107 AW868323 BF083170 AW450290 BM466817 BG255224 BE394282 AU140278 BE887464 AL042675 BI195986 BE883385 BE544751 BE270148 BM011334 AI093482 AA029903 AI610705 BE386809 F06628 AW408605 BF814085 BC007961 BM451548 BG768053 BM452948 AU140330 BG489566 BI870474 BM014013 AU131264 BG679824 BI225752 BI457400 BE410173 BM044254 BG763690 BE251495 BG179862 BE513489 |
| 400235 | 3084_1 | |

| | | | | |
|----|--------------|---|--|--|
| 5 | | | BM005937 AIO64815 BF569858 BI712614 BG655891 BG424940 BE175180 BM313160 BG471936 BM091124 BF885884 BF870522 BE004490 BE712976 BE712862 AA401033 BF569477 BE712936 BF353839 BE713042 AA316561 BE712974 BE712977 BE712938 BE712937 BE712867 BE713043 BE713023 N42463 BE712901 BE713041 BE712904 BE712895 BE713012 BE713049 BE713025 BE712998 BE712988 BE712897 BE712986 BE712984 BE712982 BE712975 BE712970 BE712953 BE712929 BE712922 BE712875 BE712866 BE712861 BE712860 BE712854 BE712853 BE712902 BE712897 BE712912 BG984910 BE712903 BE764759 BE715723 BE715745 BE712915 AA441839 BE713040 BE715755 BF872528 BF060840 BG395104 BG744878 AU124081 A1889823 A1801072 A1633102 A1678670 A1493608 AW194294 A1354559 A1686736 AW152477 A1419496 A1720319 A1866190 AA047013 AA039625 BE049622 AA369065 AA025686 A1570198 AA706304 AW439251 H64553 AW168006 A1983753 AW081999 AW082909 A1951490 BF886341 AW591246 A1190143 A1151074 A1499541 A1050934 AA402167 AA382049 T16207 T03299 A1932691 AW571663 BG479797 BE048436 BI450153 BG386046 BE616601 AW151629 BG236164 BF852743 BF852046 T57801 W37981 AA482668 H43740 W58142 W25087 BM459852 AU125403 BG767992 BE258516 A114509 BE394494 BE386905 AA450315 BG750593 AA557855 BG766487 BG766998 BF948864 BE279327 BE870900 AA577098 BF365851 AA745058 N29867 A1625038 AA641801 AA846174 H26395 AA025568 BF690282 R67845 R72666 H39554 T78959 W01317 H45860 W80837 N53985 BG757202 BE838055 BE072895 BE072668 BE867012 BM042833 AA083591 BG745462 AW374086 BG831326 BE715757 BG767243 BG763272 AA113402 A1024044 BF818501 BE081938 BF353818 AA746336 BM019086 BE712894 H16977 H45012 R10793 BE708619 BF570432 AA593938 AA064637 T28082 AA852845 T78907 AA346590 F00017 BE966368 N58726 AA732431 T54379 W80749 BF238314 BE279768 AA325106 T19241 BE409939 BF852119 W23803 T54011 AW392638 BI465185 AW516784 AA211335 BI159846 AA064680 N80615 W49676 BF851406 R88120 AA434028 H44546 T61029 N44804 AA114948 H26960 BI261965 AA582599 BG469385 BF818172 BF923672 BI042420 AW362633 BE883122 BM470779 BE935760 AW856056 AW856103 BE828607 AW381799 A1121058 BE828618 BE769545 AA102142 BG749978 BI770417 BI862544 A1110687 AF083562 BE740347 BE874864 A1305113 BE513675 BE091369 BI046660 BE091453 BI046548 A1673786 BF868704 A1025179 BF358640 BF886357 BF886313 BG951884 A1347880 AW627563 BF932536 AW820377 BF739372 BF831620 BE068264 BE613627 AA641745 W01130 H28252 | |
| 10 | 418166 | 18858_1 | AK055915 BE857252 A1523348 AA765350 BF446858 Z43675 R19529 AL133837 BG389444 AW382942 BE702956 AA081961 BE835247 BE835308 BE835295 AA376302 BE645790 AA375690 AA376592 AW954423 N85732 AA249770 A1754416 AA213816 BF592044 AA811729 AW514842 A1633486 A096810 AW183016 A1635738 N27524 BE645916 A1247842 AW991230 A1754277 H16814 A1766892 BF108422 A1800361 T95129 F11313 R97946 R93989 AA375242 BF109388 A1860939 A1680060 AW953899 BF971486 A1972337 AW953841 AA372437 A1216746 H11384 R38484 AA249043 AA249732 | |
| 15 | 455839 | 1518842_1 | BE145823 BE145830 BE145884 BE145814 BE145905 BE145833 BE145834 BE145883 BE145889 | |
| | 458997 | 11847_4 | BM453041 AA760783 BE218582 A1340046 AW166131 BF515854 A1630296 AA461307 A1090881 AW023059 AA155797 AA115486 AL597396 AW889004 AW937420 AA137082 AA013374 BG619478 BG401839 AA430373 AA968771 | |
| 20 | 406782 | 0_0 | GG775668 BG680336 AW991605 AA455904 AW265494 AW265432 BF911380 AA456370 BF911379 AA195677 BF914311 BF913866 BG775059 BG951874 A1572169 | |
| | 417324 | 292720_1 | BF036043 AW190446 BG194731 AW662036 A1445021 BE937550 AW818972 AW393132 AA834685 BF112058 AV721682 H16423 A1270167 A1857345 AA937302 AW818444 BE929780 BG498678 BF155010 BI598271 BI599811 BE161728 AW578737 AW753711 AW379707 AW381918 BG506608 AW028637 AW994240 BF887392 BF790073 AW381624 AV727105 BF439618 AA443174 A1018009 N42850 AW573242 A1417258 AA463483 A1676131 A1167170 AA836627 AA443828 AW592922 AA235129 AA730278 AW439062 AW474332 BI043239 AW474342 BG708553 AW362423 BF090028 BE827256 R16550 R39478 R39479 R94368 BG540916 BM314745 AA251087 D54231 D55274 BF085805 D31589 AW966405 AW994425 D81879 BE093545 AW901107 AA383529 BI021552 R56420 N39976 AA573281 H82595 AA234955 BE093539 AW367006 BF358697 BF366318 AA663856 BE702099 BF035969 A1267384 A1267232 BE348320 AA621574 AA861212 BF083343 BF083341 AV745131 D53074 AW954476 AW954472 AA376836 AV724531 D53063 C14928 AA093287 AA062638 BG483558 BE940050 AA765954 T70171 BE938775 BE940057 D53502 AW373300 A1118798 BM128728 AA193411 AW444709 AW952455 A1887612 BF431948 BI496876 A1264159 BM128481 A1624657 A1689301 A1969467 AA81685 AA251595 AA625761 AA872090 A1826790 AA328366 BE827416 R75951 D56918 R68122 BE827384 A1118797 A1184164 A1164411 BI495332 BE858113 A1863860 H00660 T69849 AW780389 C14667 BE934995 BI018652 R92801 AA164410 H00752 AW373305 AW373299 AW373302 BF971018 BE513812 AA133359 AW581719 BF434402 AL600619 BG699731 BI551395 AW027136 AW055130 BF939512 A1076048 H18584 AW161061 AA864334 A1616101 BE049456 AW044012 AA954079 A1274682 A1370526 AW131990 AA853195 AA853191 BG118295 AA761620 BG705371 BF355591 BF335596 AA360497 H28072 BG198352 AW364709 H40926 H44214 AA836538 BI059563 AA609784 R97304 | |
| 25 | 455839 | 1518842_1 | AL532360 BE794750 AA582906 A1015067 AW271034 BG271636 AW075177 AW071374 A1345565 A1307208 BE138953 BE049086 A1334881 AW075006 AW075181 AA464019 AW302733 AW075100 AW073433 A1802854 A1334909 A1802853 A1345036 A1348921 A1340734 A1307478 A1251289 AW302327 AW072520 A1312145 AW073656 AW072513 AW071289 A1307559 AA876186 T29587 A1307493 A1255068 A1252868 A1252839 AW074809 A1252926 A1252160 A1251662 A1251262 A1610913 A1270787 A1270156 A1252075 AW073469 AW072901 AW072496 AW071420 A1305762 A1254764 A1802837 A1251264 AW073049 AW071311 A1340643 BE138965 BE138502 AW073456 A1334733 A1054335 BE139260 A1054302 A1054060 A1054057 A1053722 A1289711 BE139228 AW470478 AW271039 AW302085 BE041872 A1254494 A1271496 A1252427 BF178773 BF178645 AW074866 BE857822 BC007350 BG766159 BG769338 BG761999 BG744385 BG770572 AW370610 AW370581 AA978353 AW327973 AW402425 A1889380 AA868504 AW612958 AA630644 A1751211 N26980 A1394506 AA747849 BF154926 BF477185 AA649647 R39135 A1750216 T35363 W36278 AW079375 AW612240 AA505495 AA515380 BG760793 AW370651 BG768029 AW370595 BF229885 BG762422 BG764907 T50662 AA025671 AW815715 AV703420 H65047 AA485582 R56186 H90385 R55913 BI261497 BI018403 BF376945 T75578 BF933325 BF932853 BG502266 AW686934 AV683504 BI018121 N41953 BF933343 BF932871 H08334 R14012 BF897622 T50816 BG698803 BF340083 Z20199 AK000695 AK000489 BC001688 BG235988 AW006329 A1887644 A1207230 A1148213 A1304333 A1634653 AW662636 A1281247 AA946921 AA424487 BE272330 A1830588 AA159183 AA977141 BG231801 AA631793 AA975194 BF817537 AA477798 BI906631 AW083424 AA625199 NM_017767 AK000334 BF984048 AW815634 AL573992 AA430612 A928390 AA464447 AW340827 AA424290 A1927759 BG951502 AW881353 BF765535 AA971409 | |
| 30 | 406782 | 0_0 | AK056315 A1015524 AA724079 BI713619 A1377728 AW293682 A1928140 A1092404 A1085630 AA731340 BM469629 AW968804 AA425558 AA769094 BF446026 AW118719 A1332765 AW500888 AW576556 A1895571 AW499664 AW614573 AW629495 AW505314 W74704 A1356361 A1923640 AW070509 A1521500 AL042095 AA609309 AA761319 A1381489 H45700 AA761333 AW265424 AA909524 AA635311 AA649040 A1392620 Z40708 A1985564 AW265313 A1913892 A1893486 AW263502 A1806164 AW291137 BI061872 BI059498 AA134476 AW084888 AA036967 AW370823 T55263 BI002756 AA489664 BF827261 W74741 BF963166 | |
| | 417324 | 292720_1 | U59185 NM_004696 AV734324 A1245349 AA369517 H88760 D79128 AA970406 H01059 H88761 H03446 BG620383 AU135008 AU136895 AU158158 AU155762 R73608 R65751 R23756 N14630 AW078687 BE439761 BE786351 R68994 BE785867 AW297502 AW297553 BG431545 AW814843 BF382644 BG429539 BE929862 BF811258 | |
| 35 | 419200 | 9531_1 | BG165971 BE143233 AL577712 A1400326 AA769318 AA427866 AW088714 A1150755 A1924874 A1186243 AA804195 AA768972 AW574769 AW341643 AW204520 AA235326 A1005076 BE826687 AW004816 AW007235 BE826639 BE826634 BF222941 BE826631 BE826643 AA292639 AW514133 A1690331 A1673409 AA627727 A1923685 AA931499 A1249783 A1810663 AA548622 AA702095 AA832395 BI259508 AA262993 AW075840 AA810885 | |
| 40 | 455705 | 77478_2 | | |
| 45 | 406851 | 0_0 | | |
| | 427239 | 20459_2 | | |
| 50 | 427289 | 1820_2 | | |
| 55 | 411825 | 7891_1 | | |
| 60 | 406827 | 0_0 | | |
| | 428342 | 6712_1 | | |
| 65 | 449444 | 2735_1 | | |
| 70 | 432665 | 27095_3 | | |
| 75 | TABLE 51C: | | | |
| | Pkey: | Unique number corresponding to an Eos probe set | | |
| | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. | | |
| | Strand: | Indicates DNA strand from which exons were predicted. | | |
| 80 | Nt_position: | Indicates nucleotide positions of predicted exons. | | |
| | Pkey | Ref | Strand | Nt_position |
| | 402075 | 8117407 | Plus | 121907-122035,122804-122921,124019-12416 |

| | | | | |
|----|--------|---------|-------|-----------------------------|
| 5 | 400860 | 9757499 | Minus | 151830-152104,152649-152744 |
| | 402609 | 9926446 | Minus | 113464-113633,114264-114654 |
| | 400750 | 8119067 | Plus | 198991-199168,199316-199548 |
| | 402994 | 2996643 | Minus | 4727-4969 |
| | 403817 | 8962065 | Plus | 110297-111052 |
| | 402829 | 8918414 | Plus | 101532-101852,102006-102263 |
| | 403532 | 8076842 | Minus | 81750-81901 |
| | 405451 | 7622517 | Minus | 145949-146227 |
| 10 | 405785 | 9581533 | Minus | 98702-98925 |
| | 405506 | 6466489 | Plus | 80014-80401,80593-81125 |
| | 405486 | 6651379 | Plus | 179441-179598 |
| | 406382 | 9256148 | Plus | 122336-122851 |
| | 401454 | 9186923 | Minus | 114659-114832 |
| 15 | 405885 | 7677703 | Minus | 42574-42998 |
| | 403969 | 8569909 | Plus | 31237-31375,32405-32506 |
| | 400533 | 6981826 | Minus | 277132-277595 |
| | 400991 | 8096825 | Plus | 159197-159320 |
| | 401591 | 9966977 | Minus | 55410-55835 |
| 20 | 404067 | 3282162 | Plus | 1415-2071 |
| | 404140 | 9843520 | Plus | 37761-38147 |
| | 401914 | 9369520 | Plus | 62537-62945,63155-63308 |
| | 404700 | 9800123 | Minus | 159621-160203 |
| 25 | 403043 | 7768753 | Minus | 314423-316252 |
| | 402408 | 9796239 | Minus | 110326-110491 |

TABLE 52A: ABOUT 204 GENES UPREGULATED IN PRIMARY MELANOMAS RELATIVE TO MELANOMA METASTASES

Table 52A lists about 204 genes upregulated in primary melanomas relative to melanoma metastases. Genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Key: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number

Unigene Title: Unigene gene title

R1: 90th percentile of primary melanoma AIs divided by the 90th percentile of melanoma metastasis AIs

R2: 90th percentile of primary melanoma AIs divided by the 90th percentile of melanoma metastasis AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

| | Pkey | ExAccn | UnigeneID | Unigene Title | R1 | R2 |
|----|--------|-----------|-----------|---|-------|-------|
| 40 | 421948 | L42583 | Hs.334309 | keratin 6A | 21.90 | 16.66 |
| | 422168 | AA586894 | Hs.112408 | S100 calcium-binding protein A7 (psorias) | 21.36 | 43.65 |
| | 401781 | | | Target Exon | 18.70 | 18.58 |
| | 401780 | | | NM_005557: Homo sapiens keratin 16 (foca | 15.34 | 16.00 |
| 45 | 431360 | NM_000427 | Hs.251680 | loricin | 12.34 | 9.86 |
| | 409632 | W74001 | Hs.55279 | serine (or cysteine) proteinase inhibito | 11.24 | 8.73 |
| | 412636 | NM_004415 | | desmoplakin (DPI, DPII) | 11.20 | 6.62 |
| | 417366 | BE185289 | Hs.1076 | small proline-rich protein 1B (comifin) | 10.46 | 12.75 |
| | 409601 | AF237621 | Hs.80828 | keratin 1 (epidermolytic hyperkeratosis) | 10.41 | 25.49 |
| 50 | 420859 | AW468397 | Hs.100000 | S100 calcium-binding protein A8 (calgran | 9.20 | 8.63 |
| | 420783 | AI659838 | Hs.99923 | lectin, galactoside-binding, soluble, 7 | 8.11 | 11.14 |
| | 422511 | AU076442 | Hs.117938 | collagen, type XVII, alpha 1 | 7.90 | 8.92 |
| | 422158 | L10343 | Hs.112341 | protease inhibitor 3, skin-derived (SKAL | 7.14 | 22.14 |
| | 427666 | AI791495 | Hs.180142 | calmodulin-like skin protein (CLSP) | 7.03 | 8.90 |
| 55 | 430686 | NM_001942 | Hs.2633 | desmoglein 1 | 6.88 | 5.39 |
| | 431369 | BE184455 | Hs.251754 | secretory leukocyte protease inhibitor (| 6.60 | 12.79 |
| | 456525 | AW468397 | Hs.100000 | S100 calcium-binding protein A8 (calgran | 6.44 | 6.19 |
| | 437191 | NM_006846 | Hs.331555 | serine protease inhibitor, Kazal type, 5 | 6.34 | 7.77 |
| | 422166 | W72424 | Hs.112405 | S100 calcium-binding protein A9 (calgran | 6.15 | 8.91 |
| 60 | 418067 | AI127958 | Hs.83393 | cystatin E/M | 6.08 | 9.24 |
| | 408536 | AW381532 | Hs.135188 | ESTs | 6.04 | 17.40 |
| | 402075 | | | ENSP00000251056: Plasma membrane calcium | 5.96 | 8.41 |
| | 413554 | AA319145 | Hs.75426 | secretogranin II (chromogranin C) | 5.46 | 3.32 |
| | 410001 | AB041036 | Hs.57771 | kallikrein 11 | 5.38 | 5.36 |
| 65 | 421100 | AW351839 | Hs.124660 | Homo sapiens cDNA: FLJ21763 fs, clone C | 5.32 | 3.84 |
| | 407788 | BE514982 | Hs.38991 | S100 calcium-binding protein A2 | 5.19 | 5.30 |
| | 419329 | AY007220 | Hs.288998 | S100-type calcium binding protein A14 | 5.03 | 7.94 |
| | 429504 | X99133 | Hs.204238 | tipocalin 2 (oncogene 24p3) (NGAL) | 4.86 | 5.22 |
| | 421773 | W69233 | Hs.112457 | ESTs | 4.82 | 12.41 |
| 70 | 442577 | AA292998 | Hs.163900 | ESTs | 4.82 | 4.40 |
| | 401760 | | | Target Exon | 4.60 | 11.03 |
| | 408522 | AI541214 | Hs.46320 | Small proline-rich protein SPRK (human, | 4.50 | 11.35 |
| | 417515 | L24203 | Hs.82237 | ataxia-telangiectasia group D-associated | 4.47 | 12.43 |
| | 431211 | M86849 | Hs.323733 | gap junction protein, beta 2, 26kD (conn | 4.45 | 2.99 |
| 75 | 446989 | AK001898 | Hs.16740 | hypothetical protein FLJ11036 | 4.39 | 4.23 |
| | 423017 | AW178761 | Hs.227948 | serine (or cysteine) proteinase inhibito | 4.38 | 4.55 |
| | 418663 | AK001100 | Hs.41690 | desmocollin 3 | 4.36 | 5.16 |
| | 424620 | AA101043 | Hs.151254 | kallikrein 7 (chymotryptic, stratum com | 4.29 | 5.19 |
| | 401747 | | | Homo sapiens keratin 17 (KRT17) | 4.28 | 5.41 |
| 80 | 414807 | AI738616 | Hs.77348 | hydroxyprostaglandin dehydrogenase 15-(N | 4.24 | 2.30 |
| | 411274 | NM_002776 | Hs.69423 | kallikrein 10 | 4.22 | 4.82 |
| | 439496 | BE616501 | Hs.32343 | Homo sapiens, Similar to RIKEN cDNA 1110 | 4.21 | 8.26 |
| | 420039 | NM_004605 | Hs.94581 | sulfotransferase family, cytosolic, 2B, | 4.18 | 4.73 |
| | 429538 | BE182592 | Hs.139322 | small proline-rich protein 2A | 4.16 | 7.30 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|-------|
| | 418686 | Z36830 | Hs.87268 | annexin A8 | 4.12 | 4.09 |
| | 407366 | AF026942 | Hs.17518 | gb:Homo sapiens cig33 mRNA, partial sequ | 4.08 | 2.13 |
| | 421733 | AL119671 | Hs.1420 | fibroblast growth factor receptor 3 (ach | 4.08 | 4.38 |
| 5 | 416091 | AF295370 | Hs.283082 | defensin, beta 3 | 4.05 | 5.38 |
| | 442757 | AI739528 | Hs.28345 | ESTs | 3.94 | 4.28 |
| | 427318 | AF186081 | Hs.175783 | zinc transporter | 3.92 | 3.07 |
| | 453309 | AI791809 | Hs.32949 | defensin, beta 1 | 3.90 | 4.30 |
| | 422192 | AA305159 | Hs.113019 | fts485 | 3.88 | 2.81 |
| 10 | 424012 | AW368377 | Hs.137569 | tumor protein 63 kDa with strong homolog | 3.86 | 5.03 |
| | 429365 | AA451798 | Hs.99249 | ESTs | 3.76 | 4.05 |
| | 423634 | AW959908 | Hs.1690 | heparin-binding growth factor binding pr | 3.72 | 6.35 |
| | 425580 | L11144 | Hs.1907 | galanin | 3.68 | 3.65 |
| | 448966 | AW372914 | Hs.86149 | phosphoinositol 3-phosphate-binding prot | 3.68 | 2.75 |
| 15 | 444946 | AW139205 | Hs.156457 | hypothetical protein FLJ22408 | 3.59 | 5.72 |
| | 408591 | AF015224 | Hs.46452 | mammaglobin 1 | 3.58 | 4.73 |
| | 431009 | BE149762 | Hs.48956 | gap junction protein, beta 6 (connexin 3 | 3.58 | 2.62 |
| | 438501 | Z44110 | Hs.86149 | phosphoinositol 3-phosphate-binding prot | 3.56 | 2.61 |
| | 421574 | AJ000152 | Hs.105924 | defensin, beta 2 | 3.56 | 4.04 |
| 20 | 402294 | | | Target Exon | 3.48 | 4.38 |
| | 428666 | AL080190 | Hs.189242 | Homo sapiens mRNA; cDNA DKFZp434A202 (fr | 3.44 | 2.95 |
| | 401785 | | | NM_002275*:Homo sapiens keratin 15 (KRT1 | 3.42 | 4.92 |
| | 418007 | M13509 | Hs.83169 | matrix metalloproteinase 1 (interstitial | 3.36 | 4.24 |
| | 418394 | AF132818 | Hs.84728 | Kruppel-like factor 5 (intestinal) | 3.31 | 5.42 |
| 25 | 452392 | L20815 | Hs.507 | corneodesmosin | 3.30 | 8.56 |
| | 445183 | AB007877 | Hs.12385 | KIAA0417 gene product | 3.30 | 2.35 |
| | 433124 | U51712 | Hs.13775 | hypothetical protein SMAP31 | 3.26 | 2.15 |
| | 419098 | AA234041 | Hs.87271 | ESTs | 3.25 | 4.34 |
| | 421978 | AJ243662 | Hs.110196 | NICE-1 protein | 3.17 | 5.86 |
| 30 | 445493 | AI915771 | | metallothionein 1E (functional) | 3.16 | 2.98 |
| | 448111 | AA053486 | Hs.20315 | interferon-induced protein with tetratri | 3.14 | 2.07 |
| | 445745 | AB007924 | Hs.13245 | KIAA0455 gene product | 3.10 | 2.39 |
| | 410268 | AA316181 | Hs.61635 | six transmembrane epithelial antigen of | 3.06 | 2.71 |
| 35 | 407839 | AA045144 | Hs.161566 | ESTs | 3.06 | 3.54 |
| | 432374 | W68815 | Hs.301885 | Homo sapiens cDNA FLJ11346 fis, clone PL | 3.04 | 4.64 |
| | 439706 | AW872527 | Hs.59761 | ESTs, Weakly similar to DAP1_HUMAN DEATH | 3.04 | 2.78 |
| | 452240 | AJ591147 | Hs.61232 | ESTs | 3.00 | 4.79 |
| | 409190 | AU076536 | Hs.50984 | sarcoma amplified sequence | 2.96 | 3.05 |
| | 408015 | AW136771 | Hs.244349 | epidermal differentiation complex protei | 2.94 | 10.53 |
| 40 | 420798 | W93774 | Hs.99936 | keratin 10 (epidermolytic hyperkeratosis | 2.91 | 3.01 |
| | 406964 | M21305 | | FGENES predicted novel secreted protein | 2.90 | 5.34 |
| | 451541 | BE279383 | Hs.26557 | plakophilin 3 | 2.89 | 6.64 |
| | 454027 | R40192 | Hs.21527 | Human DNA sequence from clone GS1-115M3 | 2.86 | 2.81 |
| | 414737 | AI160386 | Hs.125087 | ESTs | 2.84 | 1.76 |
| 45 | 428330 | L22524 | Hs.2256 | matrix metalloproteinase 7 (matrilysin, | 2.82 | 1.83 |
| | 405542 | | | Target Exon | 2.80 | 2.77 |
| | 442503 | AF147078 | Hs.150853 | p53-responsive gene 5 | 2.78 | 5.17 |
| | 402970 | | | C20000886:gil9280563[gb]AA6472.1] (AF | 2.78 | 3.37 |
| 50 | 416730 | T99937 | | gb:ye72d04.r1 Soares fetal liver spleen | 2.76 | 2.76 |
| | 433435 | BE545277 | Hs.340959 | Ts translation elongation factor, miloch | 2.75 | 2.76 |
| | 447164 | AF026941 | Hs.17518 | vipirin; similar to inflammatory respon | 2.72 | 2.86 |
| | 409453 | AI885516 | Hs.95612 | ESTs | 2.70 | 6.68 |
| | 426824 | W23624 | Hs.173059 | ESTs | 2.67 | 2.75 |
| 55 | 437233 | D81448 | Hs.339352 | Homo sapiens brother of CDO (BOC) mRNA, | 2.65 | 3.07 |
| | 430630 | AW269920 | Hs.2621 | cystatin A (stefin A) | 2.63 | 2.38 |
| | 433339 | AF019226 | Hs.8036 | glioblastoma overexpressed | 2.61 | 2.44 |
| | 444670 | H58373 | Hs.332938 | hypothetical protein MGCS370 | 2.57 | 1.74 |
| | 414602 | AW630088 | Hs.76550 | Homo sapiens mRNA; cDNA DKFZp564B1264 (f | 2.54 | 3.66 |
| | 400995 | | | C11000295:gil12737279[ref]XP_012163.1] | 2.54 | 2.93 |
| 60 | 423515 | AA327017 | Hs.176594 | ESTs | 2.53 | 7.36 |
| | 417359 | T99264 | Hs.191117 | ESTs | 2.53 | 2.54 |
| | 432426 | AW973152 | Hs.31050 | ESTs | 2.52 | 2.15 |
| | 413822 | R08950 | Hs.272044 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.52 | 3.05 |
| | 414987 | AA524394 | Hs.294022 | hypothetical protein FLJ14950 | 2.52 | 3.85 |
| 65 | 407748 | AL079409 | Hs.38176 | KIAA0606 protein; SCN Circadian Oscillat | 2.48 | 1.76 |
| | 426990 | AL044315 | Hs.173094 | Homo sapiens mRNA for KIAA1750 protein, | 2.47 | 1.92 |
| | 413392 | AW021404 | Hs.13021 | ESTs | 2.47 | 2.56 |
| | 442762 | AF035119 | Hs.8700 | deleted in liver cancer 1 | 2.46 | 1.90 |
| | 444781 | NM_014400 | Hs.11950 | GPI-anchored metastasis-associated prote | 2.46 | 7.90 |
| 70 | 424364 | AW383226 | Hs.163834 | ESTs, Weakly similar to G01763 atrophin- | 2.46 | 2.66 |
| | 420568 | F09247 | Hs.247735 | protocadherin alpha 10 | 2.46 | 3.01 |
| | 405885 | | | Target Exon | 2.46 | 2.82 |
| | 412633 | AF001691 | Hs.74304 | periplakin | 2.46 | 5.01 |
| | 429852 | AB010445 | Hs.225948 | small inducible cytokine subfamily A (Cy | 2.45 | 3.35 |
| 75 | 429624 | AA458648 | Hs.99476 | ESTs, Weakly similar to 1313184B alpha1 | 2.44 | 2.33 |
| | 407325 | AA291180 | Hs.328476 | ESTs, Weakly similar to alternatively sp | 2.44 | 2.11 |
| | 431441 | U81961 | Hs.2794 | sodium channel, nonvoltage-gated 1 alpha | 2.43 | 3.66 |
| | 432543 | AA552690 | Hs.152423 | Homo sapiens cDNA: FLJ21274 fis, clone C | 2.42 | 3.12 |
| | 430168 | AW968343 | Hs.145582 | DKFZP434I1735 protein | 2.41 | 2.75 |
| 80 | 408000 | L11690 | Hs.198689 | bulbos pemphigoid antigen 1 (230/240kD) | 2.40 | 3.67 |
| | 404049 | | | NM_018937*:Homo sapiens protocadherin be | 2.39 | 1.89 |
| | 433576 | BE080715 | Hs.161091 | ESTs | 2.39 | 1.59 |
| | 444083 | AI123195 | | gb:oo17a10.x1 Soares_NSF_F8_9W_OT_PA_P_S | 2.38 | 2.59 |
| | 408208 | BE018717 | | ESTs | 2.37 | 2.12 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|------|
| 5 | 431842 | NM_005764 | Hs.271473 | epithelial protein up-regulated in carci | 2.36 | 2.23 |
| | 453931 | AL121278 | Hs.25144 | ESTs | 2.34 | 1.99 |
| | 452308 | A1167560 | Hs.61297 | ESTs | 2.31 | 3.82 |
| | 431048 | R50253 | Hs.249129 | cell death-inducing DFFA-like effector a | 2.31 | 2.18 |
| | 403752 | | | NM_002753*:Homo sapiens mitogen-activate | 2.30 | 2.38 |
| 10 | 402525 | | | NM_002699*:Homo sapiens POU domain, clas | 2.30 | 2.36 |
| | 420223 | N27807 | | ribosomal protein L4 | 2.30 | 1.73 |
| | 452023 | AB032999 | Hs.27566 | KIAA1173 protein | 2.29 | 4.54 |
| | 443172 | AW662964 | Hs.199061 | p300/CBP-associated factor | 2.28 | 2.02 |
| | 439979 | AW600291 | Hs.6823 | hypothetical protein FLJ10430 | 2.28 | 1.71 |
| 15 | 414004 | AA737033 | Hs.7155 | ESTs, Moderately similar to 2115357A TYK | 2.27 | 1.81 |
| | 429554 | NM_012275 | Hs.207224 | interleukin 1, delta | 2.26 | 2.17 |
| | 436895 | AF037335 | Hs.5338 | carbonic anhydrase XII | 2.26 | 2.51 |
| | 404029 | | | NM_018936*:Homo sapiens protocadherin be | 2.26 | 2.19 |
| | 424049 | AB014524 | Hs.138380 | KIAA0624 protein | 2.26 | 2.99 |
| 20 | 442423 | BE326264 | Hs.246842 | ESTs | 2.26 | 1.75 |
| | 408452 | AA054683 | Hs.192455 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 2.26 | 2.29 |
| | 428471 | X57348 | Hs.184510 | stratfin | 2.25 | 2.40 |
| | 410541 | AA065003 | Hs.64179 | syntenin-2 protein | 2.24 | 2.46 |
| | 415539 | AJ733881 | Hs.72472 | BMP-R1B | 2.22 | 1.64 |
| 25 | 425701 | AA361850 | Hs.240443 | Human clone 137308 mRNA, partial cds | 2.22 | 3.04 |
| | 423973 | AF038461 | Hs.136574 | arachidonate 12-lipoxygenase, 12R type | 2.22 | 3.24 |
| | 409178 | BE393948 | Hs.50915 | kalikrein 5 | 2.19 | 4.74 |
| | 433091 | Y12642 | Hs.3185 | lymphocyte antigen 6 complex, locus D | 2.19 | 7.96 |
| | 430171 | AF086289 | Hs.234766 | skin-specific protein | 2.17 | 3.56 |
| 30 | 401994 | | | Target Exon | 2.14 | 3.34 |
| | 449228 | AJ03107 | Hs.148590 | protein related with psoriasis | 2.11 | 5.52 |
| | 446292 | AF081497 | Hs.279682 | Rh type C glycoprotein | 2.11 | 5.78 |
| | 426150 | NM_003658 | Hs.167218 | BarH-like homeobox 2 | 2.05 | 2.96 |
| | 452554 | AW452434 | Hs.58006 | ESTs, Weakly similar to ALU5_HUMAN ALU S | 2.04 | 4.17 |
| 35 | 443162 | T49951 | Hs.9029 | DKFZP434G032 protein | 1.98 | 3.20 |
| | 400304 | AF005082 | Hs.113261 | Homo sapiens skin-specific protein (xp33 | 1.94 | 3.20 |
| | 407395 | AF005082 | | gb:Homo sapiens skin-specific protein (x | 1.92 | 3.24 |
| | 412507 | L36645 | Hs.73964 | EphA4 | 1.92 | 3.06 |
| | 410310 | J02931 | Hs.62192 | coagulation factor III (thromboplastin, | 1.90 | 3.18 |
| 40 | 425415 | M13903 | Hs.157091 | involucrin | 1.89 | 5.26 |
| | 417324 | AW265494 | | ESTs | 1.88 | 3.82 |
| | 412446 | AJ768015 | | ESTs | 1.88 | 3.36 |
| | 451092 | AJ207256 | Hs.13766 | Homo sapiens mRNA for FLJ00074 protein, | 1.87 | 3.75 |
| | 444726 | NM_006147 | | interferon regulatory factor 6 | 1.86 | 4.11 |
| 45 | 424399 | AJ905687 | | AJ905687:IL-BT095-190199-019 BT095 Homo | 1.85 | 4.20 |
| | 434346 | AA630445 | | ESTs | 1.84 | 3.08 |
| | 446051 | BE048061 | Hs.37054 | ephrin-A3 | 1.83 | 3.44 |
| | 423725 | AJ403108 | Hs.132127 | hypothetical protein LOC57822 | 1.78 | 3.45 |
| | 413859 | AW992356 | Hs.8364 | Homo sapiens pyruvate dehydrogenase kina | 1.76 | 2.99 |
| 50 | 411908 | L27943 | Hs.72924 | cytidine deaminase | 1.74 | 3.60 |
| | 445656 | W22050 | Hs.21299 | ESTs, Weakly similar to AF151840 1 CG-8 | 1.71 | 3.56 |
| | 413966 | AA133935 | Hs.173704 | ESTs, Moderately similar to A53959 throm | 1.71 | 3.38 |
| | 424046 | AF027866 | Hs.138202 | serine (or cysteine) proteinase inhibito | 1.70 | 3.92 |
| | 425650 | NM_001944 | Hs.1925 | desmoglein 3 (permpigus vulgaris antigen | 1.68 | 3.25 |
| 55 | 429299 | AJ620463 | Hs.347408 | hypothetical protein MGC13102 | 1.67 | 2.92 |
| | 429002 | AW248439 | Hs.2340 | junction plakoglobin | 1.66 | 3.35 |
| | 421335 | X99977 | Hs.103505 | ARS component B | 1.68 | 4.31 |
| | 433662 | W07162 | Hs.150826 | RAB25 RAB25, member RAS oncogene family | 1.65 | 3.55 |
| | 429211 | AF052693 | Hs.198249 | gap junction protein, beta 5 (connexin 3 | 1.64 | 4.04 |
| 60 | 414214 | D49958 | Hs.75819 | glycoprotein MGA | 1.64 | 3.59 |
| | 437897 | AA770561 | Hs.146170 | hypothetical protein FLJ22969 | 1.62 | 3.13 |
| | 426350 | NM_003245 | Hs.2022 | transglutaminase 3 (E polypeptide, prote | 1.62 | 2.92 |
| | 413163 | Y00815 | Hs.75216 | protein tyrosine phosphatase, receptor t | 1.57 | 3.09 |
| | 422106 | D84239 | Hs.111732 | Fc fragment of IgG binding protein | 1.53 | 3.39 |
| 65 | 427751 | AF000152 | | conserved gene amplified in osteosarcoma | 1.52 | 3.53 |
| | 416881 | N32520 | Hs.141358 | ESTs | 1.52 | 3.06 |
| | 435013 | H91923 | Hs.110024 | NM_020142:Homo sapiens NADH:ubiquinone o | 1.49 | 2.91 |
| | 434574 | AJ424458 | Hs.33470 | ESTs | 1.48 | 3.05 |
| | 454478 | AW805749 | | superoxide dismutase 2, mitochondrial | 1.48 | 3.54 |
| 70 | 447330 | BE279949 | Hs.18141 | ladinin 1 | 1.46 | 4.48 |
| | 414583 | AA362907 | Hs.76494 | proline arginine-rich end leucine-rich r | 1.41 | 2.99 |
| | 433640 | AW390125 | Hs.240443 | Homo sapiens cDNA: FLJ23538 fis, clone L | 1.40 | 3.71 |
| | 427461 | AA531527 | Hs.332040 | hypothetical protein MGC13010 | 1.36 | 2.98 |
| | 430205 | AB025904 | Hs.235168 | carbonic anhydrase XIV | 1.36 | 3.14 |
| 75 | 450796 | NM_001988 | Hs.25482 | envoplakin | 1.34 | 3.74 |
| | 407394 | AF005081 | | gb:Homo sapiens skin-specific protein (x | 1.30 | 3.26 |
| | 430513 | AJ012008 | Hs.241586 | G6C protein | 1.28 | 3.26 |
| | 411388 | X72925 | Hs.69752 | desmocollin 1 | 1.22 | 3.64 |
| | 431089 | BE041395 | | ESTs, Weakly similar to unknown protein | 1.14 | 3.71 |
| 80 | 444107 | T46839 | Hs.10319 | UDP glycosyltransferase 2 family, polype | 1.00 | 3.20 |
| | 443672 | AA323362 | Hs.9667 | butyrobetaine (gamma), 2-oxoglutarate di | 1.00 | 3.26 |

TABLE 52B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

| Pkey | CAT Number | Accession |
|--------|------------|---|
| 412636 | 1438_1 | M77830 NM_004415 AF139065 BG681115 BG740377 BI712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 A951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599 BC005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI467252 AU159919 AI760816 BF082516 AI439101 AA451923 AI340326 AI590975 BI791553 AI700963 AI142892 AA039975 AA946936 AA644381 BM314884 AA702424 AI176112 AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI346078 W95070 AA149191 AA026864 AI830049 AW780435 AI078449 AI819984 AI858282 BI468588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 AI927207 AI205263 BF082491 AW021347 AI568096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 AI910434 BF082513 AI494069 AI270027 AI635878 AA128330 BG681425 BE706078 R20904 BG680058 BG676647 BF764409 AA026654 AV745530 BI762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 AI571075 BE067786 AV721320 AI022862 N29754 C03378 N84767 AI131077 H30146 BE714290 AI686869 AI568892 AI915596 AW105614 AI887258 AI538577 BE926474 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 BI770853 BG679406 BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040941 AA337270 AW384371 AW847442 BI058659 BE813665 W95048 W25458 AW177786 AA025851 BI367133 BF7154837 BG949393 BE714441 AW996245 BE711801 AI284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 AI498487 AV711317 AI809938 AI808768 AI240593 AI915771 H80564 T99937 T70802 BI836699 AI123195 BI757837 AW439843 AW172765 BE018717 BE464329 BE302285 H96902 BF477981 BE674508 BE670755 H95980 T15387 N27807 AA256634 BE276324 BG775668 BG680336 AW991605 AA455904 AW265494 AW265432 BF911380 AA456370 BF911379 AA195677 BF914311 BF913866 BG775059 BG951874 AI572169 BC021735 AI669212 AL120184 AI769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245 BF960659 AA987907 Z41449 BF908059 BF908053 BF908049 BE699424 BF908060 BF962832 BF952020 BF963134 BI035538 BF908052 BF908057 BF090026 BF943158 AI632924 BF512340 BF952021 BF960776 BF943437 BF942847 AI768015 F09778 F04816 F07221 AA102645 AI633838 AA617929 BF947001 BI035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815 BC285809 BE940673 BG432524 BE157554 BG676980 AU144284 AI745383 AU159045 AI693500 AW293668 AW371408 BE856107 AI338042 AW188320 AI698246 BE673290 AW297653 AA156532 AI017342 AI916754 AI190644 AI184302 AA857671 BE857018 AI307420 AI318157 AW204327 AW664668 AW274339 AA582788 AI345741 AW301433 AI873468 AW137388 BF718731 BF718413 AA877495 BF001575 AI824693 AW849604 AW849405 AW849396 AW849173 BE673179 AI611327 AA705753 BE715478 AW849414 AW849399 AI085759 AI140849 T67412 AI889885 AW104647 AI912495 AI889874 AI744241 BE717113 BE717108 BE715564 AI872527 AA029457 C00338 AI469558 BE715577 AA045413 BF843813 NM_058173 AF414087 W72837 BF742809 AW070916 BE092421 AI905687 AA340069 BE074512 AI905623 AI905633 BG202312 W72838 AI139456 BG218084 BE926938 BE186013 AW176044 AW291950 BG185269 BG197186 BG192597 BG183176 BG207535 AI127172 BE815819 AI905624 R75793 BG202313 AI905837 BE815853 AK056896 AI924216 AI660493 AI984141 AI991272 AA593860 AI983793 AI346155 AI274929 AI281211 AI821178 BC020841 BF352476 BF843140 BF917041 W80832 AA630445 BF350167 BE162052 BE931808 AI572329 BGS36379 BE875818 AW751975 W39241 BF808798 W22600 BF082190 AW031290 R42801 H98235 H17925 AI631236 AI933786 H42736 AF000152 AU123911 AW140526 BM354207 BF800492 BM142340 BE019322 AL597008 AW327818 BI041915 AW504825 AW504941 BF987969 NM_005730 U81556 AI422831 AU154008 AA147822 AA873109 AI089244 AI360868 AW168024 AI819848 AA811327 AI355616 AA281629 AI880578 AI274316 AW014622 AI268660 AI270283 AA171981 AI349410 AA402469 AI421985 AI004864 AI423497 AI361503 AI363096 AW805345 AL539979 AA553967 AW502264 AI290698 N22420 AI281054 AI500699 AW342095 C75122 AW504577 AI130811 AI423567 R79086 AI80451 BE222885 AI697830 AI279575 BF438693 AW576277 BE218210 AI952376 AA506609 AI147566 AI391690 AA991622 AI696368 AI784664 AA741555 AI002681 AW474554 AW474508 D25623 AI493929 AA179800 W73566 AW411368 AA147971 AA088581 BF804510 AI145809 AU148108 AA223219 AU157840 AW169757 AI537862 N42341 AI128667 AW327853 AA713915 W15255 W56743 AA058322 H81878 AA723464 N27523 R37745 AA613566 AI526353 AI905211 BF802713 N40338 AA249397 BF752939 BE250441 H64761 BF853011 H81877 H96088 AL576453 W73585 H39990 AW438965 BF899684 AI040299 AL561879 AA293821 H27760 BC018922 AL533396 BE513580 BF432649 AI884985 AA404264 AW024396 AW167863 AW027036 AI302177 AI660487 AW026086 BF432564 BF091011 AI193156 AA744623 AI859510 BI063081 BI061541 AA777036 BG058486 BI063555 AI349411 BF874521 AW139801 AI268585 AA401267 AI905209 R64276 N72043 AF022231 BI256540 AU134437 BG826972 BE298386 AW134499 AW206089 BF846730 AW500331 BF849336 BI041697 AI857745 AW192840 AW410527 AI697435 AW006631 AW504124 AL048926 AI085476 AW327855 AA459344 AW207516 AW204875 BM142514 BF436650 AA960980 AW242609 BI012363 AW837102 BE703126 BE814612 BE837981 BE703141 BF343101 R47375 AA031413 N40264 BG027363 BF526360 BE391263 AA280192 BE294042 BE250630 AU147734 AU146610 AA196787 N59465 AW575791 H16738 H96089 H64762 AW006603 BE857292 AI719393 AU155418 BG770385 AA339673 BG337748 H42694 BE834346 AA090896 BE619985 BM006968 R46008 BF304621 AA172280 AW957721 BF304885 BF933455 BF809973 BG386280 AW079808 T51091 AL520569 BE694350 T06360 BF347780 BE560703 BE296629 AW796921 AW798102 AW805749 AW805872 BF895060 AW794380 BF380449 AW794466 AW794538 AFD05081 BG193848 BG940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826 |

TABLE 52C:

| | |
|--------------|---|
| Pkey: | Unique number corresponding to an Eos probeset |
| Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. |
| Strand: | Indicates DNA strand from which exons were predicted. |
| Nt_position: | Indicates nucleotide positions of predicted exons. |

| | | | | |
|----|--------|---------|--------|--|
| 80 | Pkey | Ref | Strand | Nt_position |
| | 401781 | 7249190 | Minus | 83215-83435,83531-83656,83740-83901,8423 |
| | 401780 | 7249190 | Minus | 28397-28617,28920-29045,29135-29296,2941 |
| | 402075 | 8117407 | Plus | 121907-122035,122804-122921,124019-12416 |
| | 401760 | 9929699 | Plus | 83126-83250,85320-85540,94719-95287 |

| | | | |
|--------|---------|-------|--|
| 401747 | 9789672 | Minus | 118596-118816,119119-119244,119609-11976 |
| 402294 | 2282012 | Minus | 2575-3000 |
| 401785 | 7249190 | Minus | 165776-165996,166189-166314,166408-16656 |
| 405542 | 9857564 | Plus | 71331-72183 |
| 402970 | 9650703 | Minus | 124891-125049 |
| 400995 | 8099094 | Plus | 141186-141601 |
| 405885 | 7577703 | Minus | 42574-42998 |
| 404049 | 3688074 | Minus | 75765-78155 |
| 403752 | 7678857 | Plus | 33704-33828 |
| 402525 | 9800048 | Minus | 19748-20683 |
| 404029 | 7671252 | Plus | 108716-111112 |
| 401994 | 4153858 | Minus | 42904-43124,43211-43336,44607-44763,4519 |

TABLE 53A: ABOUT 298 GENES UPREGULATED IN MELANOMA METASTASES RELATIVE TO PRIMARY MELANOMAS
 Table 53A lists about 298 genes upregulated in melanoma metastases relative to primary melanomas. Genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Key:
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of melanoma metastasis AIs divided by the 90th percentile of primary melanoma AIs
 R2: 90th percentile of melanoma metastasis AIs divided by the 90th percentile of primary melanoma AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

| Pkey | ExAccn | UnigenelD | Unigene Title | R1 | R2 |
|--------|-----------|-----------|--|-------|-------|
| 407245 | X90568 | Hs.172004 | titin | 10.56 | 11.32 |
| 412228 | AW503785 | Hs.73792 | complement component (3d/Epstein Barr vi | 9.22 | 6.14 |
| 426752 | X69490 | Hs.172004 | titin | 8.78 | 10.44 |
| 418310 | AA814100 | Hs.86693 | ESTs | 8.85 | 6.49 |
| 414522 | AW518944 | Hs.76325 | immunoglobulin J chain | 8.37 | 4.39 |
| 433447 | U29195 | Hs.3281 | neuronal pentraxin II | 8.27 | 7.25 |
| 456373 | BE247706 | Hs.89751 | membrane-spanning 4-domains, subfamily A | 7.78 | 6.70 |
| 425545 | N98529 | Hs.158295 | Homo sapiens, clone MGC.12401, mRNA, com | 7.49 | 9.02 |
| 428087 | AA100573 | Hs.182421 | tropoin C2, fast | 7.45 | 7.65 |
| 436485 | X59135 | Hs.156110 | immunoglobulin kappa constant | 7.35 | 6.18 |
| 414646 | AA353776 | Hs.901 | CD48 antigen (B-cell membrane protein) | 6.97 | 5.75 |
| 412519 | AA196241 | Hs.73980 | tropoin T1, skeletal, slow | 6.15 | 6.33 |
| 430280 | AA361258 | Hs.237868 | interleukin 7 receptor | 6.07 | 3.11 |
| 449078 | AK001256 | Hs.22975 | KIAA1576 protein | 6.05 | 8.55 |
| 437952 | D63209 | Hs.5944 | solute carrier family 11 (proton-coupled | 6.03 | 5.36 |
| 412561 | NM_002286 | Hs.74011 | lymphocyte activation gene 3 | 5.85 | 5.57 |
| 431574 | AW572659 | Hs.261373 | hypothetical protein dJ434014.3 | 5.74 | 6.40 |
| 458079 | AI796870 | Hs.54277 | DNA segment on chromosome X (unique) 992 | 5.72 | 4.76 |
| 417880 | BE241595 | Hs.82848 | selectin L (lymphocyte adhesion molecule | 5.71 | 5.00 |
| 429412 | NM_006235 | Hs.2407 | POU domain, class 2, associating factor | 5.69 | 3.84 |
| 420338 | AA825595 | Hs.88269 | Homo sapiens, clone MGC.17339, mRNA, com | 5.37 | 4.12 |
| 430580 | AA806105 | Hs.300697 | immunoglobulin heavy constant gamma 3 (G | 5.31 | 6.02 |
| 428804 | AK000713 | Hs.193736 | hypothetical protein FLJ20706 | 5.29 | 7.97 |
| 410361 | BE391804 | Hs.62661 | guanylate binding protein 1, interferon- | 5.26 | 2.93 |
| 445784 | AI253155 | Hs.146065 | ESTs | 5.12 | 3.10 |
| 409461 | AA382169 | Hs.54483 | N-myc (and STAT) interactor | 5.05 | 3.41 |
| 414020 | NM_002984 | Hs.75703 | small inducible cytokine A4 (homologous | 4.59 | 4.00 |
| 420301 | AA767526 | Hs.22030 | paired box gene 5 (B-cell lineage specif | 4.47 | 3.92 |
| 453857 | AL080235 | Hs.35861 | DKFZP586E1621 protein | 4.46 | 3.61 |
| 428242 | H55709 | Hs.22250 | leukemia inhibitory factor (cholinergic | 4.37 | 3.22 |
| 414829 | AA321568 | Hs.77436 | pleckstrin | 4.35 | 3.35 |
| 417878 | U90916 | Hs.82845 | Homo sapiens cDNA: FLJ21930 6s, clone H | 4.35 | 2.68 |
| 422603 | BE242587 | Hs.118651 | hematopoietically expressed homeobox | 4.27 | 2.67 |
| 451099 | R52795 | Hs.25954 | interleukin 13 receptor, alpha 2 | 4.27 | 3.67 |
| 441623 | AA315805 | | desmoglein 2 | 4.24 | 3.66 |
| 422241 | Y00062 | Hs.170121 | protein tyrosine phosphatase, receptor I | 4.22 | 3.60 |
| 417022 | NM_014737 | Hs.80905 | Ras association (RalGDS/AF-6) domain fam | 4.20 | 2.58 |
| 426317 | AA312350 | Hs.169294 | transcription factor 7 (T-cell specific, | 4.16 | 5.82 |
| 430770 | AA765694 | Hs.123296 | ESTs | 4.15 | 5.10 |
| 420931 | AF044197 | Hs.100431 | small inducible cytokine B subfamily (Cy | 4.12 | 5.06 |
| 406707 | S73840 | Hs.931 | myosin, heavy polypeptide 2, skeletal mu | 4.11 | 3.82 |
| 444863 | AW384082 | Hs.104879 | serine (or cysteine) proteinase inhibito | 4.10 | 2.68 |
| 432306 | Y18207 | Hs.303090 | protein phosphatase 1, regulatory (inhib | 4.04 | 4.10 |
| 417105 | X60992 | Hs.81226 | CD6 antigen | 4.03 | 4.51 |
| 409041 | AB033025 | Hs.50081 | Hypothetical protein, XP_051860 (KIAA119 | 4.02 | 3.72 |
| 432485 | N90866 | Hs.276770 | CDW52 antigen (CAMPATH-1 antigen) | 3.99 | 4.87 |
| 415165 | AW887604 | Hs.78065 | complement component 7 | 3.97 | 3.98 |
| 421181 | NM_005574 | Hs.184585 | LIM domain only 2 (rhombotin-like 1) | 3.96 | 3.19 |
| 421712 | AK000140 | Hs.107139 | hypothetical protein | 3.95 | 7.34 |
| 408380 | AF123050 | Hs.44532 | diubiquitin | 3.94 | 2.45 |
| 422423 | AF283777 | Hs.116481 | CD72 antigen | 3.93 | 3.29 |
| 408989 | AW361666 | Hs.49500 | KIAA0746 protein | 3.90 | 3.02 |
| 424321 | W74048 | Hs.1765 | lymphocyte-specific protein tyrosine kin | 3.84 | 3.40 |
| 420137 | AA306478 | Hs.95327 | CD3D antigen, delta polypeptide (TIT3 co | 3.84 | 4.84 |
| 424922 | BE386547 | Hs.217112 | hypothetical protein MGC10825 | 3.78 | 3.04 |
| 400440 | X83957 | Hs.83870 | nebulin | 3.77 | 4.89 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|-------|
| | 418870 | AF147204 | Hs.89414 | chemokine (C-X-C motif), receptor 4 (fus | 3.74 | 3.91 |
| | 450293 | N36754 | Hs.171118 | hypothetical protein FLJ00026 | 3.74 | 2.89 |
| | 432606 | NM_002104 | Hs.3066 | granzyme K (serine protease, granzyme 3; | 3.72 | 2.65 |
| | 408548 | AA055449 | Hs.63187 | ESTs, Weakly similar to ALUC_HUMAN !!! | 3.72 | 2.43 |
| 5 | 429490 | AI971131 | Hs.23889 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 3.71 | 2.23 |
| | 414821 | M53835 | Hs.77424 | Fc fragment of IgG, high affinity Ia, re | 3.70 | 2.36 |
| | 419749 | X73608 | Hs.93029 | sparc/osteonectin, cwcv and kazal-like d | 3.67 | 3.30 |
| | 410016 | AA297977 | Hs.57907 | small inducible cytokine subfamily A (Cy | 3.67 | 6.72 |
| | 433658 | L03678 | Hs.156110 | immunoglobulin kappa constant | 3.66 | 2.49 |
| 10 | 424153 | AA451737 | Hs.141496 | MAGE-like 2 | 3.64 | 2.65 |
| | 421666 | AL035250 | Hs.1408 | endothelin 3 | 3.64 | 5.92 |
| | 417696 | BE241624 | Hs.82401 | CD69 antigen (p60, early T-cell activati | 3.61 | 2.69 |
| | 429732 | U20158 | Hs.2488 | lymphocyte cytosolic protein 2 (SH2 doma | 3.60 | 1.95 |
| | 422173 | BE385828 | Hs.250619 | phorbol-like protein MDS019 (CEM15) | 3.59 | 3.08 |
| 15 | 413778 | AA090235 | Hs.75535 | myosin, light polypeptide 2, regulatory, | 3.57 | 11.26 |
| | 442379 | NM_004613 | Hs.8265 | transglutaminase 2 (C polypeptide, prote | 3.56 | 4.91 |
| | 439859 | AW292872 | Hs.124554 | ESTs | 3.53 | 4.15 |
| | 453064 | R40334 | Hs.89463 | potassium large conductance calcium-acti | 3.51 | 2.88 |
| | 411252 | AB018549 | Hs.69328 | MD-2 protein | 3.46 | 1.82 |
| 20 | 414324 | Y14768 | Hs.890 | lymphotoxin beta (TNF superfamily, membe | 3.45 | 4.65 |
| | 420286 | AI796395 | Hs.111377 | ESTs | 3.42 | 2.47 |
| | 413385 | M34455 | Hs.840 | indoleamine-pyrole 2,3 dioxygenase | 3.42 | 3.09 |
| | 442104 | L20971 | Hs.188 | phosphodiesterase 4B, cAMP-specific (dun | 3.41 | 2.22 |
| | 405545 | | | Target Exon | 3.40 | 2.46 |
| 25 | 416373 | AA195845 | | ESTs, Weakly similar to S12658 cysteine- | 3.40 | 5.64 |
| | 417410 | AF063020 | Hs.82110 | PC4 and SFRS1 interacting protein 1 | 3.37 | 4.27 |
| | 418522 | AA605038 | Hs.7149 | Homo sapiens cDNA: FLJ21950 fs, clone H | 3.33 | 2.37 |
| | 433470 | AW960564 | | transmembrane 4 superfamily member 1 | 3.33 | 3.13 |
| | 416975 | NM_004131 | Hs.1051 | granzyme B (granzyme 2, cytotoxic T-lymp | 3.32 | 2.51 |
| 30 | 442149 | AB014550 | Hs.8118 | KIAA0650 protein | 3.30 | 2.29 |
| | 411852 | AA528140 | Hs.107515 | ESTs, Weakly similar to T00329 hypotheti | 3.29 | 3.85 |
| | 447023 | AA356764 | Hs.17109 | integral membrane protein 2A | 3.24 | 2.79 |
| | 421566 | NM_000399 | Hs.1395 | early growth response 2 (Krox-20 (Drosop | 3.23 | 1.78 |
| | 414176 | BE140638 | Hs.75794 | EDG-2 (endothelial differentiation, lys | 3.22 | 2.90 |
| 35 | 447513 | AW955776 | Hs.313500 | ESTs, Moderately similar to ALU7_HUMAN A | 3.18 | 4.16 |
| | 421893 | NM_001078 | Hs.109225 | vascular cell adhesion molecule 1 | 3.17 | 3.59 |
| | 424148 | BE242274 | Hs.1741 | integrin, beta 7 | 3.14 | 2.29 |
| | 406648 | AA563730 | Hs.277477 | major histocompatibility complex, class | 3.13 | 3.05 |
| 40 | 429505 | AW820035 | Hs.278679 | a disintegrin and metalloproteinase doma | 3.13 | 2.36 |
| | 446619 | AU076643 | Hs.313 | secreted phosphoprotein 1 (osteopontin, | 3.12 | 2.55 |
| | 406704 | M21665 | Hs.929 | myosin, heavy polypeptide 7, cardiac mus | 3.12 | 5.54 |
| | 443885 | H91806 | Hs.15284 | ESTs | 3.08 | 3.55 |
| | 418203 | X54942 | Hs.83758 | CDC28 protein kinase 2 | 3.08 | 2.20 |
| | 417640 | D30857 | Hs.82353 | protein C receptor, endothelial (EPCR) | 3.06 | 3.21 |
| 45 | 447232 | AW499834 | Hs.327 | interleukin 10 receptor, alpha | 3.05 | 3.36 |
| | 409103 | AF251237 | Hs.112208 | XAGE-1 protein | 3.04 | 2.07 |
| | 413719 | BE439580 | Hs.75498 | small inducible cytokine subfamily A (Cy | 3.04 | 2.24 |
| | 421834 | BE543205 | Hs.288771 | DKFZP586A0522 protein | 3.03 | 1.91 |
| | 444666 | BE293347 | Hs.11638 | long-chain fatty acid coenzyme A ligase | 3.01 | 3.43 |
| 50 | 425295 | AA431366 | Hs.37251 | ESTs | 3.01 | 3.07 |
| | 429109 | AL008637 | Hs.196352 | neutrophil cytosolic factor 4 (40kD) | 2.99 | 2.55 |
| | 420340 | NM_000734 | Hs.97087 | CD32 antigen, zeta polypeptide (TiT3 com | 2.98 | 5.98 |
| | 418968 | NM_000078 | Hs.89538 | cholesteryl ester transfer protein, plas | 2.97 | 2.68 |
| | 438914 | N93892 | Hs.10727 | ESTs | 2.97 | 2.19 |
| 55 | 418391 | NM_003281 | Hs.84673 | tropomyosin I, skeletal, slow | 2.96 | 2.68 |
| | 419056 | M89957 | Hs.89575 | CD79B antigen (immunoglobulin-associated | 2.96 | 3.94 |
| | 449523 | NM_000579 | Hs.54443 | chemokine (C-C motif) receptor 5 | 2.96 | 4.02 |
| | 450847 | NM_003155 | Hs.25590 | stanniocalcin 1 | 2.96 | 3.24 |
| 60 | 418460 | M26315 | Hs.85258 | CD8 antigen, alpha polypeptide (p32) | 2.95 | 2.73 |
| | 426711 | AA383471 | Hs.343800 | conserved gene amplified in osteosarcoma | 2.94 | 2.36 |
| | 426559 | AB001914 | Hs.170414 | paired basic amino acid cleaving system | 2.93 | 2.17 |
| | 424528 | AW073971 | Hs.238954 | ESTs, Weakly similar to KIAA1204 protein | 2.93 | 2.70 |
| | 408633 | AW963372 | Hs.46677 | PRO2000 protein | 2.92 | 2.16 |
| | 443195 | BE148235 | Hs.193063 | Homo sapiens cDNA FLJ14201 fs, clone NT | 2.92 | 2.92 |
| 65 | 425234 | AW152225 | Hs.165909 | ESTs, Weakly similar to I38022 hypotheti | 2.90 | 2.09 |
| | 437802 | AI475995 | Hs.122910 | ESTs | 2.90 | 3.71 |
| | 417771 | AA804698 | Hs.82547 | retinoic acid receptor responder (Iazaro | 2.90 | 3.56 |
| | 438000 | AI825880 | Hs.5985 | non-kinase Cdc42 effector protein SPEC2 | 2.90 | 2.60 |
| 70 | 414555 | N98569 | Hs.76422 | phospholipase A2, group IIA (platelets, | 2.87 | 2.07 |
| | 421958 | AA357185 | Hs.109918 | ras homolog gene family, member H | 2.87 | 3.48 |
| | 420224 | M84371 | Hs.96023 | CD19 antigen | 2.86 | 4.77 |
| | 434883 | AW381538 | Hs.19807 | hypothetical protein MGC12959 | 2.85 | 5.44 |
| | 452852 | AK001972 | Hs.30822 | hypothetical protein FLJ11110 | 2.84 | 2.55 |
| | 427527 | AI809057 | Hs.153261 | immunoglobulin heavy constant mu | 2.84 | 4.16 |
| 75 | 446231 | NM_002163 | Hs.14453 | interferon consensus sequence binding pr | 2.83 | 2.97 |
| | 408838 | AI669535 | Hs.40369 | ESTs | 2.82 | 1.82 |
| | 429124 | AW505086 | Hs.196914 | minor histocompatibility antigen HA-1 | 2.82 | 4.21 |
| | 425023 | AW956889 | Hs.154210 | EDG-1 (endothelial differentiation, sph | 2.79 | 4.00 |
| | 425388 | AA329384 | Hs.156110 | immunoglobulin kappa constant | 2.79 | 2.28 |
| 80 | 414290 | AI568801 | Hs.71721 | ESTs | 2.78 | 3.19 |
| | 418255 | AW135405 | Hs.37251 | ESTs | 2.76 | 3.27 |
| | 451952 | AL120173 | Hs.301663 | ESTs | 2.75 | 1.74 |
| | 424865 | AF011333 | Hs.153563 | lymphocyte antigen 75 | 2.75 | 3.10 |

| | | | | | | |
|----|--------|-----------|-----------|---|------|------|
| | 409245 | AA361037 | | IRNA isopentenylpyrophosphate transferase | 2.74 | 2.12 |
| | 453920 | AI133148 | Hs.36602 | I factor (complement) | 2.74 | 3.08 |
| | 443968 | AA287702 | Hs.10031 | KIAA0955 protein | 2.74 | 2.34 |
| 5 | 434094 | AA305599 | Hs.238205 | hypothetical protein PRO2013 | 2.73 | 1.67 |
| | 436476 | AA326108 | Hs.33829 | bHLH protein DEC2 | 2.72 | 1.70 |
| | 428398 | AI249368 | Hs.98558 | ESTs | 2.72 | 2.05 |
| | 417141 | U22662 | | nuclear receptor subfamily 1, group H, m | 2.70 | 2.55 |
| | 427080 | AV068287 | Hs.301175 | ras-related C3 botulinum toxin substrate | 2.69 | 3.15 |
| 10 | 442485 | BE092285 | Hs.29724 | hypothetical protein FLJ13187 | 2.69 | 1.99 |
| | 429317 | AA831552 | Hs.268016 | Homo sapiens cDNA: FLJ21243 fis, clone C | 2.69 | 1.70 |
| | 443998 | AI620661 | Hs.296276 | ESTs | 2.69 | 2.30 |
| | 417542 | J04129 | Hs.82269 | progesterone-associated endometrial prote | 2.68 | 3.23 |
| | 414291 | AI289619 | Hs.13040 | G protein-coupled receptor 86 | 2.68 | 3.01 |
| | 448861 | AL049951 | Hs.22370 | Homo sapiens mRNA: cDNA DKFZp56400122 (I | 2.66 | 2.51 |
| 15 | 432435 | BE218886 | Hs.282070 | ESTs | 2.65 | 3.28 |
| | 430132 | AA204686 | Hs.234149 | hypothetical protein FLJ20647 | 2.65 | 3.04 |
| | 427792 | M63928 | Hs.180841 | tumor necrosis factor receptor superfam | 2.64 | 3.82 |
| | 414696 | AF002020 | Hs.76918 | Niemann-Pick disease, type C1 | 2.64 | 1.94 |
| 20 | 420991 | AW504814 | Hs.287379 | Homo sapiens mRNA for FLJ001111 protein, | 2.64 | 2.51 |
| | 401566 | | | NM_005159:Homo sapiens actin, alpha, car | 2.63 | 3.74 |
| | 444119 | R41231 | Hs.184261 | ESTs, Weakly similar to T26886 hypotheti | 2.63 | 2.13 |
| | 425231 | AA527161 | | ESTs | 2.61 | 2.95 |
| | 417427 | M90391 | Hs.82127 | interleukin 16 (lymphocyte chemoattracta | 2.61 | 1.90 |
| 25 | 437669 | AI358105 | Hs.123164 | ESTs, Weakly similar to match to ESTs AA | 2.60 | 4.45 |
| | 413856 | D13639 | Hs.75586 | cyclin D2 | 2.60 | 5.71 |
| | 407928 | NM_002262 | Hs.41682 | killer cell lectin-like receptor subfam | 2.59 | 2.68 |
| | 443247 | BE614387 | Hs.333893 | c-Myc target JPO1 | 2.58 | 2.77 |
| | 447131 | NM_004585 | Hs.17466 | retinoic acid receptor responder (tazaro | 2.58 | 9.28 |
| 30 | 443021 | AA368546 | Hs.8904 | Ig superfamily protein | 2.58 | 4.49 |
| | 424779 | AL046851 | Hs.153053 | CD37 antigen | 2.58 | 3.88 |
| | 425235 | AA353113 | Hs.112497 | Homo sapiens cDNA: FLJ22743 fis, clone H | 2.57 | 2.09 |
| | 424265 | AF173901 | Hs.144287 | hair/eyenhancer-of-split related with YRP | 2.57 | 3.57 |
| | 426780 | BE242284 | Hs.172199 | adenylate cyclase 7 | 2.57 | 1.86 |
| 35 | 452721 | AJ269529 | Hs.301871 | solute carrier family 37 (glycerol-3-pho | 2.56 | 2.90 |
| | 442904 | AW575008 | Hs.11355 | thymopoietin | 2.56 | 3.39 |
| | 433646 | AA603319 | Hs.155195 | ESTs | 2.54 | 2.19 |
| | 417289 | D86962 | Hs.81875 | growth factor receptor-bound protein 10 | 2.53 | 4.56 |
| | 422640 | M37984 | Hs.118845 | troponin C, slow | 2.53 | 5.38 |
| 40 | 448413 | AI745379 | Hs.42911 | ESTs | 2.53 | 2.08 |
| | 429536 | AA873016 | Hs.206097 | oncogene TC21 | 2.52 | 2.49 |
| | 446272 | BE268912 | Hs.14601 | hematopoietic cell-specific Lyn substrat | 2.52 | 3.46 |
| | 424378 | W28020 | Hs.167988 | neural cell adhesion molecule 1 | 2.52 | 2.91 |
| | 410257 | BE244044 | Hs.61469 | hypothetical protein | 2.51 | 3.67 |
| 45 | 427609 | AK000436 | Hs.179791 | hypothetical protein FLJ20429 | 2.51 | 3.11 |
| | 424868 | AI568170 | Hs.96886 | ESTs | 2.51 | 2.30 |
| | 418945 | BE246762 | Hs.89499 | arachidonate 5-lipoxygenase | 2.50 | 2.64 |
| | 420899 | NM_001629 | Hs.100194 | arachidonate 5-lipoxygenase-activating p | 2.50 | 3.04 |
| | 413441 | AI929374 | Hs.75367 | Src-like-adaptor | 2.49 | 2.37 |
| 50 | 414761 | AU077228 | Hs.77256 | enhancer of zeste (Drosophila) homolog 2 | 2.49 | 1.82 |
| | 429493 | AL134708 | Hs.145998 | ESTs | 2.49 | 2.40 |
| | 419631 | AW188117 | | popeye protein 3 | 2.48 | 1.85 |
| | 437175 | AW968078 | Hs.87773 | protein kinase, cAMP-dependent, catalyti | 2.48 | 2.32 |
| | 421552 | AF026692 | Hs.105700 | secreted frizzled-related protein 4 | 2.47 | 4.17 |
| 55 | 420158 | AI791905 | Hs.95549 | hypothetical protein | 2.47 | 2.62 |
| | 453987 | AA323750 | Hs.235026 | Homo sapiens, clone IMAGE:4247529, mRNA, | 2.47 | 2.49 |
| | 429640 | U83508 | Hs.2463 | angiopoietin 1 | 2.47 | 2.57 |
| | 437330 | AL353944 | Hs.50115 | Homo sapiens mRNA: cDNA DKFZp761J1112 (I | 2.46 | 2.42 |
| | 426969 | AI936504 | | CDK-like kinase 1 | 2.46 | 2.41 |
| 60 | 427674 | NM_003528 | Hs.2178 | H2B histone family, member Q | 2.46 | 2.17 |
| | 405547 | | | NM_018833*:Homo sapiens transporter 2, A | 2.46 | 2.84 |
| | 406678 | U77534 | | gb:Human clone 1A11 immunoglobulin varia | 2.45 | 2.89 |
| | 407013 | U35637 | Hs.83870 | gb:Human nebulin mRNA, partial cds | 2.45 | 3.40 |
| | 428746 | AW503820 | Hs.192861 | Spi-B transcription factor (Spi-1/PU.1 r | 2.43 | 6.25 |
| 65 | 453953 | AW408337 | Hs.36972 | CD7 antigen (p41) | 2.39 | 4.01 |
| | 427759 | BE245578 | Hs.2200 | perforin 1 (pore forming protein) | 2.39 | 4.56 |
| | 443071 | AL080021 | Hs.8986 | complement component 1, q subcomponent, | 2.39 | 3.31 |
| | 437211 | AA382207 | Hs.5509 | ecotropic viral integration site 2B | 2.38 | 3.15 |
| | 440596 | H13032 | Hs.103378 | hypothetical protein MGC11034 | 2.37 | 3.68 |
| 70 | 452651 | AI218918 | Hs.30209 | KIAA0854 protein | 2.36 | 4.08 |
| | 421563 | NM_006433 | Hs.105806 | granulysin | 2.34 | 3.25 |
| | 421924 | BE514514 | Hs.109606 | coronin, actin-binding protein, 1A | 2.33 | 3.38 |
| | 449092 | U91641 | | alpha2,8-sialyltransferase | 2.32 | 3.53 |
| | 425367 | BE271188 | Hs.155975 | protein tyrosine phosphatase, receptor t | 2.32 | 7.02 |
| 75 | 418117 | AI922013 | Hs.83496 | linker for activation of T cells | 2.30 | 3.56 |
| | 425795 | AJ000479 | Hs.159543 | EDG-6 (endothelial differentiation, G-p | 2.26 | 3.42 |
| | 428111 | S76617 | Hs.2243 | B lymphoid tyrosine kinase | 2.25 | 3.69 |
| | 439981 | AI348408 | Hs.124675 | ESTs, Weakly similar to T14742 hypotheti | 2.25 | 4.05 |
| | 425722 | AI659076 | Hs.97031 | hypothetical protein MGC13047 | 2.25 | 3.44 |
| 80 | 436648 | R18656 | | ESTs | 2.24 | 3.23 |
| | 452250 | BE618654 | Hs.28607 | hypothetical protein A-211C6.1 | 2.23 | 3.08 |
| | 441715 | AI929453 | Hs.342655 | Homo sapiens cDNA FLJ13289 fis, clone OV | 2.23 | 3.30 |
| | 423397 | NM_001838 | Hs.1652 | chemokine (C-C motif) receptor 7 | 2.22 | 3.25 |
| | 449626 | AA774247 | Hs.301637 | zinc finger protein 258 | 2.21 | 3.14 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|-------|
| 5 | 412975 | T70956 | Hs.75106 | clusterin (complement lysis inhibitor, S | 2.18 | 3.41 |
| | 418739 | AA310964 | Hs.88012 | SHP2 interacting transmembrane adaptor | 2.15 | 3.62 |
| | 418185 | AW958272 | Hs.347326 | intercellular adhesion molecule 2 (ICAM | 2.09 | 5.21 |
| | 436420 | AA443966 | Hs.31595 | ESTs | 2.07 | 3.81 |
| | 418174 | L20688 | Hs.83656 | Rho GDP dissociation inhibitor (GDI) bet | 2.05 | 3.14 |
| | 420626 | AF043722 | Hs.99491 | RAS guanyl releasing protein 2 (calcium | 2.01 | 4.42 |
| | 428289 | M26301 | Hs.2253 | complement component 2 | 2.00 | 3.33 |
| | 429683 | AF148213 | Hs.211604 | a disintegrin-like and metalloprotease (| 2.00 | 3.75 |
| 10 | 421445 | AA913059 | Hs.104433 | Homo sapiens, clone IMAGE:4054868, mRNA | 1.96 | 3.68 |
| | 450300 | AL041440 | Hs.58210 | ESTs, Highly similar to ITH4_HUMAN INTER | 1.91 | 4.84 |
| | 416445 | AL043004 | Hs.79337 | KIAA0135 protein | 1.91 | 3.41 |
| | 409817 | BE295464 | Hs.56607 | Williams-Beuren syndrome chromosome regi | 1.87 | 3.53 |
| | 416967 | BE616731 | Hs.80645 | interferon regulatory factor 1 | 1.86 | 3.55 |
| 15 | 437740 | AA810265 | Hs.122915 | ESTs | 1.86 | 3.79 |
| | 437938 | AI950087 | Hs.1869 | gbwq05c02.x1 NCI_CGAP_Kid12 Homo sapien | 1.83 | 3.42 |
| | 425240 | AA306495 | Hs.1869 | phosphoglucosyltransferase 1 | 1.83 | 3.75 |
| | 406972 | M32053 | Hs.2556 | gbtHuman H19 RNA gene, complete cds. | 1.80 | 4.03 |
| | 430378 | Z29572 | Hs.2556 | tumor necrosis factor receptor superfam | 1.78 | 3.53 |
| 20 | 437470 | AL390147 | Hs.134742 | hypothetical protein DKFZp547D065 | 1.78 | 3.39 |
| | 416350 | AF188625 | Hs.189507 | phospholipase A2, group IID | 1.78 | 5.48 |
| | 417852 | AJ250562 | Hs.82749 | transmembrane 4 superfamily member 2 | 1.78 | 4.88 |
| | 414682 | AL021154 | Hs.76884 | inhibitor of DNA binding 3, dominant neg | 1.77 | 5.79 |
| | 444090 | S69115 | Hs.10306 | natural killer cell group 7 sequence | 1.74 | 3.41 |
| 25 | 427278 | AL031428 | Hs.174174 | KIAA0601 protein | 1.74 | 3.80 |
| | 418618 | U66097 | Hs.86724 | GTP cyclohydrolase 1 (dopa-responsive dy | 1.73 | 4.21 |
| | 420397 | NM_007018 | Hs.97437 | centrosomal protein 1 | 1.73 | 3.21 |
| | 418678 | NM_001327 | Hs.167379 | cancer/testis antigen (NY-ESO-1) | 1.73 | 3.77 |
| | 459245 | BE242623 | Hs.31939 | manic fringe (Drosophila) homolog | 1.72 | 3.12 |
| 30 | 425356 | BE244879 | Hs.155339 | inositol polyphosphate-5-phosphatase, 14 | 1.71 | 3.55 |
| | 423984 | AF163825 | Hs.136713 | pre-B lymphocyte gene 3 | 1.70 | 7.70 |
| | 422355 | AW403724 | Hs.300697 | coagulation factor VII (serum prothrombi | 1.70 | 3.10 |
| | 451579 | AW607731 | Hs.26670 | Human PAC clone RP3-515N1 from 22q11.2-q | 1.68 | 4.19 |
| | 451287 | AK002158 | Hs.26194 | likely homolog of mouse immunity-associa | 1.68 | 5.76 |
| 35 | 416819 | U77735 | Hs.80205 | pim-2 oncogene | 1.67 | 3.17 |
| | 409896 | AW205479 | Hs.279780 | NY-REN-18 antigen | 1.67 | 3.74 |
| | 447532 | AK000614 | Hs.18791 | hypothetical protein FLJ20607 | 1.66 | 3.62 |
| | 426666 | AW500131 | Hs.171763 | CD22 antigen | 1.65 | 4.67 |
| | 412265 | AA101325 | Hs.86154 | hypothetical protein FLJ12457 | 1.65 | 3.43 |
| 40 | 416971 | R34657 | Hs.80658 | uncoupling protein 2 (mitochondrial, pro | 1.64 | 3.66 |
| | 430449 | AA352723 | Hs.241471 | RN86 | 1.62 | 3.09 |
| | 424661 | M29551 | Hs.151531 | protein phosphatase 3 (formerly 2B), cat | 1.61 | 3.37 |
| | 453027 | AI879341 | Hs.539 | ribosomal protein S29 | 1.61 | 11.60 |
| | 410068 | AK633888 | Hs.58435 | FYN-binding protein (FYN-120/130) | 1.60 | 3.28 |
| 45 | 440446 | NM_013385 | Hs.7189 | pleckstrin homology, Sec7 and coiled/coi | 1.59 | 3.14 |
| | 453657 | W23237 | Hs.296162 | AD037 protein | 1.59 | 3.12 |
| | 418102 | R58958 | Hs.26608 | hypothetical protein MGC15880 | 1.58 | 3.55 |
| | 424614 | X54486 | Hs.151242 | serine (or cysteine) proteinase inhibito | 1.58 | 3.07 |
| | 406791 | AI220684 | Hs.347939 | hemoglobin, alpha 2 | 1.55 | 5.06 |
| 50 | 421703 | AI936513 | Hs.1416 | Fc fragment of IgE, low affinity II, rec | 1.53 | 3.59 |
| | 421859 | AA356620 | Hs.108947 | KIAA0050 gene product | 1.52 | 3.41 |
| | 416783 | AA206186 | Hs.79889 | monocyte to macrophage differentiation-a | 1.52 | 3.28 |
| | 456086 | AL161999 | Hs.77324 | eukaryotic translation termination facto | 1.47 | 3.34 |
| | 425783 | AI026740 | Hs.1948 | ribosomal protein S21 | 1.46 | 4.95 |
| 55 | 407682 | AL035858 | Hs.3807 | FXFD domain-containing ion transport reg | 1.46 | 3.48 |
| | 409169 | F00991 | Hs.50889 | (clone PWHLC2-24) myosin light chain 2 | 1.45 | 3.25 |
| | 435624 | AF218942 | Hs.24889 | formin 2 | 1.45 | 3.11 |
| | 413969 | X14034 | Hs.75648 | phospholipase C, gamma 2 (phosphatidyl | 1.45 | 3.33 |
| | 426530 | U24578 | Hs.278625 | complement component 4A | 1.44 | 4.27 |
| 60 | 425928 | SS5736 | Hs.238852 | ESTs, Weakly similar to hypothetical pro | 1.44 | 3.65 |
| | 418219 | AA731836 | Hs.137319 | ESTs | 1.43 | 4.01 |
| | 429071 | AW794126 | Hs.195453 | ribosomal protein S27 (metalloproteinstimuli | 1.41 | 4.23 |
| | 418473 | AA243335 | Hs.309943 | nuclear body protein Sp140 | 1.41 | 3.29 |
| | 423766 | AA303799 | Hs.300141 | ribosomal protein L39 | 1.40 | 3.22 |
| 65 | 430150 | L05148 | Hs.234569 | zeta-chain (TCR) associated protein kina | 1.39 | 3.29 |
| | 416370 | N90470 | Hs.203697 | CD38 antigen (p45) | 1.36 | 3.08 |
| | 406758 | AA552326 | Hs.77039 | ATP synthase, H transporting, mitochondr | 1.32 | 3.29 |
| | 448610 | NM_006157 | Hs.21602 | nel (chicken)-like 1 | 1.31 | 3.85 |
| | 444674 | BE562200 | Hs.244 | amino-terminal enhancer of split | 1.30 | 3.10 |
| 70 | 407694 | U77594 | Hs.37682 | retinoic acid receptor responder (tazaro | 1.30 | 3.91 |
| | 427349 | AA360154 | Hs.177415 | Finkel-Biskis-Reilly murine sarcoma viru | 1.28 | 3.59 |
| | 419032 | W81330 | Hs.99877 | ESTs, Highly similar to JAK3B [H.sapiens | 1.28 | 3.21 |
| | 436553 | AW407157 | Hs.8997 | immunoglobulin lambda locus | 1.27 | 4.00 |
| | 415138 | C18356 | Hs.295944 | tissue factor pathway inhibitor 2 | 1.24 | 3.25 |
| | 406623 | X69392 | Hs.5898 | ribosomal protein L26 | 1.24 | 3.31 |
| 75 | 437895 | AB014568 | Hs.5898 | KIAA0668 protein | 1.21 | 3.33 |
| | 421143 | AB024536 | Hs.102171 | immunoglobulin superfamily containing le | 1.18 | 3.35 |

TABLE 53B:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

Pkey CAT Number Accession

| | | |
|--------|---------|--|
| 441623 | 3362_1 | BC022413 BE395396 BF754175 AA506621 BE706665 BE706678 AA723159 BE153169 BE706729 BE706558 BE153312 BE706706 AW371853 AW371849 BE153241 BC017410 AI337912 AI090244 AW090300 BE219837 AI623661 BE501576 BE501734 AI742232 AI023964 AI458424 AA975373 AI288904 AI984583 AA890325 N32562 AI358102 AW241694 AI038448 AI672071 AI018389 AA576391 AA977874 AW189392 W37448 AA612894 AI277548 H89551 AI699774 H89355 AA315805 AW579186 BC014584 BC014581 AW780125 AI672414 BE328145 AW600919 BF031306 AW172758 BE708322 AA345675 BE875779 H28241 H25318 BF540913 BG179688 BF110202 AA528775 W37573 BE041644 AW366504 BM129522 BM129822 AI122760 BE718200 AW887496 AA149420 BE706307 BE539395 BE748765 AI373653 R75904 BF979185 BF691393 BG495595 BI094458 BE706702 BC496559 BF248373 BG494800 |
| 416373 | 3442_1 | AK056582 AW755252 AL596757 BF827376 BF827373 BF827375 BF827369 BF826900 F01252 BC022888 BI850312 AA195845 BF825671 BF574821 Z21696 F32854 AA211780 F21569 AI288453 AI803678 AA180309 AI074627 AA192950 AA661688 F36698 F32290 F28773 F22692 AA424993 AW340328 AA192247 BF672229 BF575143 BF673106 BF693623 |
| 433470 | 6624_1 | X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262377 BE044033 AW008570 AW529505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AI103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW674145 C05782 AI985264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AI136645 BF843900 AW806193 AA502832 AA649494 AI568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AJ377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 AI344943 AI348877 AI348860 BE621857 BE156280 AA450996 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI259821 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 |
| 409245 | 3199_2 | AF030234 BC017465 BG008526 AW505550 BM460141 N47324 AA361037 AA321632 N45606 AV752798 AV657116 AA296632 AU137857 AW467027 AI742080 AI624350 H58206 AA478518 AW439997 AW393555 AW393523 AI559753 AI808732 R66856 H01374 BI257369 BI259830 AW960845 BM466252 AW956813 BE768647 AV658853 BM055248 BF372070 BF372055 BF372061 AA347852 AA905863 BG505078 AV654024 BF093291 AW021929 H22650 AA459715 BG496341 BE697763 BI254209 BG499543 H42946 BI059780 BI086741 H87896 H87599 BF691752 BE768511 BG940948 W37195 BF372041 BE883796 BF372082 BF367329 BF909744 AW966003 AV714014 BI492868 BI495144 AA921845 AI693426 AI652147 AI435449 H47325 AI434429 AA573137 AI183429 AI829962 AI332526 BF513937 AI189561 AI221962 AI378034 AW118897 AW665247 AW340077 N41605 AA478519 AA63875 AI858260 AA463379 AI293205 BE045947 AA971089 AI125820 BG940947 AI080245 AA884954 AI125702 AI382934 AA31835 AI358631 AW439905 AI027833 AI399648 AI014533 AA347851 AA738261 N67374 N69081 AI768667 AA948472 AI819214 AA293133 AI186725 AA889214 AI222635 BI495143 N29605 N48812 AA769041 AI492769 D56771 AA095911 BE222062 D56772 AW372265 BM054985 DI2465 BG534562 AW003511 H87486 H42880 AW190293 BF594697 BF377611 H22043 BI255749 BI492848 H16217 H21980 H22651 H88179 H87354 H44052 H25165 H44128 |
| 417141 | 9517_1 | AJ391712 U22662 NM_005693 AW166878 BF339795 AI970974 AI521157 AI335082 AW339789 AI288682 BF477594 BF477593 AI703008 AI290961 AI049684 AW770753 AI208561 AI699406 F33996 AA630563 AI985346 AI927058 AA533982 AW204589 AI206938 AW590068 AI263769 AA991550 AI192005 AL558946 AI524337 AL516239 AL580848 AL580658 AI719135 AW026500 AI698217 AI872977 AI670983 AI654870 AA493407 AA548525 AI016420 AA843563 W15576 H61726 AA913245 BF438146 AL524338 BI762380 AU1136488 BI759892 AV655930 T78977 BI524075 BE538944 AA527161 BG211784 AA527065 AA505489 AW512550 BC022323 AF204171 NM_022361 BM264431 BE670789 AW188117 AI025298 AA861832 H84897 AI382294 AA662874 AW993380 BE813742 H84368 AI188074 N20482 H84369 |
| 426969 | 12113_1 | M59287 AI936504 AI694705 AI679216 AI679235 BF110184 AW518110 AI679811 AW054981 BE465531 BE327409 AW339105 BI714787 AI871568 AW129115 AU145080 AI223299 AW129986 AW780771 BG654629 AU144657 BF437422 AI478374 AA492513 AU157562 AI826962 AU145528 AI951093 AW513819 AA042856 AA725690 AW733176 AI028702 AI251890 AI811729 AW975208 AW339589 AI147868 AU157862 AA629327 BF476670 BE464796 AW510511 AA399098 AA398210 AI291998 AI160296 AU158075 N34811 BE326407 AI270552 AA496923 AA508002 AI270284 AI139504 BF437009 AI354626 AI936336 AA287250 AA491855 BF445818 AA688026 AA284510 AW151564 AA412072 AA709241 H89332 BF445769 BF989466 BF989472 AA631105 AI129915 W96362 AA515277 AA541513 L29222 AV758119 D82109 AL040956 BE244413 AV645640 BE246321 BE246314 D82116 AL036176 AA331779 AU100106 BE243857 AU076865 AW972327 AA497087 AI687039 AW072798 AI174455 AU156788 AA044401 AA046086 BE244986 AI634456 BE242945 BE242089 AU156034 BE244982 AL567955 BI005141 AA040426 AW630506 BF155668 AU118544 BG573573 W96436 AA373395 BE710347 AI564154 AI708332 AA729530 N92729 AI573015 T29655 H89333 H85847 AI886473 AW189980 H02905 AI811986 AU157753 W66829 AA020844 AU158204 AA057356 AA283466 AA405504 AA017027 W94754 AA226498 W72391 H66461 C00442 H01925 BI912232 U77534 U77537 |
| 406678 | 0_0 | AK056270 AV706896 AK692935 AI681140 AW162481 AW087114 AW157019 AI689795 AW251085 AW206911 BF438207 AW134945 BE041668 BF111425 U91641 NM_013305 BF968902 U55966 AU130750 BE174853 AI929731 AW161524 R43753 BE779688 |
| 449092 | 4406_1 | AJ002788 AL118666 AI381600 BE672862 AW500520 BF223709 AW593740 AA262174 AA810597 AA810596 AA810595 F09382 BF976590 AW968002 AA262288 BF931698 AW968014 R18656 BM459356 AW794189 BF954184 Z42558 BF891641 BF963380 Z45874 F05187 X93079 BF742651 BF742649 R51324 D80031 BI457883 F06613 Z43128 F12243 BF950830 H19040 BF950829 F06439 R14947 F06702 R61037 R52173 R14953 R12174 R13610 H10426 R11851 T65264 R18737 |
| 437938 | 66997_1 | U71456 AA482911 W78802 AW856538 BF737212 N36809 N35320 AA282915 AW505512 AI653832 W87891 AI961530 T85904 H59397 R97278 W01059 AI820532 T82391 AI820501 T63226 R66056 R67840 AW961101 AA337499 W37181 AA180009 AW205862 AA988777 AA856975 BF172457 BG751124 AI741346 AI950344 AI689062 AI872193 AW102898 AW173586 AI763273 AI890387 AW150329 AI762688 AA488892 AI356394 AI539642 AA642789 AI950087 BF589902 N70208 AA283144 AA488964 H60052 R97040 BF886630 AW967677 AW971573 AW967671 AI308119 AA251875 AA908598 AI819225 AI564269 AA908741 AA293273 AA969759 AW276905 AA044209 H83488 T92467 X69392 T24055 |

TABLE 53C:

Pkey:

Unique number corresponding to an Eos probelet

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.

NL_position: Indicates nucleotide positions of predicted exons.

| Pkey | Ref | Strand | NL_position |
|--------|---------|--------|--|
| 405545 | 1054740 | Plus | 118677-118807,119091-119296,121626-12182 |
| 401566 | 8469090 | Minus | 96277-96420,96979-97160 |
| 405547 | 1054740 | Plus | 124361-124520,124914-125050 |

TABLE 54A: ABOUT 161 GENES UPREGULATED IN PRIMARY MELANOMAS FROM TUMORS THAT LATER METASTASIZED RELATIVE TO PRIMARY MELANOMAS THAT DID NOT METASTASIZE LATER

Table 54A lists about 161 genes upregulated in primary melanomas from tumors that later metastasized relative to primary melanomas that did not metastasize later. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number

ExAccn: Exemplar Accession number, Genbank accession number

UnigeneID: Unigene number

Unigene Title: Unigene gene title

R1: 90th percentile of AIs for primary melanomas that later metastasized divided by the 90th percentile of AIs for primary melanomas that did not metastasize later

R2: 90th percentile of AIs for primary melanomas that later metastasized divided by the 90th percentile of AIs for primary melanomas that did not metastasize later, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

| Pkey | ExAccn | UnigeneID | Unigene Title | R1 | R2 |
|--------|----------|-----------|---|------|------|
| 448966 | AW372914 | Hs.86149 | phosphoinositol 3-phosphate-binding prot | 7.15 | 3.41 |
| 413916 | N49813 | Hs.75615 | apclipoprotein C-II | 5.93 | 6.55 |
| 414807 | A1738616 | Hs.77348 | hydroxyprostaglandin dehydrogenase 15-(N | 5.64 | 2.98 |
| 415668 | AW957684 | Hs.306814 | hypothetical protein FLJ21889 | 5.03 | 4.56 |
| 440274 | R24595 | Hs.7122 | scrapie responsive protein 1 | 4.98 | 4.83 |
| 417542 | J04129 | Hs.82269 | progesterone-associated endometrial prote | 4.96 | 7.07 |
| 427882 | AA640987 | Hs.193767 | ESTs | 4.68 | 4.68 |
| 452744 | A1267652 | Hs.246107 | Homo sapiens mRNA; cDNA DKFZp434E082 (fr | 4.29 | 3.06 |
| 407907 | A1752235 | Hs.41270 | procollagen-lysine, 2-oxoglutarate 5-dio | 3.94 | 3.86 |
| 424410 | W79027 | Hs.271762 | ESTs | 3.67 | 3.19 |
| 429083 | Y09397 | Hs.227817 | BCL2-related protein A1 | 3.46 | 2.49 |
| 407951 | W77762 | Hs.79015 | antigen identified by monoclonal antibod | 3.31 | 3.06 |
| 426330 | L22524 | Hs.2256 | matrix metalloproteinase 7 (matrilysin, | 3.27 | 2.12 |
| 440099 | AL080058 | Hs.6909 | DKFZP564G202 protein | 3.22 | 2.69 |
| 428001 | H97428 | Hs.219907 | ESTs, Moderately similar to Transforming | 3.20 | 1.85 |
| 451099 | R52795 | Hs.25954 | interleukin 13 receptor, alpha 2 | 3.18 | 4.61 |
| 442432 | BE093589 | Hs.38178 | hypothetical protein FLJ23468 | 3.13 | 2.11 |
| 430643 | AW970065 | Hs.287425 | MEGF10 protein | 3.10 | 3.31 |
| 412262 | W26406 | | seven in absentia (Drosophila) homolog 1 | 3.06 | 3.94 |
| 438328 | A1492261 | Hs.32450 | ESTs | 3.05 | 3.09 |
| 409760 | AA302840 | | gb:EST10534 Adipose tissue, white 1 Homo | 3.01 | 2.65 |
| 453912 | AL121031 | | SWI/SNF related, matrix associated, acti | 2.94 | 1.86 |
| 416426 | AA180256 | Hs.210473 | Homo sapiens cDNA FLJ14872 fs, clone PL | 2.91 | 3.70 |
| 407744 | AB020629 | Hs.38095 | ATP-binding cassette, sub-family A (ABC1 | 2.88 | 2.53 |
| 453935 | A1633770 | Hs.42572 | ESTs | 2.88 | 2.00 |
| 452689 | F33868 | Hs.284176 | transferrin | 2.84 | 6.47 |
| 449550 | AA353125 | Hs.184721 | ESTs | 2.83 | 4.74 |
| 409417 | AA156247 | Hs.104879 | serine (or cysteine) proteinase inhibito | 2.82 | 2.43 |
| 438898 | A1819863 | Hs.106243 | ESTs | 2.81 | 2.08 |
| 430191 | A1149880 | Hs.188809 | ESTs | 2.80 | 2.69 |
| 408418 | AW963897 | Hs.44743 | KIAA1435 protein | 2.79 | 1.75 |
| 450157 | AW961576 | Hs.60178 | ESTs | 2.77 | 3.40 |
| 420380 | AA640891 | Hs.102406 | ESTs | 2.77 | 4.28 |
| 443172 | AW662964 | Hs.199061 | p300/CBP-associated factor | 2.75 | 2.88 |
| 456629 | AW891965 | | histone deacetylase 3 | 2.72 | 2.24 |
| 407857 | A1928445 | Hs.92254 | synaptotagmin-like 2 | 2.72 | 1.93 |
| 421097 | A1280112 | Hs.125232 | Homo sapiens cDNA FLJ13266 fs, clone OV | 2.68 | 2.59 |
| 436280 | A1690734 | | Homo sapiens cDNA: FLJ22562 fs, clone H | 2.67 | 2.79 |
| 407550 | Y10515 | | gb:H.sapiens mRNA for CD58 T7 protein. | 2.65 | 1.98 |
| 427871 | AW992405 | Hs.59622 | Homo sapiens, clone IMAGE:3507281, mRNA, | 2.64 | 1.76 |
| 427899 | AA829286 | Hs.332053 | serum amyloid A1 | 2.59 | 3.01 |
| 442793 | A1017798 | | ESTs, Weakly similar to T147_HUMAN CARGO | 2.58 | 1.60 |
| 446619 | AU076643 | Hs.313 | secreted phosphoprotein 1 (osteopontin, | 2.57 | 1.91 |
| 444381 | BE387335 | Hs.283713 | ESTs, Weakly similar to S64054 hypotheti | 2.57 | 2.13 |
| 458247 | R14439 | Hs.209194 | ESTs | 2.56 | 2.61 |
| 451668 | Z43948 | Hs.326444 | cartilage acidic protein 1 | 2.52 | 2.74 |
| 433980 | AA137152 | Hs.286049 | phosphoserine aminotransferase | 2.51 | 1.88 |
| 412719 | AW016610 | Hs.816 | ESTs | 2.50 | 1.68 |
| 441789 | D52059 | Hs.7972 | KIAA0871 protein | 2.50 | 3.11 |
| 405885 | | | Target Exon | 2.50 | 3.15 |
| 453464 | A1884911 | Hs.32989 | receptor (calcitonin) activity modifying | 2.48 | 3.33 |
| 417821 | BE245149 | Hs.82643 | protein tyrosine kinase 9 | 2.48 | 1.66 |
| 450202 | AW969756 | Hs.34145 | ESTs, Weakly similar to B49647 GTP-bindi | 2.47 | 2.79 |
| 436825 | AW341123 | Hs.120275 | ESTs | 2.47 | 2.55 |
| 424762 | AL119442 | Hs.183684 | eukaryotic translation initiation factor | 2.42 | 2.28 |
| 432426 | AW973152 | Hs.31050 | ESTs | 2.42 | 1.76 |
| 409095 | AW337272 | Hs.293656 | ESTs, Moderately similar to S72481 proba | 2.41 | 2.41 |
| 403752 | | | NM_002753:Homo sapiens mitogen-activate | 2.41 | 2.87 |

| | | | | | |
|----|--------|-----------|--|------|------|
| | 404489 | | Target Exon | | |
| | 411690 | AA669253 | RNA, U2 small nuclear | 2.39 | 1.97 |
| | 439195 | H89360 | gb: yw28d08.s1 Morton Fetal Cochlea Homo | 2.37 | 2.54 |
| 5 | 453582 | AW854339 | hypothetical protein FLJ11937 | 2.37 | 2.27 |
| | 438461 | AW075485 | phosphoserine aminotransferase | 2.36 | 2.81 |
| | 432878 | BE386490 | Purin | 2.35 | 2.91 |
| | 416647 | BE297139 | replication protein A2 (32kD) | 2.35 | 2.28 |
| | 428666 | AL080190 | Homo sapiens mRNA: cDNA DKFZp434A202 (fr | 2.33 | 1.97 |
| 10 | 413645 | AA130992 | gb:zo15e02.s1 Stralagene colon (937204) | 2.32 | 2.92 |
| | 421282 | AA288914 | ESTs | 2.31 | 2.63 |
| | 434418 | AF134707 | a disintegrin and metalloproteinase doma | 2.31 | 1.85 |
| | 413204 | BE071603 | gb:QV3-BT0510-161299-032-03 BT0510 Homo | 2.31 | 2.21 |
| | 449720 | AA311152 | hypothetical protein FLJ21562 | 2.31 | 1.49 |
| 15 | 451838 | AW005866 | ESTs | 2.30 | 1.78 |
| | 410943 | AW968322 | low molecular mass ubiquinone-binding pr | 2.28 | 2.05 |
| | 459711 | BE386801 | trinucleotide repeat containing 3 | 2.28 | 2.39 |
| | 429489 | AF008203 | aristatless-like homeobox 3 | 2.27 | 2.39 |
| | 429493 | AL134708 | ESTs | 2.26 | 1.97 |
| 20 | 422283 | AW411307 | ESTs | 2.26 | 2.77 |
| | 441989 | AA306207 | CDC45 (cell division cycle 45, S.cerevis | 2.26 | 1.78 |
| | 419352 | AJ675008 | protein kinase, cAMP-dependent, regulato | 2.26 | 1.84 |
| | 427393 | AB029018 | ESTs | 2.25 | 1.47 |
| | 418522 | AA605038 | KIAA1095 protein | 2.25 | 1.83 |
| 25 | 433458 | AA832055 | Homo sapiens cDNA: FLJ21950 fis, clone H | 2.24 | 2.42 |
| | 452782 | AA028166 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.24 | 1.76 |
| | 443910 | AW051711 | ESTs | 2.24 | 2.34 |
| | 408832 | AW085690 | ESTs | 2.24 | 1.79 |
| 30 | 407283 | TS1008 | ESTs, Weakly similar to Z195_HUMAN ZINC | 2.22 | 1.52 |
| | 437376 | AA749400 | gb:yb55e08.s1 Stralagene ovary (937217) | 2.22 | 1.31 |
| | 450712 | AI732130 | ESTs | 2.22 | 2.44 |
| | 421362 | AK000050 | ESTs, Weakly similar to ALUB_HUMAN !!!! | 2.22 | 1.62 |
| | 445183 | AB007877 | hypothetical protein FLJ20043 | 2.22 | 2.36 |
| | 438501 | Z44110 | KIAA0417 gene product | 2.20 | 1.84 |
| 35 | 432882 | NM_013257 | phosphoinositol 3-phosphate-binding prot | 2.20 | 1.76 |
| | 414900 | AW452420 | serum/glucocorticoid regulated kinase-li | 2.19 | 1.59 |
| | 427704 | AW971063 | ESTs | 2.18 | 1.89 |
| | 404942 | | ESTs | 2.17 | 1.86 |
| 40 | 448019 | AW947164 | splicing factor, arginine/serine-rich 9 | 2.17 | 1.86 |
| | 459254 | AA694386 | ESTs, Moderately similar to I38022 hypot | 2.17 | 1.64 |
| | 418965 | AI002238 | ESTs | 2.16 | 1.61 |
| | 443357 | AW016773 | splicing factor, arginine/serine-rich 11 | 2.16 | 1.79 |
| | 412432 | AA126311 | low molecular mass ubiquinone-binding pr | 2.16 | 2.32 |
| 45 | 449567 | AI990790 | ESTs | 2.15 | 2.73 |
| | 433179 | AW362945 | ESTs | 2.08 | 2.85 |
| | 408243 | Y00787 | ESTs | 2.07 | 4.77 |
| | 435294 | T84084 | interleukin 8 | 2.05 | 3.12 |
| | 449656 | AA002008 | Homo sapiens cDNA FLJ11723 fis, clone HE | 1.97 | 2.89 |
| 50 | 412649 | NM_002206 | ESTs | 1.94 | 3.60 |
| | 445162 | AB011131 | integrin, alpha 7 | 1.93 | 2.76 |
| | 419356 | AI656166 | piccolo (presynaptic cytomatrix protein) | 1.93 | 2.66 |
| | 424263 | M77640 | hypothetical protein FLJ22316 | 1.92 | 3.39 |
| | 414694 | NM_015362 | L1 cell adhesion molecule (hydrocephalus | 1.89 | 3.10 |
| 55 | 415825 | Y18024 | HSPC002 protein | 1.88 | 4.25 |
| | 409105 | AW467539 | inositol 1,4,5-trisphosphate 3-kinase B | 1.87 | 2.66 |
| | 444784 | D12485 | ESTs | 1.87 | 2.96 |
| | 404149 | | ectonucleotide pyrophosphatase/phosphodi | 1.85 | 2.80 |
| | 406387 | | C6002509*gi 5031885 ref NP_005568.1 li | 1.84 | 2.93 |
| 60 | 420871 | AA702972 | Target Exon | 1.82 | 2.96 |
| | 455797 | BE091833 | ESTs | 1.76 | 3.12 |
| | 418751 | BE389014 | gb:IL2-BT0731-260400-076-F04 BT0731 Homo | 1.75 | 3.12 |
| | 412347 | AW970026 | phosphoinositide-3-kinase, regulatory su | 1.70 | 3.20 |
| | 413211 | AW967107 | ubiquinol-cytochrome c reductase hinge p | 1.67 | 3.65 |
| | 459317 | BRCA1b | hypothetical protein MGC4365 | 1.66 | 2.89 |
| 65 | 425525 | AA358883 | Eos Control | 1.61 | 7.34 |
| | 436823 | AW749865 | ESTs | 1.59 | 2.67 |
| | 433669 | AL047879 | ESTs, Weakly similar to I38022 hypothi | 1.56 | 2.76 |
| | 424389 | AA339786 | ESTs, Weakly similar to ALU2_HUMAN ALU S | 1.55 | 2.76 |
| | 426672 | AW270555 | lymphocyte-specific protein 1 | 1.53 | 2.95 |
| 70 | 415977 | AL037622 | hypothetical protein | 1.51 | 3.39 |
| | 404780 | | methionine aminopeptidase; eIF-2-associ | 1.47 | 2.65 |
| | 436476 | AA326108 | Target Exon | 1.43 | 2.77 |
| | 428284 | AA535762 | bHLH protein DEC2 | 1.41 | 3.04 |
| 75 | 448571 | AA486794 | NM_004545:Homo sapiens NADH dehydrogenas | 1.38 | 2.94 |
| | 428156 | BE269388 | ESTs, Weakly similar to 16.7Kd protein { | 1.37 | 2.80 |
| | 447752 | M73700 | mitochondrial ribosomal protein L20 | 1.36 | 3.29 |
| | 447455 | H38335 | lactotransferrin | 1.35 | 2.70 |
| | 453281 | W46280 | Homo sapiens mRNA for FLJ00058 protein, | 1.35 | 3.03 |
| | 413142 | M81740 | ESTs, Weakly similar to A25704 synapsin | 1.34 | 2.69 |
| 80 | 407194 | AA621644 | ornithine decarboxylase 1 | 1.33 | 2.96 |
| | 444107 | T46839 | gb:af54a01.s1 Soares_tetal_fetus_Nb2HF8_ | 1.32 | 2.70 |
| | 406797 | AI432224 | UDP glycosyltransferase 2 family, polype | 1.26 | 3.27 |
| | 406711 | N25514 | ribosomal protein L6 | 1.26 | 2.72 |
| | 414608 | BE396215 | myosin, light polypeptide 6, alkali, smo | 1.25 | 7.10 |
| | | | ATP synthase, H transporting, mitochondr | 1.24 | 2.72 |

| | | | | |
|----|--------|---------|--------|-----------------------------|
| | Pkey | Ref | Strand | NL_position |
| | 405885 | 7677703 | Minus | 42574-42998 |
| | 403752 | 7678857 | Plus | 33704-33828 |
| 5 | 404489 | 8113772 | Plus | 98183-98480 |
| | 404942 | 7382153 | Plus | 92095-92252 |
| | 404149 | 7534008 | Plus | 121831-121951,124044-124150 |
| | 406387 | 9256180 | Plus | 116229-116371,117512-117651 |
| | 404780 | 9887810 | Minus | 175708-175871 |
| 10 | 401846 | 7712190 | Minus | 82775-82823,82912-83022 |
| | 401254 | 9796309 | Plus | 152209-152383 |
| | 405752 | 9212305 | Plus | 91392-91528 |

TABLE 55A: ABOUT 201 GENES UPREGULATED IN PRIMARY MELANOMAS FROM TUMORS THAT DID NOT METASTASIZE RELATIVE TO PRIMARY MELANOMAS THAT LATER METASTASIZED

Table 55A lists about 201 genes upregulated in primary melanomas from tumors that did not metastasize relative to primary melanomas that metastasized later. Genes were selected from 59680 probesets on the Eos/Alfymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of AIs for primary melanomas that did not metastasize divided by the 90th percentile of AIs from primary melanomas that metastasized later
 R2: 90th percentile of AIs for primary melanomas that did not metastasize divided by the 90th percentile of AIs from primary melanomas that metastasized later, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

| | | | | | | |
|----|--------|-----------|-----------|--|------|------|
| | Pkey | ExAccn | UnigenelD | Unigene Title | R1 | R2 |
| | 413554 | AA319146 | Hs.75426 | secretogranin II (chromogranin C) | 8.08 | 5.48 |
| | 404854 | | | Target Exon | | |
| 30 | 406636 | L12064 | | gb:Homo sapiens (clone WR4.12VL) anti-th | 5.18 | 8.18 |
| | 433435 | BE545277 | Hs.340959 | Ts translation elongation factor, mitoch | 4.89 | 4.95 |
| | 408471 | NM_012317 | Hs.45231 | leucine zipper, down-regulated in cancer | 4.83 | 4.86 |
| | 433658 | L03678 | Hs.156110 | immunoglobulin kappa constant | 4.71 | 4.70 |
| 35 | 412802 | U41518 | Hs.74602 | aquaporin 1 (channel-forming integral pr | 4.71 | 3.85 |
| | 415801 | R24219 | Hs.278443 | Fc fragment of IgG, low affinity IIb, re | 3.98 | 4.01 |
| | 400417 | X72475 | | Target | 3.92 | 3.35 |
| | 419870 | AW403911 | Hs.266175 | phosphoprotein associated with GEMs | 3.83 | 2.78 |
| | 409190 | AU076536 | Hs.50984 | sarcoma amplified sequence | 3.67 | 2.29 |
| 40 | 408692 | AL040127 | Hs.34074 | dipeptidylpeptidase VI | 3.62 | 3.68 |
| | 423619 | T48691 | Hs.249159 | adrenergic, alpha-2A-, receptor | 3.61 | 3.89 |
| | 442117 | AW664964 | Hs.128899 | ESTs; hypothetical protein for IMAGE:447 | 3.56 | 3.61 |
| | 445745 | AB007924 | Hs.13245 | KIAA0455 gene product | 3.55 | 2.85 |
| | 406663 | U24683 | | immunoglobulin heavy constant mu | 3.38 | 2.55 |
| 45 | 414522 | AW518944 | Hs.76325 | Immunoglobulin J chain | 3.34 | 6.16 |
| | 419235 | AW470411 | Hs.288433 | neurotrimin | 3.32 | 2.75 |
| | 441598 | A1733219 | Hs.58262 | ESTs | 3.32 | 2.74 |
| | 402294 | | | Target Exon | 3.31 | 3.71 |
| | 402737 | | | Target Exon | 3.24 | 2.35 |
| 50 | 414135 | NM_004419 | Hs.2128 | dual specificity phosphatase 5 | 3.22 | 2.87 |
| | 410268 | AA316181 | Hs.61635 | six transmembrane epithelial antigen of | 3.20 | 3.04 |
| | 427335 | AA448542 | Hs.251677 | G antigen 7B | 3.18 | 2.81 |
| | 404995 | | | ENSP00000251890: Monocytic leukemia zinc | 3.17 | 4.62 |
| | 430540 | AW245422 | | Homo sapiens cDNA: FLJ22105 fis, clone H | 3.13 | 2.34 |
| 55 | 430015 | AW768399 | | ESTs | 3.12 | 2.21 |
| | 414340 | A1022656 | Hs.296272 | ESTs | 3.12 | 1.93 |
| | 400072 | | | Eos Control | 3.09 | 2.87 |
| | 422567 | AF111178 | Hs.118407 | glypican 6 | 3.08 | 3.16 |
| | 401284 | | | Target Exon | 3.06 | 2.73 |
| 60 | 455839 | BE145814 | | gb:MR0-HT0208-101299-202-a04 HT0208 Homo | 3.04 | 2.56 |
| | 454027 | R40192 | Hs.21527 | Human DNA sequence from clone GS1-115M3 | 3.02 | 2.76 |
| | 437258 | AL041243 | Hs.174104 | ESTs | 3.00 | 3.15 |
| | 445612 | N94126 | Hs.12969 | hypothetical protein | 2.99 | 2.44 |
| | 417777 | A1823763 | Hs.7055 | ESTs, Weakly similar to I78885 serine/th | 2.98 | 2.40 |
| 65 | 437723 | A1672731 | Hs.13256 | ESTs | 2.97 | 2.13 |
| | 439658 | A1091277 | Hs.302634 | frizzled (Drosophila) homolog 8 | 2.95 | 2.46 |
| | 424321 | W74048 | Hs.1765 | lymphocyte-specific protein tyrosine kin | 2.95 | 2.77 |
| | 424761 | AA534528 | Hs.152944 | loss of heterozygosity, 11, chromosomal | 2.94 | 2.68 |
| | 405757 | | | Target Exon | 2.92 | 3.81 |
| 70 | 406621 | X57809 | Hs.8997 | immunoglobulin lambda locus | 2.92 | 3.00 |
| | 409060 | A1815867 | Hs.50130 | necdin (mouse) homolog | 2.92 | 6.71 |
| | 431712 | R26584 | Hs.267993 | hypothetical protein FLJ10143 | 2.86 | 2.16 |
| | 413441 | A1929374 | Hs.75367 | Src-like-adaptor | 2.82 | 2.50 |
| | 452651 | A1218918 | Hs.30209 | KIAA0854 protein | 2.82 | 2.48 |
| 75 | 422386 | AF105374 | Hs.115830 | heparan sulfate (glucosamine) 3-O-sulfot | 2.82 | 1.13 |
| | 439778 | AL109729 | Hs.99364 | putative transmembrane protein | 2.78 | 2.77 |
| | 434293 | NM_004445 | Hs.3796 | EphB6 | 2.77 | 1.92 |
| | 406642 | AJ245210 | | gb:Homo sapiens mRNA for immunoglobulin | 2.75 | 2.89 |
| | 406638 | M13861 | | gb:Human T-cell receptor active beta-cha | 2.70 | 2.03 |
| 80 | 432331 | W37862 | Hs.274368 | MSTP032 protein | 2.69 | 2.67 |
| | 408989 | AW361666 | Hs.49500 | KIAA0746 protein | 2.68 | 3.08 |
| | 401731 | | | NM_017990: Homo sapiens hypothetical pro | 2.68 | 2.58 |
| | 401979 | | | C17000767.gil11990770[emb]CAC19651.1f (A | 2.68 | 2.53 |
| | 415539 | A1733881 | Hs.72472 | BMP-R18 | 2.68 | 3.42 |
| | | | | | 2.68 | 2.51 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|------|
| | 425032 | NM_001186 | Hs.154276 | BTB and CNC homology 1, basic leucine zi | 2.67 | 2.13 |
| | 406837 | R70292 | Hs.156110 | immunoglobulin kappa constant | 2.66 | 3.25 |
| | 422550 | BE297626 | Hs.296049 | microfibrillar-associated protein 4 | 2.66 | 2.74 |
| | 425100 | AF051850 | Hs.154567 | supervillin | 2.65 | 2.80 |
| 5 | 452933 | AW391423 | Hs.288555 | Homo sapiens cDNA: FLJ22425 fis, clone H | 2.65 | 2.63 |
| | 439706 | AW872527 | Hs.59761 | ESTs, Weakly similar to DAP1_HUMAN DEATH | 2.64 | 1.84 |
| | 447232 | AW499834 | Hs.327 | interleukin 10 receptor, alpha | 2.63 | 2.63 |
| | 425580 | L11144 | Hs.1907 | galanin | 2.62 | 2.00 |
| 10 | 450680 | AF131784 | Hs.25318 | Homo sapiens clone 25194 mRNA sequence | 2.61 | 1.80 |
| | 412482 | AI499930 | Hs.334885 | mitochondrial GTP binding protein | 2.61 | 1.82 |
| | 433470 | AW960564 | | transmembrane 4 superfamily member 1 | 2.60 | 2.44 |
| | 419138 | U48508 | Hs.89631 | ryanodine receptor 1 (skeletal) | 2.60 | 2.47 |
| | 401112 | | | NM_024997:Homo sapiens hypothetical pro | 2.60 | 2.58 |
| 15 | 411802 | AA733204 | | nuclear transcription factor Y, gamma | 2.59 | 2.32 |
| | 407856 | AA045281 | Hs.266175 | phosphoprotein associated with GEMs | 2.59 | 1.88 |
| | 425209 | AL049761 | Hs.155140 | casein kinase 2, alpha 1 polypeptide | 2.58 | 2.81 |
| | 417165 | R80137 | Hs.302738 | Homo sapiens cDNA: FLJ21425 fis, clone C | 2.56 | 2.10 |
| | 442560 | AA365042 | Hs.325531 | ESTs, Weakly similar to 2004399A chromos | 2.55 | 3.97 |
| 20 | 408491 | AI088063 | Hs.7882 | ESTs | 2.54 | 2.74 |
| | 420223 | N27807 | | ribosomal protein L4 | 2.54 | 2.02 |
| | 444467 | AI150368 | Hs.143844 | ESTs | 2.54 | 2.59 |
| | 436729 | BE621807 | | transmembrane 4 superfamily member 1 | 2.53 | 2.29 |
| | 449217 | AA278536 | Hs.23262 | ribonuclease, RNase A family, k6 | 2.53 | 1.80 |
| 25 | 453507 | AF083217 | Hs.33085 | WD repeat domain 3 | 2.52 | 1.99 |
| | 420315 | NM_006299 | Hs.96448 | zinc finger protein 193 | 2.52 | 2.50 |
| | 443060 | D78874 | Hs.8944 | procollagen C-endopeptidase enhancer 2 | 2.50 | 2.35 |
| | 453500 | AI478427 | Hs.43125 | esophageal cancer related gene 4 protein | 2.50 | 2.44 |
| | 402692 | | | Target Exon | 2.50 | 1.73 |
| 30 | 427792 | M63928 | Hs.180841 | tumor necrosis factor receptor superfam | 2.50 | 4.55 |
| | 440065 | W03476 | Hs.266331 | hypothetical protein MGC4595 | 2.49 | 2.95 |
| | 420568 | F09247 | Hs.247735 | protocadherin alpha 10 | 2.49 | 3.55 |
| | 444115 | AW954585 | Hs.271920 | ESTs, Weakly similar to Z195_HUMAN ZINC | 2.49 | 2.52 |
| | 404049 | | | NM_018937:Homo sapiens protocadherin be | 2.48 | 2.67 |
| 35 | 417694 | R09486 | Hs.193118 | ESTs | 2.48 | 2.09 |
| | 420600 | BE011657 | Hs.165695 | ESTs, Weakly similar to unnamed protein | 2.48 | 2.00 |
| | 429922 | Z97630 | Hs.226117 | H1 histone family, member 0 | 2.47 | 2.01 |
| | 404752 | | | NM_024778:Homo sapiens hypothetical prot | 2.47 | 3.07 |
| | 421429 | NM_014922 | Hs.104305 | death effector filament-forming Ced-4-i | 2.47 | 2.46 |
| 40 | 436378 | AJ227874 | Hs.99244 | ESTs | 2.46 | 1.88 |
| | 429852 | AB010445 | Hs.225948 | small inducible cytokine subfamily A (Cy | 2.44 | 2.98 |
| | 431190 | AL134172 | Hs.120852 | ESTs | 2.44 | 2.48 |
| | 439979 | AW600291 | Hs.6823 | hypothetical protein FLJ10430 | 2.44 | 2.96 |
| | 436608 | AA628990 | Hs.192371 | down syndrome critical region protein DS | 2.44 | 3.16 |
| 45 | 445547 | D86181 | Hs.273 | galactosylceramidase (Krabbe disease) | 2.43 | 3.33 |
| | 443030 | R58048 | Hs.9238 | hypothetical protein FLJ23516 | 2.43 | 2.07 |
| | 416908 | AA333990 | Hs.80424 | coagulation factor XIII, A1 polypeptide | 2.43 | 3.36 |
| | 406782 | AAA30373 | | gb:zw20111.s1 Soares ovary tumor NbHOT H | 2.40 | 3.38 |
| | 407260 | L09095 | | gb:Homo sapiens mRNA fragment | 2.38 | 3.78 |
| 50 | 419556 | U29615 | Hs.91093 | chitinase 1 (chitotriosidase) | 2.36 | 3.56 |
| | 431365 | AA504080 | Hs.191958 | immunoglobulin superfamily receptor tran | 2.34 | 2.84 |
| | 414555 | N98569 | Hs.76422 | phospholipase A2, group IIA (platelets, | 2.33 | 3.21 |
| | 436485 | X59135 | Hs.156110 | immunoglobulin kappa constant | 2.31 | 2.94 |
| | 403632 | | | Target Exon | 2.27 | 2.80 |
| 55 | 434232 | AW297064 | Hs.131862 | ESTs | 2.24 | 2.98 |
| | 428114 | AI821548 | Hs.98363 | ESTs, Weakly similar to I38022 hypotheti | 2.23 | 2.81 |
| | 403294 | | | Target Exon | 2.19 | 2.81 |
| | 429249 | X81479 | Hs.2375 | egl-like module containing, mucin-like, | 2.16 | 3.13 |
| | 403295 | | | Target Exon | 2.15 | 2.95 |
| 60 | 427817 | AA503373 | Hs.186678 | ESTs | 2.13 | 2.80 |
| | 425154 | NM_001851 | Hs.154850 | collagen, type IX, alpha 1 | 2.08 | 3.28 |
| | 443176 | AI696081 | Hs.223770 | ESTs | 2.04 | 3.50 |
| | 401770 | | | C17001739:gi 2327052 gb AAC48759.1 (U9 | 2.04 | 5.39 |
| | 407124 | R08160 | | gb:yf18a07.s1 Soares fetal liver spleen | 2.03 | 2.95 |
| 65 | 456060 | C14904 | Hs.45184 | Homo sapiens cDNA FLJ12284 fis, clone MA | 2.03 | 2.97 |
| | 413053 | AW963263 | Hs.65377 | ESTs, Moderately similar to KIAA1399 pro | 2.01 | 3.42 |
| | 426653 | AA530892 | Hs.171695 | dual specificity phosphatase 1 | 2.01 | 3.05 |
| | 410677 | NM_003278 | Hs.65424 | tetranectin (plasminogen-binding protein | 2.01 | 3.58 |
| | 401673 | | | C16001416:gi 12743112 ref XP_010131.2 | 1.99 | 4.99 |
| 70 | 420983 | W95228 | Hs.100764 | cathepsin G | 1.95 | 5.47 |
| | 413624 | BE177019 | Hs.75445 | SPARC-like 1 (mast9, hev9) | 1.94 | 4.58 |
| | 433554 | AW957666 | Hs.8108 | disabled (Drosophila) homolog 1 | 1.93 | 2.82 |
| | 405121 | | | mitogen-activated protein kinase 8 inter | 1.92 | 2.82 |
| | 436456 | AW292677 | Hs.248122 | G protein-coupled receptor 24 | 1.92 | 2.80 |
| 75 | 450852 | AI983354 | Hs.7740 | oxysterol binding protein-like 1 | 1.91 | 5.08 |
| | 432902 | U75697 | | histone deacetylase 3 | 1.90 | 2.84 |
| | 422100 | AI096988 | Hs.111554 | ADP-ribosylation factor-like 7 | 1.89 | 3.04 |
| | 420162 | BE378432 | Hs.95577 | cyclin-dependent kinase 4 | 1.87 | 2.85 |
| | 424398 | BE397787 | Hs.146393 | homocysteine-inducible, endoplasmic reti | 1.85 | 3.71 |
| 80 | 416714 | AF283770 | Hs.79630 | CD79A antigen (immunoglobulin-associated | 1.85 | 3.38 |
| | 433465 | AV657778 | Hs.3314 | selenoprotein P, plasma, 1 | 1.85 | 3.57 |
| | 447990 | BE048821 | Hs.20144 | small inducible cytokine subfamily A (Cy | 1.82 | 6.17 |
| | 421563 | NM_006433 | Hs.105806 | granulysin | 1.80 | 3.50 |
| | 453804 | AA300204 | Hs.35276 | KIAA0852 protein | 1.78 | 2.87 |

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|--------|-----------|-----------|---|------|------|
| 429412 | NM_006235 | Hs.2407 | POU domain, class 2, associating factor | 1.78 | 3.54 |
| 437866 | AA156781 | | metallothionein 1E (functional) | 1.77 | 2.97 |
| 427751 | AF000152 | | conserved gene amplified in osteosarcoma | 1.75 | 6.89 |
| 400442 | | | DKFZP586G1722 protein | 1.74 | 3.60 |
| 456898 | NM_001928 | Hs.155597 | D component of complement (adipsin) | 1.74 | 3.45 |
| 414477 | U41635 | Hs.76228 | amplified in osteosarcoma | 1.71 | 4.99 |
| 432870 | AW974124 | | gb:EST386227 MAGE resequences, MAGM Homo | 1.68 | 2.86 |
| 456642 | AW451623 | Hs.109752 | putative c-Myc-responsive | 1.68 | 3.09 |
| 456694 | AW016382 | Hs.105642 | Homo sapiens cDNA: FLJ23271 fls, clone H | 1.66 | 2.83 |
| 430449 | AA352723 | Hs.241471 | RNB6 | 1.65 | 2.84 |
| 401029 | | | v-myc avian myelocytomatosis viral relat | 1.65 | 2.88 |
| 402742 | | | NM_002508:Homo sapiens nidogen (enactin) | 1.64 | 3.37 |
| 402559 | | | Rho GTPase activating protein 1 | 1.63 | 3.07 |
| 418271 | NM_000919 | Hs.83920 | peptidylglycine alpha-amidating monooxyg | 1.62 | 3.11 |
| 406851 | AA609784 | | major histocompatibility complex, class | 1.62 | 2.86 |
| 450912 | AW939251 | Hs.25647 | v-fos FBJ murine osteosarcoma viral onco | 1.60 | 3.94 |
| 447029 | AL137281 | Hs.17110 | Homo sapiens mRNA; cDNA DKFZp434C2016 (f | 1.60 | 3.75 |
| 417739 | Z43995 | | gb:HSC1QB121 normalized infant brain cDN | 1.59 | 2.96 |
| 452950 | AA428123 | Hs.302766 | tyrosine 3-monooxygenase/tryptophan 5-mo | 1.58 | 2.95 |
| 427461 | AA531527 | Hs.332040 | hypothetical protein MGC13010 | 1.58 | 4.11 |
| 444182 | AW160432 | Hs.296460 | craniofacial development protein 1 | 1.57 | 2.98 |
| 407815 | AW373860 | Hs.183860 | hypothetical protein FLJ20277 | 1.57 | 3.88 |
| 452887 | AI702223 | Hs.107253 | hypothetical protein DKFZp761F241 | 1.56 | 2.88 |
| 416819 | U77735 | Hs.80205 | pim-2 oncogene | 1.56 | 3.59 |
| 414583 | AA362907 | Hs.76494 | proline arginine-rich end leucine-rich r | 1.55 | 4.38 |
| 426104 | AI204418 | Hs.190080 | ESTs | 1.55 | 3.47 |
| 441591 | AF055992 | Hs.183 | Duffy blood group | 1.52 | 4.28 |
| 446406 | AI553681 | | Arg/Abi-interacting protein ArgBP2 | 1.49 | 2.87 |
| 427343 | AI880044 | Hs.176977 | protein kinase C binding protein 2 | 1.49 | 2.88 |
| 415550 | L13720 | Hs.78501 | growth arrest-specific 6 | 1.47 | 4.82 |
| 411961 | AA78432 | Hs.72956 | hypermethylated in cancer 1 | 1.46 | 3.48 |
| 406213 | | | ENSP00000246202:DJ63M2.2 (similar to AC | 1.42 | 3.19 |
| 400847 | | | NM_003105:Homo sapiens sortilin-related | 1.41 | 2.97 |
| 404642 | | | NM_021965:Homo sapiens phosphoglucomuta | 1.40 | 3.02 |
| 452650 | AW270150 | Hs.254516 | ESTs | 1.40 | 2.86 |
| 432894 | AW167668 | Hs.279772 | brain specific protein | 1.37 | 5.52 |
| 404030 | | | NM_015669:Homo sapiens protocadherin be | 1.37 | 3.03 |
| 422033 | AW245805 | Hs.110903 | claudin 5 (transmembrane protein deleted | 1.35 | 3.15 |
| 413762 | AW411479 | Hs.848 | FK506-binding protein 4 (59kD) | 1.34 | 3.09 |
| 425367 | BE271188 | Hs.155975 | protein tyrosine phosphatase, receptor t | 1.32 | 3.29 |
| 415198 | AW009480 | Hs.943 | natural killer cell transcript 4 | 1.32 | 2.89 |
| 406908 | Z25437 | | gb:H.sapiens protein-tyrosine kinase gen | 1.31 | 2.89 |
| 423959 | AA333025 | | gb:EST37122 Embryo, 8 week I Homo sapien | 1.31 | 2.88 |
| 408135 | AA317248 | Hs.42957 | methyltransferase-like 1 | 1.29 | 3.81 |
| 427523 | BE242779 | Hs.179526 | upregulated by 1,25-dihydroxyvitamin D-3 | 1.29 | 3.25 |
| 415512 | Y16270 | Hs.78482 | paralemnin | 1.29 | 2.85 |
| 413531 | AL036958 | Hs.75416 | DAZ associated protein 2 | 1.28 | 3.06 |
| 419608 | AL037237 | Hs.91586 | transmembrane 9 superfamily member 1 | 1.27 | 2.80 |
| 424614 | X54486 | Hs.151242 | serine (or cysteine) proteinase inhibitor | 1.26 | 2.90 |
| 422934 | BE244189 | Hs.122492 | hypothetical protein | 1.25 | 3.41 |
| 450935 | BE514743 | | tumor suppressor deleted in oral cancer- | 1.25 | 3.63 |
| 416630 | H69392 | Hs.174051 | small nuclear ribonucleoprotein 70kD pol | 1.24 | 2.93 |
| 416950 | AL049798 | Hs.80552 | dermatopontin | 1.22 | 2.81 |
| 412558 | AW962019 | | gb:EST374092 MAGE resequences, MAGG Homo | 1.21 | 3.02 |
| 419593 | W73092 | Hs.58282 | ESTs | 1.19 | 2.84 |
| 403470 | | | Target Exon | 1.14 | 2.82 |
| 402230 | | | Fgenesh predicted: CYTOCHROME P450 4F5 (| 1.12 | 2.96 |
| 400559 | | | Target Exon | 1.00 | 2.90 |
| 412695 | AW984439 | | gb:PM3-HN0011-220300-002-c05 HN0011 Homo | 1.00 | 2.84 |
| 427072 | H38046 | Hs.293981 | ESTs | 1.00 | 2.89 |
| 430439 | AL133561 | | DKFZP4348061 protein | 1.00 | 3.09 |
| 418183 | NM_001772 | Hs.83731 | CD33 antigen (gp67) | 1.00 | 2.93 |

TABLE 558:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

| | | | |
|----|--------|------------|---|
| 70 | Pkey | CAT Number | Accession |
| | 406636 | 0_0 | L12064 L12083 L12065 L12075 L12066 L12085 L12072 L12082 L12081 L12062 L12080 |
| | 430540 | 713_2 | BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 |
| | | | BM045810 AU120387 BG770238 BG686740 BG913323 BI759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 |
| 75 | | | AI365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903567 |
| | | | BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF986930 BM475542 AW246215 BE501897 BE903610 |
| | | | BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI458099 BE391391 BE259420 |
| | | | BE298109 AW245422 AI423847 AI914618 H80534 BE301004 AL531791 AI435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296 |
| | | | AI359493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AI421728 BG767231 BM462953 |
| 80 | | | BC340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512 |
| | | | W58732 W85690 BG958989 AI205206 H19721 W17051 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 |
| | | | F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114 |
| | | | AI243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103 |

| | | | |
|--------|--------|-----------|---|
| | | | AW008188 R07703 AA989120 AA746235 AW028983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 B1860809 BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591 BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 BM045010 AU120387 BG770238 BG686740 BG913323 B1759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 AI770171 BF196861 BE856897 AA463876 AJ375927 AA648810 AA948193 AA490916 AI459893 AI458188 AI240408 AI191843 AI131029 AW766399 AI365196 AW337984 AW026150 BE465591 BE674599 AI818438 AA772197 AI651927 AW151143 B1198825 BG819083 BM458764 BE903567 BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610 BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 BE298109 AW245422 AJ423847 AJ914618 H80534 BE301004 AL531791 AI435581 BF793112 AL577303 AA373265 BE746985 BF743630 BE879296 AI359493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AI421728 BG767231 BM462953 BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512 W58732 W85690 BG958989 AJ205206 H19721 W17051 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114 AI243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103 AW008188 R07703 AA989120 AA746235 AW028983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 B1860809 BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591 BE145823 BE145830 BE145884 BE145814 BE145905 BE145833 BE145834 BE145883 BE145889 AJ245210 AJ245212 AJ245211 AJ245213 M13861 |
| 430015 | 713_2 | | |
| 5 | | | |
| 10 | | | |
| 15 | | | |
| | 455839 | 1518842_1 | |
| | 406642 | 0_0 | |
| | 406638 | 0_0 | |
| | 433470 | 6624_1 | |
| 20 | | | |
| 25 | | | |
| 30 | | | |
| 35 | | | |
| 40 | | | |
| 45 | | | |
| | 411802 | 609_6 | |
| 50 | | | |
| | 420223 | 191648_1 | |
| | 436729 | 6624_1 | |
| 55 | | | |
| 60 | | | |
| 65 | | | |
| 70 | | | |
| 75 | | | |
| 80 | 406782 | 0_0 | |
| | 432902 | 35601_1 | |
| | | | X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H80983 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW671415 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL762600 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AI568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI601827 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 BF345917 AL549635 BI040919 AA733204 AA232382 T34425 T32000 BF906697 Z42382 BI544863 AL548378 AW816536 AW816719 BE152340 BF375392 AW816716 BE152336 BF375367 N27807 AA256634 BE276324 X75684 AL573167 AI445461 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI678712 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA706057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI799814 AA129575 AI671727 AI470033 BE646195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA962397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692846 AI061065 H80983 R79933 AI950693 AI245632 AI349390 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872628 AI927217 AI453453 AI189366 AW338678 AI261359 AI500576 BF477735 AI032569 AI972899 AI985583 Z28771 AI363829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 AI650338 BE773499 AI745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI565439 AI918453 AI472527 AI446740 AA035576 AA191414 AW671415 C05782 AI589264 D57558 AI468237 AI432033 AA989662 R21752 BF002457 AA988297 AL574095 AL576200 AL571074 AL574525 AL578810 BG498381 AI928364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA129574 AA136645 BF843900 AW806193 AA502832 AA649494 AI568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 AI377596 C06111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI248307 BE773483 AI567995 W60075 BF941183 AI738844 BE811458 BE773481 AI262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW806183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 BI755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 BI601827 BG741786 BI868522 AU135866 BI552770 BI259210 BI256520 BI255569 BG485098 BI258228 BG498501 BM044512 AU133984 AL556586 BE745111 BI222633 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF691383 BG721129 BG541578 BE906666 BG751098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI260895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088544 AI815987 BG528631 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D56120 AA343532 AA308636 F00242 AA376086 AA316968 AA343799 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088854 AA921353 R21800 AA011222 T97525 AA430373 AA968771 U75697 AI362269 AW575181 AL035820 AF039703 NM_003883 U66914 BE513355 BE302938 BE302936 BE303018 AA094475 F08725 R98879 R18769 BE019412 AA045846 AL120913 BE168807 BE168812 R21136 BE168915 H71247 N59055 AA533007 AW938705 BE260952 BE313803 AA307436 AW951917 AW581926 AW277164 AI439049 AW581905 AI744899 AW804572 BE004443 AA335928 AA486355 AA115468 AA312123 R77086 AA595186 AW166991 AI952071 AW593311 AW571813 AI749734 AI674761 AI560970 AI480266 AA534470 AA737815 BE300597 AW022818 |

| | | | | | | |
|----|--------------|---|--|--|--|--|
| 5 | 437866 | 34267_1 | BE300599 AA911621 AJ074678 BE300694 A1187018 R98969 AA456572 AJ032111 AJ830414 AA045874 AA932352 AJ81262 T78896 AA714518 AW009272 T17250 R76914 AW317029 H71248 AA931900 AA282808 AJ032140 AJ208512 AJ244759 AJ20456 AJ208085 AJ283758 AJ369297 R46731 H79779 AJ349348 AW273644 AJ555914 AJ220114 AW615802 AA887531 AA810217 AA832227 AJ567776 AJ918324 AA862566 AA831038 AW246807 W78118 R43091 Z41762 AW135694 AW263376 AA115046 T34171 T34077 N53974 W79902 BE514017 BE513761 H79778 AW878598 U52054 AL581000 AA156850 AW293839 BI335865 AA024963 BF149420 BE073977 AW602574 BE164012 BE163992 BE163974 AW402161 BM194134 AW966609 W84374 BF916380 AA385173 W84366 AA383743 BF903598 AA043776 W84421 AA778446 AW444904 BF446960 AA837481 AV755539 AW468444 AW468002 AA811830 AA581806 AI866686 AJ572124 AA687333 D20160 AA812489 AU185248 AU186004 AA156781 AJ536733 BM144850 AJ471883 AA040926 BF507639 AA043777 AW874142 BE832523 BE163972 BI022546 BI021204 BE875818 AW751975 W39241 BF808798 W22600 BF082190 AA031290 R42801 H98235 H17925 AJ631236 AJ933786 H42736 AF000152 AU123911 AW410526 BM354207 BF800492 BM142340 BE019322 AL597008 AW327818 BI041915 AW504825 AW504941 BF987969 NM_005730 UB1556 AA422831 AU154008 AA147822 AA873109 AJ089244 AJ360868 AW168024 AJ819848 AA811327 AJ355616 AA281629 AI880578 AJ274316 AW014622 AI268660 AJ270283 AA171981 AJ349410 AA402469 AJ421985 AJ004864 AJ423497 AJ361503 AJ363096 AW805345 AL539979 AA553967 AW502264 AI290698 N22420 AI281054 AJ500699 AW342095 C75122 AW504577 AJ130811 AJ423567 R79086 AJ860451 BE222885 AJ697830 AJ279575 BF438693 AW576277 BE218210 AJ952376 AA506609 AJ147566 AJ391690 AA991622 AJ696368 AJ784664 AA741555 AJ002681 AW474554 AW474508 D25623 AI493929 AW179800 W73566 AW411368 AA147971 AA088581 BF804510 AU145809 AU148108 AA223219 AU157840 AW169757 AJ537862 N42341 AI128667 AW327853 AA713915 W15255 W56743 AA058322 H81878 AA723464 N27523 R37745 AA613566 AL526353 AJ905211 BF802713 N40338 AA248397 BF752939 BE250441 H64761 BF853011 H81877 H96088 AL576453 W73585 H39990 AW438965 BF899684 AJ040299 AL561879 AA293821 H27760 BC018922 AL533396 BE513580 BF432649 AJ884985 AA404264 AW024396 AW167863 AW027036 AJ302177 AI660487 AW026086 BF432564 BF091011 AI193156 AA744623 AJ859510 BI063081 BI061541 AA777036 BG058486 BI063555 AJ349411 BF874521 AW139801 AI268585 AA401267 AJ905209 R64276 N72043 AF022231 BI256540 AU134437 BG826972 BE298386 AW134499 AW206089 BF846730 AW500331 BF849336 BI041697 AI857745 AW192840 AW410527 AJ697435 AW006631 AW504124 AL048926 A085476 AW327855 AA459344 AW207516 AW204875 BM142514 BF436650 AA960980 AW242609 BI012363 AW837102 BE703126 BE814612 BE837981 BE703141 BF343101 R47375 AA031413 N40264 BG027363 BF526360 BE391263 AA280192 BE294042 BE250630 AU147734 AU146610 AA196787 N59465 AW575791 H16738 H96089 H46762 AW006603 BE857292 AW179393 AU155418 BG777035 AA339673 BG337748 H42694 BE834346 AA090896 BE619985 BM006968 R46008 BF304621 AA172280 AW957721 BF304885 BF933455 BF809973 BG386280 AW079808 T51091 AL520569 BE694350 T06360 BF347780 BE560703 BE296629 AW974124 AA572989 AA569080 AA609784 R97304 R12357 R34740 Z43995 BG105015 R45824 AJ659533 AW022952 BM312713 C04108 AU159507 AW290967 AW235078 AW271693 AA999835 AL134290 AW235222 BM312405 AJ480093 AJ469044 AJ308242 AJ274858 AJ824850 AJ093881 BE857254 AW235980 AJ985474 AI540755 W17232 D56716 BE835412 AA091594 BE769194 BE769189 BE765413 BE766491 BF154895 BE765626 BF372247 BE769079 BE769122 BF154873 BF154880 Z26986 BE768478 BF372008 T34949 BE768476 BE768462 BF370113 BE835323 BE769217 BE769113 AA093838 BE769188 N88480 AA093969 AA092843 BE273069 AA333025 BE349913 BC002850 BC016704 NM_005851 AF089814 AK001498 AL537879 BG754157 AJ129659 AJ261895 BG397540 BF663515 AW517226 BG677982 AJ435188 AJ453123 AI198380 AA524481 BC981512 AW269638 AJ348113 AJ095743 AA457108 AW044584 AU151602 AJ744572 AJ078741 AI879729 AJ089613 AJ568618 BF109806 AW440972 AA401965 AI027227 AJ127506 AA434027 BF732901 AW264768 AA833667 AL038554 AJ568161 AI350340 AA402084 BE677778 AA933621 BF663514 BG763563 AL574521 BG177226 BG759860 BE906329 AW161323 AJ879350 BF946477 BF766208 AA633194 AL537880 AL038553 BG468205 BG761617 BI762655 BG436637 N49458 BI834722 BG397879 BI258799 AW004930 AA902847 AI832036 AW167549 AA743167 AA848017 AA365434 AI819503 AA767866 AI582000 N33615 AJ950146 AA444029 AA227130 AA041525 AW339842 AA865972 AA838006 AW157822 AI890994 BI771150 BI821666 BE779491 AW962019 BE389091 AW984433 AW984393 AW984439 AW984451 AW984371 AW984349 AW984356 AW984444 AW984443 AW984449 AL133561 AL117481 AL122069 AW435292 AJ968826 AL041090 | | | |
| 10 | 427751 | 15028_1 | | | | |
| 15 | | | | | | |
| 20 | | | | | | |
| 25 | 432870 | 1238170_1 | | | | |
| | 406851 | 0_0 | | | | |
| | 417739 | 2145372_1 | | | | |
| | 445406 | 11004_1 | | | | |
| 30 | | | | | | |
| 35 | 423959 | 887999_1 | | | | |
| | 450935 | 4469_1 | | | | |
| 40 | | | | | | |
| | 412558 | 1227364_1 | | | | |
| | 412695 | 1243394_1 | | | | |
| | 430439 | 6750_2 | | | | |
| 45 | TABLE 55C: | | | | | |
| | Pkey: | Unique number corresponding to an Eos probe set | | | | |
| | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA | | | | |
| | Strand: | sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. | | | | |
| 50 | NL_position: | Indicates DNA strand from which exons were predicted. | | | | |
| | | Indicates nucleotide positions of predicted exons. | | | | |
| 55 | Pkey | Ref | Strand | NL_position | | |
| | 404854 | 7143420 | Plus | 14260-14537 | | |
| | 402294 | 2282012 | Minus | 2575-3000 | | |
| | 402737 | 9212184 | Minus | 13358-13552 | | |
| | 404995 | 6006247 | Minus | 154015-154123 | | |
| | 401284 | 9800819 | Minus | 101307-101421 | | |
| | 405757 | 3334694 | Minus | 66825-70466 | | |
| 60 | 401731 | 9690317 | Plus | 43830-43963,44787-44935,45698-45810,4741 | | |
| | 401979 | 2826778 | Minus | 75693-75851,76977-77112 | | |
| | 401112 | 9966198 | Minus | 60628-61041 | | |
| | 402692 | 8468956 | Plus | 124606-125387 | | |
| | 404049 | 3688074 | Minus | 75765-78155 | | |
| 65 | 404752 | 7109522 | Minus | 120168-120326 | | |
| | 403632 | 8572864 | Minus | 35197-35358 | | |
| | 403294 | 8096496 | Plus | 41565-41881 | | |
| | 403295 | 8096528 | Plus | 22386-22708 | | |
| | 401770 | 9958312 | Plus | 183424-183576 | | |
| 70 | 401673 | 7689903 | Minus | 122587-122705,122765-123047 | | |
| | 405121 | 8102330 | Minus | 35816-36004,36587-36684 | | |
| | 400442 | 9887672 | Plus | 59362-59574 | | |
| | 401029 | 8117523 | Plus | 41999-42172 | | |
| | 402742 | 9212200 | Minus | 23487-23613 | | |
| 75 | 402559 | 9864273 | Plus | 33539-33715 | | |
| | 406213 | 7342019 | Plus | 25921-26612,34539-35161 | | |
| | 400847 | 9188605 | Plus | 44643-44835 | | |
| | 404642 | 9796810 | Plus | 102999-103145 | | |
| | 404030 | 7671252 | Plus | 149362-151749 | | |
| 80 | 403470 | 9929739 | Minus | 8376-8552 | | |
| | 402230 | 9966312 | Minus | 29782-29932 | | |
| | 400559 | 9843598 | Plus | 75483-75584 | | |

TABLE 56A: ABOUT 277 GENES UPREGULATED IN MELANOMA METASTASES RELATIVE TO BENIGN NEVI

Table 56A lists about 277 genes upregulated in melanoma metastases relative to benign nevi. Genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

| | | |
|----|----------------|---|
| 5 | Key: | Unique Eos probeset identifier number |
| | ExAccn: | Exemplar Accession number, Genbank accession number |
| | UnigenelD: | Unigene number |
| | Unigene Title: | Unigene gene title |
| 10 | R1: | 70th percentile of melanoma metastasis AIs divided by the maximum of benign nevi AIs |
| | R2: | 70th percentile of melanoma metastasis AIs divided by the maximum of benign nevi AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator |

| | | | | | | |
|----|--------|-----------|-----------|--|-------|-------|
| | Key | ExAccn | UnigenelD | Unigene Title | R1 | R2 |
| | 422424 | A1186431 | Hs.296638 | prostate differentiation factor | 13.73 | 17.18 |
| 15 | 446619 | AU076643 | Hs.313 | secreted phosphoprotein 1 (osteopontin, | 11.67 | 13.25 |
| | 407846 | AA426202 | Hs.40403 | Cbp/p300-interacting transactivator, wit | 9.35 | 8.75 |
| | 444381 | BE387335 | Hs.283713 | ESTs, Weakly similar to S64054 hypothesi | 8.63 | 6.22 |
| | 417880 | BE241595 | Hs.82848 | selectin L (lymphocyte adhesion molecule | 8.21 | 8.65 |
| 20 | 424321 | W74048 | Hs.1765 | lymphocyte-specific protein tyrosine kin | 7.13 | 5.04 |
| | 447210 | AF035269 | Hs.17752 | phosphatidylserine-specific phospholipas | 6.79 | 7.12 |
| | 417693 | AW959741 | Hs.40368 | adaptor-related protein complex 1, sigma | 6.55 | 5.94 |
| | 429500 | X78565 | Hs.289114 | hexabrachion (tenascin C, cytactin) | 6.43 | 3.46 |
| | 414812 | X72755 | Hs.77367 | monokine induced by gamma interferon | 6.43 | 5.44 |
| 25 | 451736 | AW080356 | Hs.23889 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 6.31 | 6.08 |
| | 418870 | AF147204 | Hs.89414 | chemokine (C-X-C motif), receptor 4 (fus | 6.20 | 6.04 |
| | 428291 | AA534009 | Hs.183487 | interferon stimulated gene (20kD) | 6.03 | 4.72 |
| | 417308 | H50720 | Hs.81892 | KIAA0101 gene product | 6.01 | 7.07 |
| | 448569 | BE382657 | Hs.21486 | signal transducer and activator of trans | 5.99 | 8.88 |
| 30 | 439310 | AF086120 | Hs.102793 | ESTs | 5.95 | 6.63 |
| | 452838 | U65011 | Hs.30743 | preferentially expressed antigen in mela | 5.95 | 3.77 |
| | 422241 | Y00062 | Hs.170121 | protein tyrosine phosphatase, receptor t | 5.76 | 6.37 |
| | 442379 | NM_004613 | Hs.8265 | transglutaminase 2 (C polypeptide, prote | 5.76 | 3.14 |
| | 409274 | NM_003930 | Hs.52644 | SKAP55 homologue | 5.65 | 5.01 |
| 35 | 442739 | NM_007274 | Hs.8679 | cytosolic acyl coenzyme A thioester hydr | 5.58 | 3.50 |
| | 442711 | AF151073 | Hs.8645 | hypothetical protein | 5.45 | 5.84 |
| | 425118 | AU076611 | Hs.154672 | methylene tetrahydrofolate dehydrogenase | 5.42 | 5.75 |
| | 412918 | BE563957 | | activated RNA polymerase II transcrip | 5.35 | 4.94 |
| | 428125 | AA393071 | Hs.182579 | leucine aminopeptidase | 5.33 | 5.34 |
| 40 | 446921 | AB012113 | Hs.16530 | small inducible cytokine subfamily A (Cy | 5.33 | 4.98 |
| | 431183 | NM_006855 | Hs.250696 | KDEL (Lys-Asp-Glu-Leu) endoplasmic retic | 5.30 | 6.25 |
| | 414219 | W20010 | Hs.75823 | ALL1-fused gene from chromosome 1q | 5.16 | 5.33 |
| | 426600 | NM_003378 | Hs.171014 | VGF nerve growth factor inducible | 5.05 | 8.77 |
| | 415444 | BE247295 | Hs.78452 | solute carrier family 20 (phosphate tran | 5.03 | 5.17 |
| 45 | 436701 | AW959032 | | ESTs, Moderately similar to I78885 serin | 5.03 | 4.17 |
| | 406648 | AA563730 | Hs.277477 | major histocompatibility complex, class | 4.99 | 5.08 |
| | 410850 | AW362867 | Hs.302738 | Homo sapiens cDNA: FLJ21425 fis, clone C | 4.98 | 4.71 |
| | 418299 | AA279530 | Hs.83968 | integrin, beta 2 (antigen CD18 (p95), ty | 4.98 | 4.08 |
| | 432469 | AL080084 | | CGI-100 protein | 4.97 | 4.70 |
| | 404854 | | | Target Exon | 4.85 | 4.07 |
| 50 | 415701 | NM_003878 | Hs.78619 | gamma-glutamyl hydrolase (conjugase, fol | 4.82 | 4.90 |
| | 425397 | J04088 | Hs.156346 | topoisomerase (DNA) II alpha (170kD) | 4.81 | 3.45 |
| | 408958 | T99607 | Hs.49346 | signal recognition particle 54kD | 4.78 | 2.34 |
| | 453949 | AU077146 | Hs.36927 | heat shock 105kD | 4.78 | 6.32 |
| 55 | 458079 | AJ796870 | Hs.54277 | DNA segment on chromosome X (unique) 992 | 4.77 | 6.57 |
| | 440245 | AK001913 | Hs.7100 | hypothetical protein | 4.74 | 3.83 |
| | 412228 | AW503785 | Hs.73792 | complement component (3d/Epstein Barr vi | 4.74 | 5.53 |
| | 417834 | BE172058 | Hs.82689 | tumor rejection antigen (gp96) 1 | 4.73 | 4.35 |
| | 451003 | AF058696 | Hs.25812 | Nijmegen breakage syndrome 1 (nibrin) | 4.67 | 4.60 |
| | 424571 | BE379766 | | polymerase (RNA) II (DNA directed) polyp | 4.62 | 3.50 |
| 60 | 434203 | BE262677 | Hs.283558 | hypothetical protein PRO1855 | 4.61 | 5.67 |
| | 452268 | NM_003512 | Hs.28777 | H2A histone family, member L | 4.60 | 3.79 |
| | 421311 | N71848 | Hs.283609 | hypothetical protein PRO2032 | 4.60 | 3.58 |
| | 410491 | AA465131 | Hs.64001 | Homo sapiens clone 25218 mRNA sequence | 4.60 | 4.68 |
| 65 | 425706 | AW406678 | Hs.122559 | hypothetical protein FLJ22570 | 4.59 | 3.83 |
| | 450293 | N36754 | Hs.171118 | hypothetical protein FLJ00026 | 4.57 | 5.40 |
| | 406836 | AW514501 | Hs.156110 | immunoglobulin kappa constant | 4.57 | 6.33 |
| | 413441 | AJ929374 | Hs.75367 | Src-like-adaptor | 4.53 | 4.77 |
| | 431129 | AL137751 | Hs.263671 | Homo sapiens mRNA; cDNA DKFp434I0812 (f | 4.48 | 4.89 |
| 70 | 418506 | AA084248 | Hs.85339 | G protein-coupled receptor 39 | 4.47 | 4.17 |
| | 411060 | NM_005074 | Hs.318501 | Homo sapiens mRNA full length insert cDN | 4.47 | 4.33 |
| | 417501 | AL041219 | Hs.82222 | sema domain, immunoglobulin domain (Ig), | 4.45 | 3.32 |
| | 437763 | AA469369 | Hs.5831 | tissue inhibitor of metalloproteinase 1 | 4.43 | 4.43 |
| | 448883 | BE614989 | Hs.7503 | hypothetical protein FLJ14153 | 4.42 | 3.91 |
| 75 | 417274 | N92036 | Hs.81848 | RAD21 (S. pombe) homolog | 4.41 | 4.09 |
| | 419285 | D31887 | Hs.89868 | KIAA0062 protein | 4.40 | 3.56 |
| | 418321 | D63477 | Hs.84087 | KIAA0143 protein | 4.38 | 3.00 |
| | 430154 | AW583058 | Hs.234726 | serine (or cysteine) proteinase inhibito | 4.37 | 4.26 |
| 80 | 428450 | NM_014791 | Hs.184339 | KIAA0175 gene product | 4.36 | 4.90 |
| | 428297 | AA236291 | Hs.183583 | serine (or cysteine) proteinase inhibito | 4.36 | 3.57 |
| | 447232 | AW499834 | Hs.327 | interleukin 10 receptor, alpha | 4.36 | 4.07 |
| | 409598 | NM_014018 | Hs.55097 | mitochondrial ribosomal protein S28 | 4.35 | 3.29 |
| | 442432 | BE093589 | Hs.38178 | hypothetical protein FLJ23468 | 4.34 | 5.80 |
| | 407047 | XG5965 | | gb:H.sapiens SOD-2 gene for manganese su | 4.33 | 3.51 |

| | | | | | | |
|----|--------|-----------|-----------|---|------|-------|
| 5 | 443991 | NM_002250 | Hs.10082 | potassium intermediate/small conductance | | |
| | 452322 | BE566343 | Hs.28988 | glutaredoxin (thioltransferase) | 4.33 | 4.23 |
| | 420991 | AW504814 | Hs.287379 | Homo sapiens mRNA for FLJ00111 protein, | 4.32 | 2.68 |
| | 449722 | BE280074 | Hs.23960 | cyclin B1 | 4.32 | 4.54 |
| | 408380 | AF123050 | Hs.44532 | diubiquitin | 4.31 | 3.73 |
| | 427127 | AW802282 | Hs.22265 | pyruvate dehydrogenase phosphatase | 4.30 | 5.74 |
| | 417933 | X02308 | Hs.82962 | thymidylate synthetase | 4.28 | 4.80 |
| | 432828 | AB042326 | Hs.287402 | chondroitin 4-sulfotransferase | 4.28 | 3.59 |
| 10 | 450306 | AL080080 | Hs.24766 | thioredoxin domain-containing | 4.25 | 4.15 |
| | 440266 | AA088809 | Hs.19525 | hypothetical protein FLJ22794 | 4.24 | 3.15 |
| | 407951 | W77762 | Hs.79015 | antigen identified by monoclonal antibody | 4.23 | 4.12 |
| | 427337 | Z46223 | Hs.176663 | Fc fragment of IgG, low affinity IIb, r | 4.22 | 4.64 |
| | 408989 | AW361666 | Hs.49500 | KIAA0746 protein | 4.20 | 4.62 |
| 15 | 449626 | AA774247 | Hs.301637 | zinc finger protein 258 | 4.20 | 4.92 |
| | 422846 | BE513934 | Hs.1583 | neutrophil cytosolic factor 1 (47kD, chr | 4.19 | 3.17 |
| | 415726 | T89844 | Hs.78712 | aminolevulinic, delta-, synthase 1 | 4.18 | 8.91 |
| | 444207 | AI565004 | | cathepsin D (lysosomal aspartyl protease | 4.16 | 4.21 |
| | 416980 | AA381133 | Hs.80684 | high-mobility group (nonhistone chromoso | 4.16 | 1.89 |
| 20 | 438718 | AL040058 | Hs.6375 | uncharacterized hypothalamus protein HT0 | 4.14 | 3.30 |
| | 437802 | AI475995 | Hs.122910 | ESTs | 4.14 | 3.04 |
| | 446392 | AF142419 | Hs.15020 | homolog of mouse quaking QKI (KH domain | 4.12 | 5.13 |
| | 409461 | AA382169 | Hs.54483 | N-myc (and STAT) interactor | 4.12 | 3.87 |
| | 427247 | AW504221 | Hs.174103 | integrin, alpha L (antigen CD11A (p180), | 4.11 | 4.96 |
| 25 | 414359 | M62194 | Hs.75929 | cadherin 11, type 2, OB-cadherin (osteob | 4.11 | 6.37 |
| | 450071 | AA018283 | Hs.24359 | Homo sapiens cDNA FLJ11174 fis, clone PL | 4.10 | 4.16 |
| | 452882 | AW972990 | Hs.196270 | folate transporter/carrier | 4.10 | 2.35 |
| | 414522 | AW518944 | Hs.76325 | immunoglobulin J chain | 4.10 | 4.50 |
| | 407756 | AA116021 | Hs.38260 | ubiquitin specific protease 18 | 4.09 | 6.07 |
| 30 | 405506 | | | Target Exon | 4.09 | 5.03 |
| | 417497 | AW402482 | Hs.82212 | CD53 antigen | 4.08 | 3.71 |
| | 413715 | AW851121 | Hs.75497 | Homo sapiens cDNA: FLJ22139 fis, clone H | 4.07 | 8.61 |
| | 421508 | NM_004833 | Hs.105115 | absent in melanoma 2 | 4.06 | 4.05 |
| | 445701 | AF055581 | Hs.13131 | lymphocyte adaptor protein | 4.05 | 4.61 |
| 35 | 443071 | AL080021 | Hs.8986 | complement component 1, q subcomponent, | 4.02 | 4.56 |
| | 417615 | BE548641 | Hs.82314 | hypoxanthine phosphoribosyltransferase 1 | 4.00 | 8.91 |
| | 444371 | BE540274 | Hs.239 | forkhead box M1 | 3.99 | 4.15 |
| | 450515 | AW304226 | | biphenyl hydrolase-like (serine hydrolas | 3.86 | 4.58 |
| | 446506 | AI123118 | Hs.15159 | chemokine-like factor, alternatively spl | 3.85 | 4.26 |
| 40 | 410668 | BE379794 | Hs.159651 | hypothetical protein | 3.81 | 4.06 |
| | 443710 | AI928136 | Hs.9691 | Homo sapiens cDNA: FLJ23249 fis, clone C | 3.80 | 6.84 |
| | 406837 | R70292 | Hs.156110 | immunoglobulin kappa constant | 3.77 | 4.46 |
| | 419381 | AB023420 | Hs.90093 | heat shock 70kD protein 4 | 3.77 | 6.44 |
| | 402474 | | | NM_004079: Homo sapiens cathepsin S (CTSS | 3.76 | 4.00 |
| 45 | 454080 | AI199711 | Hs.576 | fucosidase, alpha-L-1, tissue | 3.76 | 4.67 |
| | 409264 | NM_014937 | Hs.52463 | KIAA0966 protein | 3.74 | 6.22 |
| | 428398 | AI249368 | Hs.98558 | ESTs | 3.69 | 4.36 |
| | 423494 | AW504365 | Hs.24143 | Wiskott-Aldrich syndrome protein interac | 3.68 | 5.18 |
| | 414829 | AA321568 | Hs.77436 | pleckstrin | 3.67 | 4.12 |
| 50 | 437239 | AW503395 | Hs.5541 | ATPase, Ca transporting, ubiquitous | 3.65 | 4.45 |
| | 433867 | AK000696 | Hs.3618 | hippocalcin-like 1 | 3.63 | 4.84 |
| | 432485 | N90866 | Hs.276770 | CDW52 antigen (CAMPATH-1 antigen) | 3.59 | 4.49 |
| | 418310 | AA814100 | Hs.86693 | ESTs | 3.54 | 5.31 |
| | 406868 | AA505445 | Hs.300697 | immunoglobulin heavy constant gamma 3 (G | 3.49 | 4.57 |
| 55 | 438746 | AI885815 | Hs.184727 | Human melanoma-associated antigen p97 (m | 3.48 | 4.33 |
| | 427527 | AI809067 | Hs.153261 | immunoglobulin heavy constant mu | 3.47 | 6.87 |
| | 442485 | BE092285 | Hs.29724 | hypothetical protein FLJ13187 | 3.44 | 10.42 |
| | 432606 | NM_002104 | Hs.3066 | granzyme K (serine protease, granzyme 3; | 3.41 | 4.60 |
| | 435080 | AI831760 | Hs.155111 | hypothetical protein FLJ14428 | 3.40 | 4.50 |
| 60 | 436810 | AA353044 | Hs.5321 | ARP3 (actin-related protein 3, yeast) ho | 3.40 | 4.22 |
| | 422545 | X02761 | Hs.287820 | fibronectin 1 | 3.40 | 5.03 |
| | 409142 | AL136877 | Hs.50758 | SMC4 (structural maintenance of chromoso | 3.39 | 7.32 |
| | 434826 | AF155661 | Hs.22265 | pyruvate dehydrogenase phosphatase | 3.36 | 4.47 |
| | 416975 | NM_004131 | Hs.1051 | granzyme B (granzyme 2, cytotoxic T-lymp | 3.34 | 5.02 |
| 65 | 448410 | AK000227 | Hs.21126 | hypothetical protein FLJ20220 | 3.34 | 4.24 |
| | 432642 | BE297635 | Hs.3069 | heat shock 70kD protein 98 (mortalin-2) | 3.33 | 4.29 |
| | 425234 | AW152225 | Hs.165909 | ESTs, Weakly similar to I38022 hypothe | 3.32 | 4.48 |
| | 443623 | AA345519 | Hs.9641 | complement component 1, q subcomponent, | 3.24 | 4.64 |
| | 426490 | NM_001621 | Hs.170087 | aryl hydrocarbon receptor | 3.23 | 13.58 |
| 70 | 443958 | BE241880 | Hs.10029 | cathepsin C | 3.23 | 4.20 |
| | 407862 | BE548267 | Hs.337986 | Homo sapiens cDNA FLJ10934 fis, clone OV | 3.16 | 5.05 |
| | 412577 | Z22968 | Hs.74076 | CD163 antigen | 3.15 | 4.04 |
| | 414050 | NM_004766 | Hs.75724 | coatomer protein complex, subunit beta 2 | 3.14 | 5.32 |
| | 442904 | AW575008 | Hs.11355 | thymopoietin | 3.13 | 4.65 |
| 75 | 421633 | AF121860 | Hs.106260 | sorting nexin 10 | 3.13 | 4.34 |
| | 413936 | AF113676 | Hs.297681 | serine (or cysteine) proteinase inhibitor | 3.12 | 4.99 |
| | 428797 | AA496205 | Hs.193700 | Homo sapiens mRNA: cDNA DKFZp586I0324 (f | 3.11 | 5.47 |
| | 408515 | AI289507 | Hs.295883 | hypothetical protein FLJ23399 | 3.10 | 4.30 |
| | 409442 | AA310162 | Hs.169248 | cytochrome c | 3.10 | 4.03 |
| 80 | 456373 | BE247706 | Hs.89751 | membrane-spanning 4-domains, subfamily A | 3.07 | 4.00 |
| | 430413 | AW842182 | Hs.241392 | small inducible cytokine A5 (RANTES) | 3.04 | 4.38 |
| | 418526 | BE019020 | Hs.85838 | solute carrier family 16 (monocarboxylic | 3.04 | 5.53 |
| | 452139 | AA099959 | Hs.16331 | Homo sapiens cDNA: FLJ21482 fis, clone C | 3.03 | 4.97 |
| | 430478 | NM_014349 | Hs.241535 | apolipoprotein L 3 | 3.01 | 4.87 |
| | | | | | 2.98 | 4.44 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|-------|
| | 439237 | AW408158 | Hs.318893 | ESTs, Weakly similar to A47582 B-cell gr | 2.95 | 7.45 |
| | 406782 | AA430373 | | gb:zw20111.s1 Soares ovary tumor NbHOT H | 2.93 | 8.49 |
| | 450455 | AL117424 | Hs.25035 | chloride intracellular channel 4 | 2.90 | 5.08 |
| 5 | 422530 | AW972300 | Hs.118110 | bone marrow stromal cell antigen 2 | 2.87 | 7.07 |
| | 429490 | AI971131 | Hs.23889 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 2.87 | 4.29 |
| | 410231 | AA314163 | Hs.61153 | proteasome (prosome, macropain) 26S subu | 2.82 | 5.53 |
| | 419956 | AL137939 | Hs.40096 | cadherin 19, type 2 | 2.80 | 4.26 |
| | 416511 | NM_006762 | Hs.79356 | Lysosomal-associated multispanning membr | 2.79 | 5.55 |
| 10 | 421712 | AK000140 | Hs.107139 | hypothetical protein | 2.79 | 6.29 |
| | 429732 | U20158 | Hs.2488 | lymphocyte cytosolic protein 2 (SH2 doma | 2.78 | 4.74 |
| | 448517 | AA082750 | Hs.42194 | hypothetical protein FLJ22649 similar to | 2.78 | 4.69 |
| | 427792 | M63928 | Hs.180841 | tumor necrosis factor receptor superfam | 2.77 | 5.18 |
| | 446272 | BE268912 | Hs.14601 | hematopoietic cell-specific Lyn substrat | 2.75 | 4.90 |
| 15 | 422173 | BE385828 | Hs.250619 | phorbol-in-like protein MDS019 (CEM15) | 2.75 | 4.33 |
| | 446566 | H95741 | Hs.17914 | membrane-spanning 4-domains, subfamily A | 2.72 | 4.19 |
| | 429402 | AF116571 | Hs.201671 | SRY (sex determining region Y)-box 13 | 2.72 | 5.15 |
| | 421360 | AA297012 | Hs.103839 | erythrocyte membrane protein band 4.1-f | 2.71 | 4.82 |
| | 425762 | BE244076 | Hs.159578 | AT-hook transcription factor AKNA | 2.71 | 4.61 |
| 20 | 429412 | NM_006235 | Hs.2407 | POU domain, class 2, associating factor | 2.69 | 4.45 |
| | 409202 | AA236881 | Hs.51043 | hexosaminidase B (beta polypeptide) | 2.68 | 4.89 |
| | 426124 | AI268389 | Hs.250697 | phosphatidylinositol glycan, class F | 2.68 | 4.25 |
| | 422672 | X12784 | Hs.119129 | collagen, type IV, alpha 1 | 2.67 | 5.00 |
| | 417389 | BE260964 | Hs.82045 | midkine (neurite growth-promoting factor | 2.65 | 9.54 |
| 25 | 445784 | AI253155 | Hs.146065 | ESTs | 2.65 | 4.11 |
| | 410341 | AW499985 | Hs.42915 | ARP2 (actin-related protein 2, yeast) ho | 2.64 | 4.50 |
| | 422603 | BE242587 | Hs.118651 | hematopoietically expressed homeobox | 2.63 | 4.17 |
| | 424687 | J05070 | Hs.151738 | matrix metalloproteinase 9 (gelatinase B | 2.62 | 5.80 |
| | 410016 | AA297977 | Hs.57907 | small inducible cytokine subfamily A (Cy | 2.61 | 5.57 |
| 30 | 424779 | AL046851 | Hs.153053 | CD37 antigen | 2.60 | 5.72 |
| | 420224 | M84371 | Hs.96023 | CD19 antigen | 2.60 | 4.02 |
| | 421924 | BE514514 | Hs.109606 | coronin, actin-binding protein, 1A | 2.57 | 4.83 |
| | 426143 | BE379836 | | proteasome (prosome, macropain) subunit, | 2.56 | 4.50 |
| | 421563 | NM_006433 | Hs.105806 | granulysin | 2.56 | 5.35 |
| 35 | 425593 | AA278921 | Hs.1908 | proteoglycan 1, secretory granule | 2.55 | 4.32 |
| | 428169 | AI928984 | Hs.182793 | golgi phosphoprotein 2 | 2.54 | 5.78 |
| | 417022 | NM_014737 | Hs.80905 | Ras association (RalGDS/AF-6) domain fam | 2.54 | 4.09 |
| | 414646 | AA353776 | Hs.901 | CD48 antigen (B-cell membrane protein) | 2.53 | 4.41 |
| | 429800 | AA333375 | Hs.223014 | antizyme inhibitor | 2.50 | 5.68 |
| 40 | 407241 | M34516 | | gb:Human omega light chain protein 14.1 | 2.50 | 4.69 |
| | 421739 | AB004550 | Hs.107526 | UDP-Gal:betaGlcNAc beta 1,4-galactosylt | 2.45 | 4.35 |
| | 412819 | T25829 | Hs.24048 | FK506 binding protein precursor | 2.45 | 4.66 |
| | 435523 | T62849 | Hs.11090 | membrane-spanning 4-domains, subfamily A | 2.44 | 4.91 |
| | 434883 | AW381538 | Hs.19807 | hypothetical protein MGC12959 | 2.41 | 4.80 |
| 45 | 420340 | NM_000734 | Hs.97087 | CD32 antigen, zeta polypeptide (TIT3 com | 2.41 | 4.00 |
| | 449296 | AL137257 | Hs.23458 | Homo sapiens cDNA: FLJ23015 fis, clone L | 2.41 | 4.77 |
| | 417370 | T26651 | Hs.82030 | tryptophanyl-tRNA synthetase | 2.41 | 4.04 |
| | 400223 | | | Eos Control | 2.39 | 5.47 |
| | 431629 | AU077025 | Hs.265827 | interferon, alpha-inducible protein (clo | 2.38 | 7.67 |
| 50 | 414622 | AI752666 | Hs.76669 | nicotinamide N-methyltransferase | 2.38 | 5.32 |
| | 415149 | X12451 | Hs.78056 | cathepsin L | 2.37 | 8.07 |
| | 435099 | AC004770 | Hs.4756 | flap structure-specific endonuclease 1 | 2.37 | 5.23 |
| | 454390 | AB020713 | Hs.56966 | KIAA0906 protein | 2.35 | 4.57 |
| | 427407 | BE268649 | Hs.177766 | ADP-ribosyltransferase (NAD; poly (ADP-r | 2.31 | 5.48 |
| 55 | 449029 | N28989 | Hs.22891 | solute carrier family 7 (cationic amino | 2.24 | 4.08 |
| | 438956 | W00847 | Hs.135056 | Human DNA sequence from clone RPS-850E9 | 2.23 | 4.02 |
| | 423397 | NM_001838 | Hs.1652 | chemokine (C-C motif) receptor 7 | 2.23 | 4.90 |
| | 416232 | AW502678 | Hs.79090 | exportin 1 (CRM1, yeast, homolog) | 2.18 | 4.97 |
| | 436692 | AW243158 | Hs.5297 | DKFZP564A2416 protein | 2.17 | 4.13 |
| 60 | 420842 | AI083668 | Hs.50601 | hypothetical protein MGC10986 | 2.14 | 5.14 |
| | 428227 | AA321649 | Hs.2248 | small inducible cytokine subfamily B (Cy | 2.13 | 4.43 |
| | 429642 | X68264 | Hs.211579 | melanoma cell adhesion molecule (MCAM) (| 2.11 | 5.42 |
| | 416448 | L13210 | Hs.79339 | lectin, galactoside-binding, soluble, 3 | 2.10 | 6.36 |
| | 416714 | AF283770 | Hs.79630 | CD79A antigen (immunoglobulin-associated | 2.10 | 4.06 |
| 65 | 409220 | BE243323 | Hs.51233 | tumor necrosis factor receptor superfam | 2.09 | 4.67 |
| | 414045 | NM_002951 | Hs.75722 | ribophorin II | 2.07 | 4.32 |
| | 422451 | AA310753 | Hs.42491 | ESTs, Weakly similar to S65657 alpha-1C- | 2.07 | 4.24 |
| | 441211 | AW946155 | Hs.7750 | hypothetical protein AL133206 | 2.06 | 4.64 |
| | 434692 | H06586 | Hs.94 | DnaJ (Hsp40) homolog, subfamily A, membe | 2.05 | 4.33 |
| 70 | 452363 | AI582743 | Hs.94953 | Homo sapiens, Similar to complement comp | 2.04 | 13.36 |
| | 438393 | AA351815 | Hs.50740 | Homo sapiens cDNA: FLJ22272 fis, clone H | 2.03 | 4.52 |
| | 413313 | NM_002047 | Hs.283108 | glycyl-tRNA synthetase | 2.02 | 4.11 |
| | 452700 | AI859390 | Hs.288940 | five-span transmembrane protein M83 | 2.00 | 4.04 |
| | 406621 | X57809 | Hs.8997 | immunoglobulin lambda locus | 1.99 | 4.35 |
| 75 | 424415 | NM_001975 | Hs.146580 | enolase 2, (gamma, neuronal) | 1.98 | 4.52 |
| | 429451 | BE409861 | Hs.202833 | heme oxygenase (decycling) 1 | 1.95 | 5.60 |
| | 416967 | BE616731 | Hs.80645 | interferon regulatory factor 1 | 1.95 | 5.38 |
| | 414945 | BE076358 | Hs.77667 | lymphocyte antigen 6 complex, locus E | 1.93 | 4.69 |
| | 418917 | X02994 | Hs.1217 | adenosine deaminase | 1.91 | 4.32 |
| 80 | 445411 | AL137255 | Hs.12646 | hypothetical protein FLJ22693 | 1.91 | 4.48 |
| | 413945 | NM_000591 | Hs.75627 | CD14 antigen | 1.90 | 6.03 |
| | 429119 | AV660012 | Hs.196437 | hypothetical protein FLJ10788 | 1.90 | 4.08 |
| | 413317 | U53225 | Hs.75283 | sorting nexin 1 | 1.89 | 4.06 |
| | 427239 | BE270447 | | ubiquitin carrier protein | 1.87 | 5.98 |

| | | | | | | |
|----|--------|-----------|-----------|---|------|------|
| 5 | 450440 | AB024334 | Hs.25001 | tyrosine 3-monooxygenase/tryptophan 5-mo | 1.87 | 6.33 |
| | 413142 | M81740 | Hs.75212 | ornithine decarboxylase 1 | 1.85 | 4.21 |
| | 447131 | NM_004585 | Hs.17466 | retinoic acid receptor responder (lazarro | 1.84 | 5.07 |
| | 430040 | AW503115 | Hs.227823 | pMS protein | 1.83 | 5.57 |
| | 416819 | U77735 | Hs.80205 | pim-2 oncogene | 1.83 | 4.12 |
| | 425356 | BE244879 | Hs.155939 | inositol polyphosphate-5-phosphatase, 14 | 1.82 | 5.71 |
| | 414570 | Y00285 | Hs.76473 | insulin-like growth factor 2 receptor | 1.81 | 4.73 |
| | 443639 | BE269042 | Hs.9661 | proteasome (prosome, macropain) subunit, | 1.80 | 4.71 |
| 10 | 418707 | U97502 | Hs.87497 | butyrophilin, subfamily 3, member A2 | 1.78 | 5.16 |
| | 425367 | BE271188 | Hs.155975 | protein tyrosine phosphatase, receptor I | 1.78 | 7.00 |
| | 409154 | U72882 | Hs.50842 | interferon-induced protein 35 | 1.74 | 5.10 |
| | 444954 | AW247076 | Hs.12163 | eukaryotic translation initiation factor | 1.71 | 5.15 |
| | 424825 | AF207069 | Hs.153357 | procollagen-lysine, 2-oxoglutarate 5-dio | 1.70 | 4.43 |
| 15 | 428385 | AF112213 | Hs.184062 | putative Rab5-interacting protein | 1.69 | 4.06 |
| | 427378 | BE515037 | Hs.177556 | melanoma antigen, family D, 1 | 1.67 | 5.68 |
| | 413322 | AA380158 | Hs.75290 | ADP-ribosylation factor 4 | 1.67 | 4.56 |
| | 442414 | BE408758 | Hs.8297 | ribonuclease 6 precursor | 1.65 | 4.40 |
| | 410129 | BE244074 | Hs.58831 | regulator of Fas-induced apoptosis | 1.64 | 4.02 |
| 20 | 452472 | AW957300 | Hs.294142 | ESTs, Weakly similar to C55663 oligodend | 1.63 | 4.49 |
| | 446143 | BE245342 | Hs.306079 | sec61 homolog | 1.62 | 4.73 |
| | 413511 | AI627178 | Hs.75412 | arginine-rich, mutated in early stage tu | 1.60 | 4.19 |
| | 415017 | F06434 | Hs.77805 | ATPase, H transporting, lysosomal (vacuo | 1.60 | 4.61 |
| | 410361 | BE391804 | Hs.62661 | guanylate binding protein 1, interferon- | 1.59 | 4.26 |
| 25 | 410068 | AI633888 | Hs.58435 | FYN-binding protein (FYB-120/130) | 1.56 | 4.10 |
| | 419489 | AW411280 | Hs.90693 | replication initiation region protein (6 | 1.55 | 4.30 |
| | 439627 | BE621702 | Hs.29076 | hypothetical protein FLJ21841 | 1.55 | 6.54 |
| | 414427 | L19711 | Hs.76111 | dystroglycan 1 (dystrophin-associated gl | 1.53 | 4.00 |
| | 416971 | R34657 | Hs.80658 | uncoupling protein 2 (mitochondrial, pro | 1.53 | 4.79 |
| 30 | 426059 | BE292842 | Hs.166120 | interferon regulatory factor 7 | 1.51 | 4.12 |
| | 418879 | AW162087 | Hs.5437 | Tax1 (human T-cell leukemia virus type I | 1.50 | 4.93 |
| | 433271 | BE621697 | Hs.14317 | nucleolar protein family A, member 3 (H | 1.45 | 4.15 |
| | 422481 | AL050163 | Hs.117339 | DNAX-activation protein 10 | 1.45 | 4.03 |
| | 432805 | X94630 | Hs.3107 | CD97 antigen | 1.43 | 4.11 |
| 35 | 447150 | AI439011 | Hs.86386 | myeloid cell leukemia sequence 1 (BCL2-r | 1.43 | 4.08 |
| | 421975 | AW961017 | Hs.6459 | hypothetical protein FLJ11856 | 1.41 | 4.36 |
| | 427458 | BE208364 | Hs.29283 | ESTs, Weakly similar to LKHU proteoglyca | 1.41 | 4.10 |
| | 412968 | AW500508 | Hs.75102 | alanine-tRNA synthetase | 1.40 | 4.25 |
| | 428511 | AA019912 | Hs.184693 | transcription elongation factor B (SIII) | 1.38 | 4.91 |
| 40 | 413825 | BE299181 | Hs.75564 | CD151 antigen | 1.37 | 4.46 |
| | 427496 | D21260 | Hs.178710 | clathrin, heavy polypeptide (Hc) | 1.30 | 4.04 |
| | 407143 | CA1076 | Hs.332329 | EST | 1.29 | 4.37 |

TABLE 56B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

| | | | |
|----|--------|------------|---|
| 45 | Pkey | CAT Number | Accession |
| | 412918 | 2764_3 | BE784583 AL519009 AV755430 AV756363 AV711927 BI523434 AI521453 AA845815 AW024829 AW949702 BG218926 AA626658 AI445621 AI452815 AA946555 AA723580 AA612925 BG105326 BG532618 AW513994 AW602165 AI373448 AA907901 AW135104 BG186662 W69205 BG219754 BE774875 BG190378 AA483898 BE066066 BE066067 BE066068 AW304207 BE939361 AW795569 BG210592 AW795644 BE939358 AW102886 BE065977 BG182971 H97042 D58090 BI046351 H81248 AI750112 AW372079 C05492 D58287 D57835 AA935095 BF700910 BG215802 BG195459 AW368467 BG495535 BG533177 BI087962 BE541579 BF130753 269892 AA210833 BM353155 AI473754 AI147901 AI803109 AA843296 AA418925 AI478552 AI400067 AI360304 AA418828 AW301673 BE218952 AI532804 BF433234 AA394157 BF378047 BE467036 AA319724 AW290940 AI222671 AI347724 AW001711 AI028652 AA398130 AI470582 AI915936 AA908929 C75102 N36920 H50440 AI919034 AI004399 AI383862 AI123606 AA648518 AA516258 AI855321 N22865 AA848101 AI589792 AA758196 AA214530 AI373911 AW194733 AA213447 AI290291 BF437165 AA757592 BF086904 AW959032 AW992466 BF446888 AI936337 BE938849 AW149064 AI701629 N90021 BC016556 BC016365 NM_016040 AF151858 BI561037 AW966873 AW967497 BE219482 BE018650 AW770511 AW469095 AW470133 BM150181 BM193977 AI824135 AI632346 AI129838 BM147664 AI292112 BE244667 AA251084 AW503659 BM193866 BM194481 BF446862 AL597435 BF000262 AI824386 AI990100 AW087624 AA668793 AL080084 BI335866 BI820940 BG779242 BM069854 AA282620 AA256771 AW964511 AA451623 H00335 AW370399 AW954201 BM145846 BG111760 AI750065 BG555794 AA564086 BG494071 BM069606 AI675331 BE302224 AI476466 AI625980 BM144854 AI184602 AI343932 AW136586 AW029464 AI708651 AA824243 BM145917 AA662210 AA825708 AI335858 AI273704 AA662171 N48971 AA976614 AI344537 AA609603 AI873901 AI859995 AA833589 AA765811 AI150322 AI926816 BM148634 N98862 AA019347 AA897062 AA831100 N69889 BE243185 AA282179 AA831098 AA112676 AI702407 BG621752 BE006492 AA353202 BG674256 N46921 BI048774 AW300233 BF739890 AW966879 AA393405 BF115146 AA910851 AA013099 N28878 AA287713 BE348728 BG616446 AL599953 AL599952 BF381073 AW505056 AA094735 H03613 AA287714 H27168 R54718 BF792697 AV693603 AV685883 BG619956 BF541504 BF216789 AA319751 BM452652 BF335838 AA280397 BG171509 BF571997 AA490239 AW388161 BE842126 BG165309 N71903 AI955397 AI536898 BE242040 F09718 AA772421 AA450218 M78543 BE241414 AA013098 H00297 AW576477 AW150918 AW591371 AI382711 N71926 H72497 AI285602 AA745055 AI281647 BF377670 T65207 BG532880 BG721680 AA285143 H27167 AW500235 BG494497 BF668899 BE379766 AW152643 AI803450 AI564343 AI092711 AI140525 AW152156 AI620740 AI554689 AI161209 AI290242 AI339745 AI374611 AI347388 AI858296 AI140529 AI366124 AA493912 AA406235 AA493889 AI057160 AW022264 AI097277 AI141126 AI080051 AA983529 AA860507 N53469 AA843767 N81163 N70628 AA424577 AA583537 BF003004 AA526688 AA235977 AI057152 AI095366 AI095356 AA458646 AW194479 AA150439 AI375272 AW571777 AI359198 AA953793 BE614394 BE738239 AA127883 AI034344 T59504 D81608 AA908704 AW051665 AA382785 AA307208 N24639 AI370715 BE244980 AA548596 AW449675 AI91008 BF223749 N70752 N22266 AI91012 AA028001 AI419106 BF215661 BF591548 BG942356 AI474968 BE858217 BF793358 AV756756 BG483603 AI093724 BF693395 BG545345 AI744294 T59549 AA811773 BG499757 BE739425 AA514221 AA865491 AI828293 AA470456 AI276739 AA169357 BE932464 AA514889 AW819039 AW819083 BE843048 AI432496 AI470335 AI247243 BG533994 AA513783 AI887309 AA528036 AW972006 AW873028 AI924914 AI818810 AW152378 AW084946 AI521413 AI669583 BE932521 AI581370 BE180238 AW089750 AW771461 AW089714 AI590949 AI819148 AA731056 BF815234 BF911506 AA235803 AA485373 AI735658 AW393133 AW073080 AI707637 BF353320 BE843111 AW819036 AW393135 BG697291 AV648670 AV654332 AV687530 BG566964 AI807430 AI676072 AA837010 AI452482 AI625817 AW241750 BE048616 AI290928 AI680714 AA485530 BE175687 AV648513 AW130312 AI000556 AA632893 BE674169 BF001208 AA948166 BE175650 AA524664 AA490345 AI244948 AA602956 AA483492 AA918178 AW802049 BG675859 AV658871 BG678060 AI565004 AW819026 BE843092 AV686437 AV723049 BG616948 AI911647 AI743490 AI091096 BE857251 AI962074 AA040027 AW769317 |

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|----|--------|---------|---|--|--|--|
| 5 | 450515 | 13638_2 | AA343477 AA640112 BF876213 R82948 H26425 H82876 BE843095 BE843140 BG536641 BG617830 AA235802 BE774985 BE006682 BF342375 AA903144 BF338083 BF984258 AV657996 AI749532 BE768614 BE857252 BE932516 BE768573 AV657993 AV657777 AV752631 BE774974 T55847 BF095761 BF911511 BE710793 BE180119 BG617338 H45942 T55897 AV657718 BG563497 BE299605 AJ589870 AA847598 AI470122 BF933896 AI304356 BE223045 BF435800 AI394207 AJ708171 AW025415 AJ079409 AW008420 AW304226 N34543 AW603578 AA526961 AA983631 N99134 AA626645 R45023 AA902417 AW672925 AA449985 AA953982 AW675471 AA010062 N80194 H14620 H28475 H26247 BF333581 AW842369 H06848 H05608 H81745 H15016 R51905 AA860423 AJ860904 AA876023 AA430373 AA968771 BC005265 BG176720 AW006027 BM352064 AW026316 AI635822 AI880584 AI693769 AJ092211 BI492387 AI400449 AV166297 BF939910 AA232282 AW021432 AI333893 AA494308 AA854899 AI436795 AW069256 AA682373 AI092748 AA993184 AI126077 AI081758 AI240686 AI261863 AJ378423 AA465237 AI376096 AA035579 AJ087306 AA448162 AA129977 AI090903 AI080686 AI288939 N33004 AI801240 AW021546 AI370773 AI086064 AA669528 AI250053 AJ870113 AA853181 AA858014 BG055562 BG939559 AW080765 AA032283 AW467587 H40506 D00762 NM_002788 AA641134 AI582295 AI417525 AI563975 AI093566 AJ070743 AI290741 AW073417 BE875418 BM264076 BG876884 AI680535 AW854219 BE774635 AW854212 BG952443 AW854221 AW854208 BE156348 BE843056 AW858991 BE937569 BG878291 BG876450 AW819099 AJ908570 AA449871 AU135228 BM478404 BF126296 AA375499 AA248473 NM_005648 BC013809 L34587 BF103775 BG702618 BG716553 BI667090 BG505863 BF983483 BG718195 BI857891 BG501016 BM043599 AL521812 BG705730 BI495545 BI495546 BF112248 BM023182 BM023123 AI075173 AW051799 BF058224 BI324885 BF436008 AA398446 BG822375 BM019558 BM023382 BG164174 N56909 BI457064 BM023464 AI207475 BM311415 BG758430 BG758807 AJ934826 N90351 BG422026 BE910312 AI027778 AJ081950 AI360890 BM009115 AI191829 BG759697 AI138728 AA399403 AI355589 AI336427 AA868702 AA393660 AA025127 BG027630 AA962774 AA631224 BG940967 BE791087 AA573315 W81685 AA393525 BG944103 AI339125 AI149864 AA977655 N90314 BE612839 BG491847 AI129091 AA461234 AA781198 AA759256 AA88954 AA975844 AI184099 AJ018025 AA398363 AJ003331 AJ193380 AA626020 AI244475 AI601114 AW135664 AJ206607 AW263599 AA813219 AI684453 AA878626 AA772222 AI085496 AI630226 BG940966 AI022010 AA770649 AA887624 AA491739 AA974295 BG530040 AA037091 AA019912 BI160457 H64512 BG503896 427239 20459_2 AL532360 BE794750 AA582906 AI015067 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE138953 BE049086 AI334881 AW075005 AW075181 AA464019 AW302733 AW075100 AW073433 AI802854 AI334909 AI802853 AI345036 AI348921 AI340734 AI307478 AI251289 AW302327 AW072520 AI312145 AW073656 AW072513 AW071289 AI307559 AA876186 T29587 AI307493 AI255068 AI252868 AI252839 AW074809 AI252926 AI252160 AI251662 AI251262 AI610913 AI270787 AI270156 AI252075 AW073469 AW072901 AW072496 AW071420 AI305762 AI254764 AI802837 AI251264 AW073049 AW071311 AI340643 BE138965 BE138502 AW073456 AI334733 AI054335 BE139260 AI054302 AI054060 AI054057 AI053722 AI289711 BE139228 AW470478 AW271039 AW302085 BE041872 AI254494 AI271496 AI252427 BF718773 BF718645 AW074866 BE857822 | | | |
| 10 | 406782 | 0_0 | | | | |
| | 426143 | 3806_1 | | | | |
| 15 | 400223 | 2368_1 | | | | |
| | | | | | | |
| 20 | | | | | | |
| | | | | | | |
| 25 | 427239 | 20459_2 | | | | |
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| 30 | | | | | | |
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| 35 | | | | | | |
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| 40 | | | | | | |
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TABLE 56C:

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

| Pkey | Ref | Strand | Nt_position |
|--------|---------|--------|-------------------------------------|
| 404854 | 7143420 | Plus | 14260-14537 |
| 405506 | 6466489 | Plus | 80014-80401,80593-81125 |
| 402474 | 7547175 | Minus | 53526-53628,55755-55920,57530-57757 |

TABLE 57A: ABOUT 304 GENES UPREGULATED IN MELANOMA METASTASES RELATIVE TO NORMAL SKIN

Table 57A lists about 304 genes upregulated in melanoma metastases relative to normal skin. Genes were selected from 59680 probesets on the Eos/Atfymatrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of melanoma metastasis AIs divided by the 90th percentile of normal skin AIs
 R2: 90th percentile of melanoma metastasis AIs divided by the 90th percentile of normal skin AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

| Pkey | ExAccn | UnigenelD | Unigene Title | R1 | R2 |
|--------|-----------|-----------|---|-------|-------|
| 422424 | AI186431 | Hs.296638 | prostate differentiation factor | 18.94 | 25.00 |
| 438549 | BE386801 | Hs.21858 | trinucleotide repeat containing 3 | 17.45 | 18.47 |
| 417880 | BE241595 | Hs.82848 | selectin L (lymphocyte adhesion molecule | 14.05 | 11.15 |
| 452838 | U65011 | Hs.30743 | preferentially expressed antigen in mela | 13.91 | 15.41 |
| 446519 | AJ076643 | Hs.313 | secreted phosphoprotein 1 (osteopontin, | 13.41 | 9.73 |
| 426555 | NM_000372 | Hs.2053 | tyrosinase (oculocutaneous albinism IA) | 12.24 | 7.33 |
| 439310 | AF086120 | Hs.102793 | ESTs | 10.12 | 10.80 |
| 414020 | NM_002984 | Hs.75703 | small inducible cytokine A4 (homologous | 9.74 | 10.16 |
| 447210 | AF035269 | Hs.17752 | phosphatidylserine-specific phospholipas | 9.43 | 11.69 |
| 414812 | X72755 | Hs.77367 | monokine induced by gamma interferon | 9.28 | 10.97 |
| 430377 | NM_001922 | Hs.301865 | dopachrome tautomerase (dopachrome delta | 9.07 | 7.96 |
| 426600 | NM_003378 | Hs.171014 | VEGF nerve growth factor inducible | 9.06 | 19.93 |
| 453857 | AL080235 | Hs.35861 | DKFZP586E1621 protein | 8.66 | 5.87 |
| 418310 | AA814100 | Hs.86693 | ESTs | 8.65 | 6.62 |
| 433447 | U29195 | Hs.3281 | neuronal pentraxin II | 8.27 | 4.68 |
| 430280 | AA361258 | Hs.237868 | interleukin 7 receptor | 8.01 | 6.37 |
| 430822 | AJ005371 | Hs.248017 | glyceraldehyde-3-phosphate dehydrogenase | 7.80 | 6.10 |
| 456373 | BE247706 | Hs.89751 | membrane-spanning 4-domains, subfamily A | 7.78 | 7.60 |
| 415752 | BE314524 | Hs.78776 | putative transmembrane protein | 7.68 | 5.41 |
| 419628 | H67546 | Hs.49768 | ESTs | 7.66 | 8.96 |
| 417355 | D13168 | Hs.82002 | endothelin receptor type B | 7.56 | 4.59 |
| 424321 | W74048 | Hs.1765 | lymphocyte-specific protein tyrosine kin | 7.48 | 5.77 |
| 412228 | AW503785 | Hs.73792 | complement component (3d/Epstein Barr vi | 7.43 | 4.93 |
| 436485 | X59135 | Hs.156110 | immunoglobulin kappa constant | 7.35 | 7.98 |
| 414646 | AA353776 | Hs.901 | CD48 antigen (B-cell membrane protein) | 6.97 | 5.06 |
| 422241 | Y00062 | Hs.170121 | protein tyrosine phosphatase, receptor I | 6.83 | 5.20 |
| 429170 | NM_001394 | Hs.2359 | dual specificity phosphatase 4 | 6.67 | 3.77 |
| 417542 | J04129 | Hs.82269 | progesterone-associated endometrial prote | 6.67 | 15.22 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|------|
| 5 | 428398 | AI249368 | Hs.98558 | ESTs | | |
| | 409899 | AW361666 | Hs.49500 | KIAA0746 protein | 6.57 | 3.60 |
| | 417022 | NM_014737 | Hs.80905 | Ras association (RalGDS/AF-6) domain fam | 6.48 | 4.93 |
| | 449644 | AW560707 | Hs.148324 | ESTs | 6.38 | 3.65 |
| | 412326 | R07566 | Hs.73817 | small inducible cytokine A3 (homologous | 6.35 | 5.84 |
| | 457211 | AW972565 | Hs.32399 | ESTs, Weakly similar to S51797 vasodilat | 6.30 | 7.18 |
| | 420991 | AW504814 | Hs.287379 | Homo sapiens mRNA for FLJ00111 protein, | 6.25 | 7.21 |
| | 428227 | AA321649 | Hs.2248 | small inducible cytokine subfamily B (Cy | 6.25 | 5.36 |
| 10 | 432828 | AB042326 | Hs.287402 | chondroitin 4-sulfotransferase | 6.18 | 6.01 |
| | 449078 | AK001256 | Hs.22975 | KIAA1576 protein | 6.12 | 6.51 |
| | 436856 | AI469355 | Hs.127310 | ESTs | 6.05 | 8.55 |
| | 433658 | L03678 | Hs.156110 | immunoglobulin kappa constant | 6.00 | 5.54 |
| | 424247 | X14008 | Hs.234734 | lysozyme (renal amyloidosis) | 5.92 | 7.18 |
| 15 | 409417 | AA156247 | Hs.104879 | serine (or cysteine) proteinase inhibito | 5.89 | 4.07 |
| | 431574 | AW572659 | Hs.261373 | hypothetical protein dJ434O14.3 | 5.86 | 6.07 |
| | 458079 | AI796870 | Hs.54277 | DNA segment on chromosome X (unique) 992 | 5.74 | 6.03 |
| | 440274 | R24595 | Hs.7122 | scrapie responsive protein 1 | 5.72 | 5.92 |
| | 429412 | NM_006235 | Hs.2407 | POU domain, class 2, associating factor | 5.69 | 3.22 |
| 20 | 432606 | NM_002104 | Hs.3066 | granzyme B (serine protease, granzyme 3; | 5.69 | 5.17 |
| | 436315 | BE390513 | Hs.27935 | hypothetical protein MGC4837 | 5.68 | 3.35 |
| | 452973 | H88409 | Hs.40527 | ESTs | 5.67 | 4.56 |
| | 426559 | AB001914 | Hs.170414 | paired basic amino acid cleaving system | 5.63 | 5.50 |
| | 406663 | U24683 | | immunoglobulin heavy constant mu | 5.62 | 3.09 |
| 25 | 416975 | NM_004131 | Hs.1051 | granzyme B (granzyme 2, cytotoxic T-lymp | 5.54 | 9.68 |
| | 408380 | AF123050 | Hs.44532 | diubiquitin | 5.52 | 6.42 |
| | 418299 | AA279530 | Hs.83968 | integrin, beta 2 (antigen CD18 (p95), ly | 5.51 | 4.49 |
| | 429500 | X78565 | Hs.289114 | hexabrachion (tenascin C, cytotoxic) | 5.43 | 4.50 |
| | 446341 | AL040763 | Hs.310735 | ESTs, Moderately similar to ALU7_HUMAN A | 5.42 | 3.54 |
| 30 | 425234 | AW152225 | Hs.165909 | ESTs, Weakly similar to I38022 hypothe | 5.41 | 5.29 |
| | 434203 | BE262677 | Hs.283558 | hypothetical protein PRO1855 | 5.40 | 4.35 |
| | 420338 | AA825595 | Hs.88269 | Homo sapiens, clone MGC:17339, mRNA, com | 5.38 | 4.16 |
| | 430580 | AA806105 | Hs.300697 | immunoglobulin heavy constant gamma 3 (G | 5.37 | 5.77 |
| | 428804 | AK000713 | Hs.193736 | hypothetical protein FLJ20706 | 5.31 | 5.32 |
| 35 | 447735 | AA775268 | Hs.6127 | Homo sapiens cDNA: FLJ23020 fis, clone L | 5.29 | 4.80 |
| | 410491 | AA465131 | Hs.64001 | Homo sapiens clone 25218 mRNA sequence | 5.29 | 3.61 |
| | 410361 | BE391804 | Hs.62661 | guanylate binding protein 1, interferon- | 5.27 | 5.35 |
| | 412561 | NM_002286 | Hs.74011 | lymphocyte-activation gene 3 | 5.26 | 6.00 |
| | 450293 | N36754 | Hs.171118 | hypothetical protein FLJ00026 | 5.26 | 5.04 |
| 40 | 400750 | | | Target Exon | 5.23 | 3.60 |
| | 417933 | X02308 | Hs.82962 | thymidylate synthetase | 5.18 | 3.62 |
| | 413385 | M34455 | Hs.840 | indoleamine-pyrrole 2,3 dioxygenase | 5.14 | 3.33 |
| | 445784 | AI253155 | Hs.146085 | ESTs | 5.12 | 5.36 |
| | 420602 | AF060877 | Hs.99236 | regulator of G-protein signalling 20 | 5.12 | 4.06 |
| 45 | 421508 | NM_004833 | Hs.105115 | absent in melanoma 2 | 5.06 | 7.68 |
| | 434826 | AF155661 | Hs.22265 | pyruvate dehydrogenase phosphatase | 5.03 | 5.59 |
| | 402474 | | | NM_004079:Homo sapiens cathepsin S (CTSS | 4.96 | 6.25 |
| | 400417 | X72475 | | Target | 4.95 | 5.13 |
| 50 | 420137 | AA306478 | Hs.95327 | CD30 antigen, delta polypeptide (TIT3 co | 4.90 | 3.93 |
| | 409264 | NM_014937 | Hs.52463 | KIAA0966 protein | 4.88 | 6.81 |
| | 418460 | M26315 | Hs.85258 | CD8 antigen, alpha polypeptide (p32) | 4.88 | 3.18 |
| | 418506 | AA084248 | Hs.85339 | G protein-coupled receptor 39 | 4.87 | 4.20 |
| | 409142 | AL136877 | Hs.50758 | SMC4 (structural maintenance of chromoso | 4.85 | 5.86 |
| | 425088 | AA663372 | Hs.169395 | hypothetical protein FLJ12015 | 4.83 | 5.94 |
| 55 | 405506 | | | Target Exon | 4.82 | 5.19 |
| | 409512 | AW979187 | Hs.293591 | melanoma differentiation associated prot | 4.74 | 4.09 |
| | 430838 | N46664 | Hs.169395 | hypothetical protein FLJ12015 | 4.74 | 3.72 |
| | 439963 | AW247529 | Hs.6793 | platelet-activating factor acetylhydrola | 4.73 | 3.50 |
| | 421379 | Y15221 | Hs.103982 | small inducible cytokine subfamily B (Cy | 4.72 | 3.66 |
| 60 | 447217 | BE465754 | Hs.17778 | neuropilin 2 | 4.71 | 5.16 |
| | 422309 | U79745 | Hs.114924 | solute carrier family 16 (monocarboxylic | 4.70 | 4.52 |
| | 413670 | AB000115 | Hs.75470 | hypothetical protein, expressed in osteo | 4.69 | 3.51 |
| | 419956 | AL137939 | Hs.40096 | cadherin 19, type 2 | 4.68 | 3.69 |
| | 429903 | AL134197 | Hs.93597 | cyclin-dependent kinase 5, regulatory su | 4.68 | 5.83 |
| 65 | 449217 | AA278536 | Hs.23262 | ribonuclease, RNase A family, k6 | 4.68 | 5.29 |
| | 449722 | BE280074 | Hs.23960 | cyclin B1 | 4.66 | 3.84 |
| | 424006 | AF054815 | Hs.137548 | CD84 antigen (leukocyte antigen) | 4.64 | 4.29 |
| | 407846 | AA426202 | Hs.40403 | Cbp/p300-interacting transactivator, wit | 4.62 | 4.54 |
| | 414821 | M63835 | Hs.77424 | Fc fragment of IgG, high affinity Ia, re | 4.62 | 6.78 |
| 70 | 406673 | M34996 | Hs.198253 | major histocompatibility complex, class | 4.59 | 5.81 |
| | 431620 | AA126109 | Hs.264981 | Z'-5'-oligoadenylate synthetase 2 (69-71 | 4.57 | 5.60 |
| | 441224 | AU076964 | Hs.7753 | calumenin | 4.56 | 4.44 |
| | 442739 | NM_007274 | Hs.8679 | cytosolic acyl coenzyme A thioester hydr | 4.56 | 3.75 |
| | 444371 | BE540274 | Hs.239 | forkhead box M1 | 4.56 | 3.22 |
| 75 | 448719 | AA033627 | Hs.21858 | trinucleotide repeat containing 3 | 4.53 | 5.28 |
| | 420301 | AA767526 | Hs.22030 | paired box gene 5 (B-cell lineage specif | 4.48 | 9.08 |
| | 430294 | AI538226 | Hs.32976 | guanine nucleotide binding protein 4 | 4.47 | 5.61 |
| | 428513 | BE220806 | Hs.184697 | Homo sapiens clone 23785 mRNA sequence | 4.43 | 4.11 |
| | 445006 | NM_004403 | Hs.13530 | deafness, autosomal dominant 5 | 4.41 | 4.43 |
| 80 | 432485 | N90866 | Hs.276770 | CDW52 antigen (CAMPATH-1 antigen) | 4.39 | 3.99 |
| | 428242 | H55709 | Hs.2250 | leukemia inhibitory factor (choleergic | 4.38 | 5.50 |
| | 421633 | AF121850 | Hs.105260 | sorting nexin 10 | 4.37 | 3.25 |
| | 414829 | AA321568 | Hs.77436 | pleckstrin | 4.36 | 6.23 |
| | 417166 | AA431323 | Hs.42146 | ESTs | 4.35 | 2.91 |
| | | | | | 4.35 | 4.08 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|-------|
| 5 | 448410 | AK000227 | Hs.21126 | hypothetical protein FLJ20220 | 4.34 | 5.35 |
| | 419381 | AB023420 | Hs.90093 | heat shock 70kD protein 4 | 4.34 | 3.72 |
| | 411305 | BE241596 | Hs.69547 | myelin basic protein | 4.32 | 4.18 |
| | 425289 | AW139342 | Hs.155530 | interferon, gamma-inducible protein 16 | 4.28 | 2.44 |
| | 451099 | R52795 | Hs.25954 | interleukin 13 receptor, alpha 2 | 4.27 | 4.48 |
| | 432642 | BE297635 | Hs.3069 | heat shock 70kD protein 9B (mortalin-2) | 4.25 | 2.69 |
| | 422282 | AF019225 | Hs.114309 | apolipoprotein L | 4.25 | 3.75 |
| | 433867 | AK000596 | Hs.3618 | hippocatin-like 1 | 4.23 | 5.13 |
| 10 | 415817 | U88967 | Hs.78867 | protein tyrosine phosphatase, receptor-t | 4.20 | 2.15 |
| | 438619 | AB032773 | | TU12B1-TY protein | 4.19 | 3.32 |
| | 426317 | AA312350 | Hs.169294 | transcription factor 7 (T-cell specific, | 4.16 | 5.14 |
| | 420208 | BE276055 | Hs.95972 | silver (mouse homolog) like | 4.16 | 5.08 |
| | 416602 | NM_006159 | Hs.79389 | Protein kinase C-binding protein NELL2 | 4.16 | 2.38 |
| 15 | 430770 | AA765694 | Hs.123296 | ESTs | 4.15 | 3.67 |
| | 424541 | AW392551 | Hs.180559 | ESTs, Weakly similar to A56194 thromboxa | 4.15 | 3.98 |
| | 427337 | Z46223 | Hs.176663 | Fc fragment of IgG, low affinity IIb, r | 4.14 | 3.51 |
| | 456760 | AW961251 | Hs.127828 | guanine nucleotide binding protein (G pr | 4.14 | 4.42 |
| | 406868 | AA505445 | Hs.300697 | immunoglobulin heavy constant gamma 3 (G | 4.13 | 5.07 |
| 20 | 420931 | AF044197 | Hs.100431 | small inducible cytokine B subfamily (Cy | 4.12 | 6.43 |
| | 410016 | AA297977 | Hs.57907 | small inducible cytokine subfamily A (Cy | 4.11 | 8.73 |
| | 452698 | NM_001295 | Hs.301921 | chemokine (C-C motif) receptor 1 | 4.11 | 4.48 |
| | 444863 | AW384082 | Hs.104879 | serine (or cysteine) proteinase inhibito | 4.10 | 4.78 |
| | 435080 | AI831760 | Hs.155111 | hypothetical protein FLJ14428 | 4.07 | 2.76 |
| 25 | 442711 | AF151073 | Hs.8645 | hypothetical protein | 4.06 | 3.49 |
| | 423605 | AF047826 | Hs.129887 | cadherin 19, type 2 | 4.06 | 2.42 |
| | 409038 | T97490 | Hs.50002 | small inducible cytokine subfamily A (Cy | 4.05 | 3.26 |
| | 421712 | AK000140 | Hs.107139 | hypothetical protein | 4.02 | 7.60 |
| | 422283 | AW411307 | Hs.114311 | CDC45 (cell division cycle 45, S.cerevis | 4.00 | 3.87 |
| 30 | 409415 | AA579258 | Hs.6083 | Homo sapiens cDNA: FLJ21026 fs, clone C | 4.00 | 5.87 |
| | 412719 | AW016610 | Hs.816 | ESTs | 3.99 | 5.46 |
| | 437179 | AA393508 | | serologically defined colon cancer antig | 3.96 | 4.51 |
| | 420319 | AW406289 | Hs.96593 | hypothetical protein | 3.95 | 5.47 |
| | 438380 | T06430 | Hs.6194 | chondroitin sulfate proteoglycan BEHAB/b | 3.91 | 4.58 |
| 35 | 418064 | BE387287 | Hs.83384 | S100 calcium-binding protein, beta (neur | 3.84 | 4.42 |
| | 420286 | AI796395 | Hs.111377 | ESTs | 3.83 | 4.56 |
| | 410600 | AW575742 | | ESTs, Moderately similar to S65657 alpha | 3.80 | 5.70 |
| | 410326 | AI368909 | Hs.47650 | ESTs | 3.76 | 4.86 |
| | 424779 | AL046851 | Hs.153053 | CD37 antigen | 3.70 | 8.72 |
| 40 | 452194 | AI694413 | | Ubiquitin-like protein FAT10777 - diubiq | 3.69 | 6.38 |
| | 411027 | AF072099 | Hs.67846 | leukocyte immunoglobulin-like receptor, | 3.65 | 5.40 |
| | 412140 | AA219691 | Hs.73625 | RAB5 interacting, kinesin-like (rabkines | 3.65 | 4.48 |
| | 424153 | AA451737 | Hs.141496 | MAGE-like 2 | 3.64 | 5.82 |
| | 421666 | AL035250 | Hs.1408 | endothelin 3 | 3.64 | 5.52 |
| 45 | 429732 | U20158 | Hs.2488 | lymphocyte cytosolic protein 2 (SH2 doma | 3.60 | 5.56 |
| | 421713 | BE385828 | Hs.250619 | phorbol-like protein MDS019 (CEM15) | 3.59 | 4.35 |
| | 421563 | NM_006433 | Hs.105806 | granulysin | 3.49 | 7.38 |
| | 453837 | AL138387 | Hs.256126 | baculoviral IAP repeat-containing 7 (liv | 3.49 | 6.13 |
| | 424326 | NM_014479 | Hs.145296 | ADAM-like disintegrin protease, decysin | 3.48 | 4.23 |
| 50 | 427247 | AW504221 | Hs.174103 | integrin, alpha L (antigen CD11A (p180), | 3.47 | 5.38 |
| | 408838 | AI669535 | Hs.40369 | ESTs | 3.45 | 4.59 |
| | 402829 | | | C1002500.gij6754254[ref]NP_034610.1[hea | 3.42 | 5.01 |
| | 418918 | X07871 | Hs.89476 | CD2 antigen (p50), sheep red blood cell | 3.42 | 8.14 |
| | 430594 | AK000790 | Hs.246885 | hypothetical protein FLJ20783 | 3.40 | 4.35 |
| 55 | 429714 | BE561801 | Hs.2484 | T-cell leukemia/lymphoma 1A | 3.36 | 4.84 |
| | 414324 | Y14768 | Hs.890 | lymphotoxin beta (TNF superfamily, membe | 3.35 | 4.45 |
| | 421958 | AA357185 | Hs.109918 | ras homolog gene family, member H | 3.35 | 4.28 |
| | 428291 | AA534009 | Hs.183487 | interferon stimulated gene (20kD) | 3.34 | 5.18 |
| | 424687 | J05070 | Hs.151738 | matrix metalloproteinase 9 (gelatinase B | 3.31 | 8.00 |
| 60 | 451736 | AW080356 | Hs.23889 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 3.29 | 4.50 |
| | 412790 | NM_014767 | Hs.74583 | KIAA0275 gene product | 3.28 | 5.42 |
| | 404854 | | | Target Exon | 3.28 | 4.28 |
| | 400860 | | | Target Exon | 3.26 | 4.41 |
| 65 | 430413 | AW842182 | Hs.241392 | small inducible cytokine A5 (RANTES) | 3.24 | 5.65 |
| | 438209 | AL120659 | Hs.6111 | aryl-hydrocarbon receptor nuclear transl | 3.24 | 4.35 |
| | 422846 | BE513934 | Hs.1583 | neutrophil cytosolic factor 1 (47kD, chr | 3.24 | 4.90 |
| | 440065 | W03476 | Hs.266331 | hypothetical protein MGC4595 | 3.20 | 6.21 |
| | 440704 | M69241 | Hs.162 | insulin-like growth factor binding prote | 3.20 | 4.72 |
| | 411088 | BE247593 | Hs.145053 | ESTs | 3.18 | 4.20 |
| 70 | 447513 | AW955776 | Hs.313500 | ESTs, Moderately similar to ALU7_HUMAN A | 3.18 | 4.68 |
| | 413190 | AA151802 | Hs.40368 | adaptor-related protein complex 1, sigma | 3.15 | 4.27 |
| | 430017 | AA263172 | Hs.35 | protein tyrosine phosphatase, non-recept | 3.15 | 4.28 |
| | 406837 | R70292 | Hs.156110 | immunoglobulin kappa constant | 3.12 | 4.09 |
| | 409103 | AF251237 | Hs.112208 | XAGE-1 protein | 3.04 | 4.04 |
| 75 | 425706 | AW406678 | Hs.122559 | hypothetical protein FLJ22570 | 3.04 | 4.28 |
| | 447656 | NM_003726 | Hs.19126 | src kinase-associated phosphoprotein of | 3.03 | 4.30 |
| | 427792 | M63928 | Hs.180841 | tumor necrosis factor receptor superfam | 3.01 | 4.82 |
| | 402994 | | | NM_002463*:Homo sapiens myxovirus (infl | 2.99 | 5.74 |
| | 434276 | AF123659 | Hs.93605 | leucine zipper, putative tumor suppresso | 2.97 | 5.07 |
| 80 | 449523 | NM_000579 | Hs.54443 | chemokine (C-C motif) receptor 5 | 2.96 | 4.15 |
| | 439237 | AW408158 | Hs.318893 | ESTs, Weakly similar to A47582 B-cell gr | 2.96 | 5.81 |
| | 406621 | X57809 | Hs.8997 | immunoglobulin lambda locus | 2.93 | 7.88 |
| | 447131 | NM_004585 | Hs.17466 | retinoic acid receptor responder (tazaro | 2.91 | 13.22 |
| | 426322 | J05068 | Hs.2012 | transcobalamin I (vitamin B12 binding pr | 2.90 | 8.37 |

| | | | | | | |
|----|--------|-----------|-----------|---|------|-------|
| | 448275 | BE514434 | Hs.20830 | kinesin-like 2 | | |
| | 423397 | NM_001838 | Hs.1652 | chemokine (C-C motif) receptor 7 | 2.87 | 4.15 |
| | 406782 | AA430373 | | gb:zw2011.1.s1 Soares ovary tumor NbHOT H | 2.86 | 5.53 |
| 5 | 414915 | NM_002462 | Hs.76391 | myxovirus (influenza) resistance 1, homo | 2.81 | 4.60 |
| | 412819 | T25829 | Hs.24048 | FK506 binding protein precursor | 2.80 | 5.89 |
| | 432886 | BE159028 | Hs.279704 | chromatin accessibility complex 1 | 2.78 | 4.90 |
| | 428380 | NM_004271 | Hs.184018 | MD-1, RP105-associated | 2.76 | 4.21 |
| | 408209 | NM_004454 | Hs.43697 | ets variant gene 5 (ets-related molecule | 2.76 | 5.15 |
| 10 | 416511 | NM_006762 | Hs.79356 | Lysosomal-associated multispinning membr | 2.76 | 4.30 |
| | 422530 | AW972300 | Hs.118110 | bone marrow stromal cell antigen 2 | 2.75 | 4.13 |
| | 428746 | AW503820 | Hs.192861 | Spi-B transcription factor (Spi-1/PU.1 r | 2.74 | 5.05 |
| | 453953 | AW408337 | Hs.36972 | CD7 antigen (p41) | 2.73 | 9.20 |
| | 407241 | M34516 | | gb:Human omega light chain protein 14.1 | 2.72 | 4.38 |
| 15 | 437669 | AI358105 | Hs.123164 | ESTs, Weakly similar to match to ESTs AA | 2.68 | 4.07 |
| | 453779 | N35187 | Hs.43388 | 28kD interferon responsive protein | 2.66 | 4.71 |
| | 432874 | W94322 | Hs.279651 | melanoma inhibitory activity | 2.65 | 4.31 |
| | 410129 | BE244074 | Hs.58831 | regulator of Fas-induced apoptosis | 2.64 | 4.15 |
| | 412926 | AI879076 | Hs.75061 | macrophage myristoylated alanine-rich C | 2.62 | 7.36 |
| 20 | 418739 | AA310964 | Hs.88012 | SHP2 interacting transmembrane adaptor | 2.62 | 4.43 |
| | 424825 | AF207069 | Hs.153357 | procollagen-lysine, 2-oxoglutarate 5-dio | 2.61 | 5.42 |
| | 417370 | T28651 | Hs.82030 | tryptophanyl-tRNA synthetase | 2.60 | 9.69 |
| | 411358 | R47479 | Hs.94761 | KIAA1691 protein | 2.60 | 5.17 |
| | 425367 | BE271188 | Hs.155975 | protein tyrosine phosphatase, receptor t | 2.59 | 4.01 |
| 25 | 426470 | AA528794 | Hs.128644 | ESTs | 2.58 | 13.24 |
| | 425535 | AB007937 | Hs.158287 | KIAA0468 gene product | 2.54 | 4.52 |
| | 431629 | AU077025 | Hs.265827 | interferon, alpha-inducible protein (clo | 2.52 | 11.31 |
| | 425722 | AI659076 | Hs.97031 | hypothetical protein MGC13047 | 2.50 | 7.80 |
| | 438291 | BE514605 | Hs.289092 | Homo sapiens cDNA: FLJ22380 fis, clone H | 2.49 | 4.25 |
| 30 | 416426 | AA180256 | Hs.210473 | Homo sapiens cDNA: FLJ14872 fis, clone PL | 2.49 | 4.04 |
| | 441859 | AW194364 | Hs.94814 | ESTs, Weakly similar to FIG1 MOUSE FIG-1 | 2.48 | 4.08 |
| | 416714 | AF283770 | Hs.79630 | CD79A antigen (immunoglobulin-associated | 2.48 | 5.25 |
| | 431186 | NM_012249 | Hs.250697 | ras-like protein | 2.48 | 4.88 |
| | 417389 | BE260964 | Hs.82045 | midkine (neurite growth-promoting factor | 2.46 | 6.04 |
| 35 | 424481 | R19453 | Hs.1787 | proteolipid protein 1 (Pelizaeus-Merzbac | 2.45 | 5.34 |
| | 428437 | AV656017 | Hs.184325 | CGI-76 protein | 2.43 | 6.57 |
| | 427634 | AI399745 | Hs.18449 | hypothetical protein MGC10820 | 2.42 | 4.96 |
| | 420842 | AI083668 | Hs.50601 | hypothetical protein MGC10986 | 2.39 | 8.46 |
| | 428289 | M26301 | Hs.2253 | complement component 2 | 2.38 | 5.90 |
| 40 | 417929 | R27219 | Hs.74647 | Human T-cell receptor active alpha-chain | 2.38 | 5.32 |
| | 413278 | BE563085 | Hs.833 | interferon-stimulated protein, 15 kDa | 2.37 | 6.99 |
| | 433671 | AW138797 | Hs.132906 | 19A24 protein | 2.34 | 9.69 |
| | 432403 | AA550815 | Hs.124840 | ESTs | 2.34 | 4.81 |
| | 427759 | BE245578 | Hs.2200 | perforin 1 (pore forming protein) | 2.34 | 4.99 |
| 45 | 419870 | AW403911 | Hs.266175 | phosphoprotein associated with GEMs | 2.32 | 4.56 |
| | 421445 | AA913059 | Hs.104433 | Homo sapiens, clone IMAGE:4054868, mRNA | 2.30 | 4.22 |
| | 401591 | | | Target Exon | 2.30 | 6.18 |
| | 451708 | AI306536 | Hs.60975 | ESTs | 2.29 | 7.01 |
| | 452700 | AI859390 | Hs.288940 | five-span transmembrane protein M83 | 2.26 | 4.50 |
| 50 | 424618 | L29472 | Hs.1802 | major histocompatibility complex, class | 2.24 | 4.90 |
| | 409208 | Y00093 | | integrin, alpha X (antigen CD11C (p150), | 2.22 | 5.40 |
| | 436456 | AW292677 | Hs.248122 | G protein-coupled receptor 24 | 2.21 | 4.74 |
| | 419741 | NM_007019 | Hs.93002 | ubiquitin carrier protein E2-C | 2.19 | 4.61 |
| | 416448 | L13210 | Hs.79339 | lectin, galactoside-binding, soluble, 3 | 2.17 | 7.43 |
| 55 | 438555 | AI222089 | Hs.143878 | Homo sapiens mRNA for FLJ00024 protein, | 2.16 | 5.58 |
| | 407260 | L09095 | | gb:Homo sapiens mRNA fragment | 2.13 | 4.26 |
| | 448243 | AW369771 | | integrin, beta 8 | 2.13 | 4.00 |
| | 437938 | AI950087 | | gb:wq05c02.x1 NCI_CGAP_Kid12 Homo sapien | 2.10 | 4.03 |
| | 425262 | D87119 | Hs.155418 | GS3955 protein | 2.07 | 4.45 |
| 60 | 414945 | BE076358 | Hs.77667 | lymphocyte antigen 6 complex, locus E | 2.06 | 4.36 |
| | 400261 | | | Eos Control | 2.05 | 4.66 |
| | 432468 | AW402155 | Hs.3003 | CD3E antigen, epsilon polypeptide (TTT3 | 2.04 | 4.22 |
| | 416967 | BE616731 | Hs.80645 | interferon regulatory factor 1 | 2.02 | 4.23 |
| 65 | 420626 | AF043722 | Hs.99491 | RAS guanyl releasing protein 2 (calcium | 1.99 | 4.45 |
| | 440672 | AF083811 | Hs.7345 | MAD1 (mitotic arrest deficient, yeast, h | 1.98 | 4.42 |
| | 452923 | BE276018 | Hs.288940 | five-span transmembrane protein M83 | 1.98 | 4.55 |
| | 452244 | N33530 | Hs.176674 | ESTs | 1.96 | 4.54 |
| | 427239 | BE270447 | | ubiquitin carrier protein | 1.95 | 4.23 |
| | 418678 | NM_001327 | Hs.167379 | cancer/testis antigen (NY-ESO-1) | 1.94 | 4.93 |
| 70 | 431836 | AF178532 | Hs.271411 | beta-site APP-cleaving enzyme 2 | 1.94 | 5.28 |
| | 444090 | S69115 | Hs.10306 | natural killer cell group 7 sequence | 1.93 | 4.17 |
| | 404067 | | | Target Exon | 1.93 | 5.06 |
| | 426890 | AA393167 | Hs.41294 | ESTs | 1.92 | 6.16 |
| | 453597 | BE281130 | Hs.33713 | myo-inositol 1-phosphate synthase A1 | 1.91 | 4.23 |
| 75 | 401914 | | | Target Exon | 1.91 | 4.10 |
| | 448499 | BE613280 | Hs.77550 | hypothetical protein MGC1780 | 1.87 | 4.76 |
| | 439627 | BE621702 | Hs.29076 | hypothetical protein FLJ21841 | 1.87 | 5.17 |
| | 425923 | NM_005026 | Hs.162808 | phosphoinositide-3-kinase, catalytic, de | 1.85 | 6.59 |
| | 416819 | U77735 | Hs.80205 | pim-2 oncogene | 1.85 | 4.03 |
| | 425069 | AA687465 | Hs.298184 | potassium voltage-gated channel, shaker- | 1.84 | 4.57 |
| 80 | 430378 | Z29572 | Hs.2556 | tumor necrosis factor receptor superfam | 1.84 | 6.40 |
| | 435968 | AW161481 | Hs.111577 | integral membrane protein 3 | 1.78 | 4.02 |
| | 410423 | AW402432 | Hs.63489 | protein tyrosine phosphatase, non-recept | 1.76 | 5.26 |
| | 434224 | AA380731 | Hs.84 | interleukin 2 receptor, gamma (severe co | 1.75 | 4.30 |
| | | | | | 1.74 | 4.91 |

| | | | | | | |
|----|--------------|---|---|--|------|------|
| 5 | 413566 | AW604451 | Hs.285814 | sprouty (Drosophila) homolog 4 | 1.71 | 6.00 |
| | 430148 | BE387620 | Hs.234489 | lactate dehydrogenase B | 1.70 | 4.34 |
| | 410068 | AI533888 | Hs.58435 | FYN-binding protein (FYB-120/130) | 1.69 | 4.04 |
| | 437696 | Z83844 | Hs.5790 | hypothetical protein dJ37E16.5 | 1.66 | 5.95 |
| | 423984 | AF163825 | Hs.136713 | pre-B lymphocyte gene 3 | 1.64 | 6.26 |
| | 426666 | AW500131 | Hs.171763 | CD22 antigen | 1.63 | 4.33 |
| | 406908 | Z25437 | | gb:H.sapiens protein-tyrosine kinase gen | 1.62 | 7.19 |
| | 440087 | W28969 | Hs.7718 | hypothetical protein FLJ22678 | 1.61 | 4.33 |
| 10 | 421859 | AA356620 | Hs.108947 | KIAA0050 gene product | 1.59 | 4.30 |
| | 415198 | AW009480 | Hs.943 | natural killer cell transcript 4 | 1.56 | 4.12 |
| | 406827 | AA971409 | | gb:op92c04.s1 NCI_CGAP_Lu5 Homo sapiens | 1.55 | 4.29 |
| | 413969 | X14034 | Hs.75648 | phospholipase C, gamma 2 (phosphatidyl | 1.53 | 4.63 |
| | 456086 | AL161999 | Hs.77324 | eukaryotic translation termination facto | 1.52 | 4.11 |
| 15 | 433320 | D60647 | Hs.250879 | ESTs, Highly similar to CTXN RAT CORTEXI | 1.52 | 4.36 |
| | 406906 | Z25424 | | gb:H.sapiens protein-serine/threonine ki | 1.50 | 8.67 |
| | 406885 | D28423 | | gb:Human mRNA for pre-mRNA splicing fact | 1.49 | 5.07 |
| | 443759 | BE390832 | Hs.134729 | FXYD domain-containing ion transport reg | 1.48 | 4.50 |
| | 452423 | AA991724 | Hs.180535 | hypothetical protein MGC10966 | 1.48 | 4.91 |
| 20 | 448143 | AF039704 | Hs.20478 | ceroid-lipofuscinosis, neuronal 2, late | 1.43 | 4.26 |
| | 451524 | AK001466 | Hs.26516 | hypothetical protein FLJ10604 | 1.43 | 4.74 |
| | 417287 | AI831678 | Hs.285714 | KIAA1599 protein | 1.41 | 4.01 |
| | 432665 | AW603880 | | ATPase, H transporting, lysosomal (vacuo | 1.38 | 4.07 |
| | 403043 | | | Target Exon | 1.36 | 4.89 |
| 25 | 407239 | AA076350 | Hs.67846 | leukocyte immunoglobulin-like receptor, | 1.32 | 4.57 |
| | 436553 | AW407157 | Hs.8997 | immunoglobulin lambda locus | 1.30 | 4.00 |
| | 422934 | BE244189 | Hs.122492 | hypothetical protein | 1.30 | 4.37 |
| | 442680 | BE270707 | Hs.8583 | similar to APOBEC1 | 1.26 | 4.48 |
| 30 | TABLE 57B: | | | | | |
| | Pkey: | Unique Eos probeset identifier number | | | | |
| | CAT number: | Gene cluster number | | | | |
| | Accession: | Genbank accession numbers | | | | |
| 35 | Pkey | CAT Number | Accession | | | |
| | 438619 | 35124_1 | NM_016575 AB032773 AI765521 BF593742 AI497757 AI761233 AW467938 BF000670 AI818496 N24761 AL043306 BF476138 BF593836 AA132787 | | | |
| | | | AI147248 AI086795 AA151317 T95298 AW083548 AA058371 N27951 AI769860 AI784548 AW205506 AI800679 AI041733 AI459902 BE327641 | | | |
| | | | AI865829 AI254736 AI302433 AI744176 AI241825 AA027842 AL524933 AL524932 BF947764 BF340737 BF948700 BG996395 NS3455 N21027 | | | |
| | | | AI127616 N35901 AA682443 AA678249 AA719371 AA132582 T15981 H99958 N40717 AW959402 AI267251 BF909329 AI142035 T95379 H29420 | | | |
| | | | R59632 H17318 H17331 H29327 R40829 R43395 R59573 AI749561 R56599 H16755 AI694500 AA027907 | | | |
| 40 | 437179 | 12239_1 | AK055109 BC019085 AA187684 BG656226 BM023227 AI932311 AW264381 AA398371 BM021483 AI432433 AI375777 AI129580 AW262782 | | | |
| | | | AA134107 BM023515 AA977504 AI859222 AI348454 R69725 AA975268 BM021207 AL080074 AA129218 AW207842 N90581 AA771919 AI092259 | | | |
| | | | AI028416 AI074114 BG656536 BE501677 AW193419 AA917040 W90430 AI342984 AI378957 AL036486 AW020068 BI491093 BF476021 R41226 | | | |
| | | | R69631 F04125 C02343 AA115589 R56480 AI400988 R54266 R31422 | | | |
| 45 | 410600 | 497855_1 | BF347859 AW499616 AA191322 AW499617 AL601010 AW575742 AA729043 BE463447 AA086179 BE549623 AI335824 AW08712 BM149172 | | | |
| | 452194 | 90339_1 | AI694413 AW994700 AI912946 N73548 AI082035 AW271652 W24189 W24182 AI719718 AA024658 AW810120 AW015394 T79755 AA988043 | | | |
| | | | AI709339 | | | |
| | 406782 | 0_0 | AA430373 AA968771 | | | |
| | 409208 | 10117_2 | AK074047 AI144342 AW014280 BM145128 N28267 AW206231 AA989041 H93197 AW594063 BG236296 AW236606 AW081031 AA765843 BM144372 | | | |
| 50 | | | AA989341 AI824838 AI963970 AI637671 AW196330 BG427526 BM148789 BF893644 BF881946 | | | |
| | 448243 | 13061_2 | BG166513 AA479726 BE622314 AL134913 BE006305 BE006312 BE006298 AA044582 AW994956 AA234175 AA043906 BE006303 BF327669 | | | |
| | | | BE006317 BF326759 BF541959 | | | |
| | 437938 | 66997_1 | U71456 AA482911 W78802 AW856538 BF737212 N36809 N35320 AA282915 AW505512 AI653832 W87891 AI961530 T85904 H59397 R97278 | | | |
| | | | W01059 AI820532 T82391 AI820501 T63226 R66056 R67840 AW961101 AA337499 W37181 AA180009 AW205862 AA988777 AA856975 BF172457 | | | |
| 55 | | | BG751124 AI741346 AI950344 AI689062 AI872193 AW102898 AW173586 AI763273 AI890387 AW150329 AI762688 AA488892 AI356394 AI539642 | | | |
| | | | AA642789 AI950087 BF589902 N70208 AA283144 AA488954 H60052 R97040 BF886630 AW967677 AW971573 AW967671 AI308119 AA251875 | | | |
| | | | AA908598 AI819225 AI564269 AA908741 AA293273 AA969759 AW276905 AA044209 H83488 T92487 | | | |
| | 400261 | 23110_1 | BC006097 X03066 NM_002120 M26040 AW469119 AW469127 AI299772 AW518149 AI144456 AW628070 AI629032 AI358810 AI880433 AI440472 | | | |
| | | | AI357070 AI865365 AW014799 AI767973 AW518041 AA909398 AW768606 | | | |
| 60 | 427239 | 20459_2 | AL532360 BE794750 AA582906 AI015067 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE138953 BE049086 AI334881 | | | |
| | | | AW075006 AW075181 AA464019 AW302733 AW075100 AW073433 AI802854 AI334909 AI802853 AI345036 AI348921 AI340734 AI307478 AI251289 | | | |
| | | | AW302327 AW072520 AI312145 AW073656 AW072513 AW071289 AI307559 AA876186 T29587 AI307493 AI255068 AI252868 AI252839 AW074809 | | | |
| | | | AI252926 AI252160 AI251662 AI251262 AI610913 AI270787 AI270156 AI252075 AW073469 AW072901 AW072496 AW071420 AI305762 AI254764 | | | |
| | | | AI802837 AI251264 AW073049 AW071311 AI340643 BE138965 BE138502 AW073456 AI334733 AI054335 BE139260 AI054302 AI054060 AI054057 | | | |
| | | | AI053722 AI289711 BE139228 AW470478 AW271039 AW302085 BE041872 AI254494 AI271496 AI252427 BF718773 BF718645 AW074856 BE857822 | | | |
| 65 | 406827 | 0_0 | AA971409 | | | |
| | 432665 | 27095_3 | BG165971 BE143233 AL577712 AI400326 AA769318 AA427866 AW088714 AI150755 AI924874 AI186243 AA804195 AA768972 AW574769 | | | |
| | | | AW341643 AW204520 AA235326 AI005076 BE826687 AW004816 AW007235 BE826639 BE826634 BF222941 BE826631 BE826643 AA292639 | | | |
| | | | AW514133 AI690331 AI673409 AA627727 AI923685 AA931499 AI249783 AI810663 AA548622 AA702095 AA832395 BI259508 AA262993 AW075840 | | | |
| | | | AA810885 | | | |
| 70 | TABLE 57C: | | | | | |
| | Pkey: | Unique number corresponding to an Eos probeset | | | | |
| | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA | | | | |
| | | sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495. | | | | |
| 75 | Strand: | Indicates DNA strand from which exons were predicted. | | | | |
| | NI_position: | Indicates nucleotide positions of predicted exons. | | | | |
| 80 | Pkey | Ref | Strand | NI_position | | |
| | 400750 | 8119067 | Plus | 198991-199168, 199316-199548 | | |
| | 402474 | 7547175 | Minus | 53526-53628, 55755-55920, 57530-57757 | | |
| | 405506 | 6466489 | Plus | 80014-80401, 80593-81125 | | |
| | 402829 | 8918414 | Plus | 101532-101852, 102006-102263 | | |
| | 404854 | 7143420 | Plus | 14260-14537 | | |

| | | | | |
|---|--------|---------|-------|-----------------------------|
| 5 | 400860 | 9757499 | Minus | 151830-152104,152649-152744 |
| | 402994 | 2996643 | Minus | 4727-4969 |
| | 401591 | 9966977 | Minus | 55410-55835 |
| | 404067 | 3282162 | Plus | 1415-2071 |
| | 401914 | 9369520 | Plus | 62537-62945,63155-63308 |
| | 403043 | 7768753 | Minus | 314423-316252 |

10 TABLE 58A: ABOUT 183 GENES UPREGULATED IN MELANOMA METASTASES FROM PATIENTS WITH LIMITED DISEASE RELATIVE TO MELANOMA METASTASES FROM PATIENTS WITH PROGRESSIVE DISEASE

Table 58A lists about 183 genes upregulated in melanoma metastases from patients with limited disease relative to melanoma metastases from patients with progressive disease. Genes were selected from 59680 probesets on the Eos/Alfymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

15 Pkey: Unique Eos probeset identifier number
 ExAccon: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of AIs for metastases from patients with limited disease divided by 90th percentile of AIs for metastases from patients with progressive disease
 R2: 90th percentile of AIs for metastases from patients with limited disease divided by 90th percentile of AIs for metastases from patients with progressive disease, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

| Pkey | ExAccon | UnigeneID | Unigene Title | R1 | R2 |
|--------|-----------|-----------|--|-------|-------|
| 415668 | AW957684 | Hs.306814 | hypothetical protein FLJ21889 | 12.74 | 12.92 |
| 447414 | D82343 | Hs.74376 | neuroblastoma (nerve tissue) protein | 7.66 | 5.88 |
| 412659 | AW753865 | Hs.74376 | octadecanoyl related ER localized protei | 7.23 | 5.76 |
| 430154 | AW583058 | Hs.234726 | serine (or cysteine) proteinase inhibito | 6.91 | 14.26 |
| 414430 | AJ346201 | Hs.76118 | ubiquitin carboxyl-terminal esterase L1 | 6.86 | 7.10 |
| 436485 | X59135 | Hs.156110 | immunoglobulin kappa constant | 6.85 | 6.81 |
| 426600 | NM_003378 | Hs.171014 | VGF nerve growth factor inducible | 6.73 | 11.21 |
| 430822 | AJ005371 | Hs.248017 | glyceraldehyde-3-phosphate dehydrogenase | 5.53 | 4.63 |
| 416426 | AA180256 | Hs.210473 | Homo sapiens cDNA FLJ14872 fis, clone PL | 5.48 | 7.08 |
| 423858 | AL137326 | Hs.133483 | Homo sapiens mRNA; cDNA DKFZp43480650 (f | 5.27 | 5.94 |
| 433658 | L03678 | Hs.156110 | immunoglobulin kappa constant | 4.78 | 3.07 |
| 452436 | BE077546 | Hs.31447 | ESTs, Moderately similar to A46010 X-fin | 4.68 | 3.27 |
| 413916 | N49813 | Hs.75615 | apolipoprotein C-II | 4.62 | 4.82 |
| 407825 | NM_006152 | Hs.40202 | lymphoid-restricted membrane protein | 4.55 | 3.12 |
| 406648 | AA563730 | Hs.277477 | major histocompatibility complex, class | 4.31 | 4.15 |
| 409060 | AJ815867 | Hs.50130 | necdin (mouse) homolog | 4.23 | 3.44 |
| 401941 | | | Target Exon | 3.89 | 3.19 |
| 447471 | AF039843 | Hs.18676 | sprouty (Drosophila) homolog 2 | 3.88 | 2.43 |
| 419628 | H67546 | Hs.49768 | ESTs | 3.66 | 4.16 |
| 414863 | AW131473 | Hs.106185 | rat guanine nucleotide dissociation stim | 3.63 | 2.81 |
| 423416 | NM_004920 | Hs.128316 | apoptosis-associated tyrosine kinase | 3.47 | 3.06 |
| 400275 | | | NM_006513*:Homo sapiens seryl-tRNA synth | 3.47 | 3.43 |
| 426283 | NM_003937 | Hs.169139 | kynureninase (L-kynurenine hydrolase) | 3.42 | 1.96 |
| 442117 | AW664964 | Hs.128899 | ESTs; hypothetical protein for IMAGE:447 | 3.41 | 2.89 |
| 411763 | AW862589 | | gb:QV0-CT0387-180300-167-a07 CT0387 Homo | 3.37 | 6.31 |
| 402007 | | | C18000503*:gij8922165[ref]NP_060080.1 h | 3.34 | 3.74 |
| 424775 | AB014540 | Hs.153026 | SWAP-70 protein | 3.30 | 2.00 |
| 424036 | AA770688 | | H2A histone family, member L | 3.30 | 3.16 |
| 453464 | AJ884911 | Hs.32989 | receptor (calcitonin) activity modifying | 3.30 | 5.58 |
| 401739 | | | NM_005622*:Homo sapiens SA (rat hyperten | 3.30 | 3.23 |
| 440274 | R24595 | Hs.7122 | scrapie responsive protein 1 | 3.27 | 2.47 |
| 413398 | D21262 | Hs.75337 | nucleolar and coiled-body phosphoprotein | 3.26 | 2.61 |
| 417165 | R80137 | Hs.302738 | Homo sapiens cDNA: FLJ21425 fis, clone C | 3.26 | 2.58 |
| 418478 | U38945 | Hs.1174 | cyclin-dependent kinase inhibitor 2A (me | 3.14 | 4.04 |
| 436965 | Z11894 | Hs.156110 | gb:H.sapiens rearranged mRNA for immunog | 3.13 | 2.38 |
| 453857 | AL080235 | Hs.35861 | DKFZP586E1621 protein | 3.13 | 2.47 |
| 404405 | | | Target Exon | 3.11 | 4.69 |
| 413719 | BE439580 | Hs.75498 | small inducible cytokine subfamily A (Cy | 3.11 | 2.10 |
| 443247 | BE614387 | Hs.333893 | c-Myc target JPO1 | 3.10 | 2.26 |
| 400417 | X72475 | | Target | 3.08 | 2.32 |
| 401512 | | | NM_014080:Homo sapiens dual oxidase-like | 3.07 | 2.87 |
| 423242 | AL039402 | Hs.125783 | DEME-6 protein | 3.06 | 2.78 |
| 417501 | AL041219 | Hs.82222 | sema domain, immunoglobulin domain (Ig), | 3.06 | 2.81 |
| 451952 | AL120173 | Hs.301663 | ESTs | 3.05 | 2.65 |
| 427419 | NM_000200 | Hs.177888 | histatin 3 | 3.05 | 4.24 |
| 406663 | U24683 | | immunoglobulin heavy constant mu | 3.05 | 4.55 |
| 442104 | L20971 | Hs.188 | phosphodiesterase 4B, cAMP-specific (dun | 3.03 | 1.90 |
| 451993 | AA765776 | Hs.122983 | ESTs | 3.02 | 1.71 |
| 421097 | AJ280112 | Hs.125232 | Homo sapiens cDNA FLJ13266 fis, clone OV | 3.01 | 3.11 |
| 430129 | BE301708 | Hs.233955 | hypothetical protein FLJ20401 | 3.00 | 3.47 |
| 427700 | AA262294 | Hs.180383 | dual specificity phosphatase 6 | 3.00 | 2.22 |
| 400237 | | | NM_001087*:Homo sapiens angio-associated | 2.98 | 3.43 |
| 414063 | H26904 | Hs.75736 | apolipoprotein D | 2.97 | 5.76 |
| 426153 | AF057169 | Hs.182771 | viteliform macular dystrophy (Best dise | 2.94 | 2.38 |
| 414781 | D50917 | Hs.77293 | KIAA0127 gene product | 2.94 | 2.88 |
| 445823 | AJ478563 | Hs.145519 | FKSG87 protein | 2.92 | 1.98 |
| 404439 | | | ENSP00000067222*:Mitochondrial 28S ribos | 2.92 | 2.57 |
| 421218 | NM_000499 | Hs.72912 | cytochrome P450, subfamily I (aromatic c | 2.90 | 2.47 |
| 420350 | AW406896 | Hs.88269 | Homo sapiens, clone MGC:17339, mRNA, com | 2.90 | 3.87 |
| 424855 | AW204725 | Hs.25560 | ESTs | 2.89 | 2.61 |
| 436700 | AJ693690 | Hs.301406 | hypothetical protein PP3501 | 2.88 | 3.63 |

| | | | | | | |
|----|--------|-----------|-----------|---|------|------|
| | 451131 | AI267586 | Hs.268012 | fatty-acid-Coenzyme A ligase, long-chain | 2.87 | 2.92 |
| | 427157 | U51166 | Hs.173824 | thymine-DNA glycosylase | 2.87 | 2.11 |
| | 402273 | | | Target Exon | 2.87 | 2.48 |
| 5 | 414135 | NM_004419 | Hs.2128 | dual specificity phosphatase 5 | 2.83 | 3.09 |
| | 430643 | AW970065 | Hs.287425 | MEGF10 protein | 2.83 | 3.04 |
| | 451979 | F06972 | Hs.27372 | endothelial tyrosine kinase (ETk) (BMX) | 2.82 | 2.12 |
| | 406642 | AJ245210 | | gb:Homo sapiens mRNA for immunoglobulin | 2.81 | 2.88 |
| | 407360 | X13075 | | gb:Human 2a12 mRNA for kappa-immunoglobulin | 2.81 | 3.43 |
| | 405441 | | | Target Exon | 2.80 | 3.15 |
| 10 | 450816 | BE271927 | Hs.87385 | ESTs | 2.80 | 2.48 |
| | 435675 | AA694099 | Hs.266820 | ESTs | 2.78 | 2.70 |
| | 426495 | NM_001151 | Hs.2043 | solute carrier family 25 (mitochondrial) | 2.78 | 2.53 |
| | 441623 | AA315805 | | desmoglein 2 | 2.78 | 2.27 |
| | 413336 | AI569936 | Hs.296178 | hypothetical protein FLJ22637 | 2.76 | 3.18 |
| 15 | 408527 | AL135018 | Hs.33074 | Homo sapiens, clone IMAGE:3606519, mRNA, | 2.76 | 1.92 |
| | 437740 | AA810265 | Hs.122915 | ESTs | 2.76 | 1.88 |
| | 426322 | J05068 | Hs.2012 | transcobalamin I (vitamin B12 binding pr | 2.75 | 8.06 |
| | 411852 | AA528140 | Hs.107515 | ESTs, Weakly similar to T00329 hypotheti | 2.74 | 3.30 |
| | 428422 | AI557280 | Hs.184270 | capping protein (actin filament) muscle | 2.73 | 2.31 |
| 20 | 426793 | X89887 | Hs.172350 | HIR (histone cell cycle regulation defec | 2.72 | 2.19 |
| | 401454 | | | NM_014226*:Homo sapiens renal tumor anti | 2.72 | 1.99 |
| | 436825 | AW341123 | Hs.120275 | ESTs | 2.72 | 2.89 |
| | 407705 | AB023139 | Hs.37892 | KIAA0922 protein | 2.72 | 2.48 |
| 25 | 416782 | L35035 | Hs.79886 | ribose 5-phosphate isomerase A (ribose 5 | 2.72 | 2.63 |
| | 449151 | AI632331 | Hs.196038 | ESTs | 2.72 | 2.99 |
| | 433464 | N92481 | | gb:zb12g02.s1 Soares_fetal_lung_NbHL19W | 2.69 | 3.17 |
| | 401009 | | | Target Exon | 2.69 | 3.28 |
| | 427227 | AF103803 | Hs.283690 | hypothetical protein | 2.68 | 2.02 |
| 30 | 405268 | | | ENSP00000223174*:KIAA0783 PROTEIN. | 2.67 | 2.18 |
| | 410295 | AA741357 | | nidogen (enactin) | 2.65 | 2.06 |
| | 435905 | AW997484 | Hs.5003 | KIAA0456 protein | 2.65 | 2.12 |
| | 430378 | Z29572 | Hs.2556 | tumor necrosis factor receptor superfam | 2.65 | 2.52 |
| | 457423 | AK000642 | Hs.265018 | hypothetical protein FLJ20635 | 2.64 | 2.51 |
| | 448752 | AA593867 | Hs.300842 | KIAA1608 protein | 2.63 | 2.20 |
| 35 | 414931 | AK000342 | Hs.77646 | Homo sapiens mRNA; cDNA DKFZp761M0223 (f | 2.63 | 1.83 |
| | 441283 | AA927670 | Hs.131704 | ESTs | 2.62 | 1.92 |
| | 439352 | BE614347 | Hs.169615 | hypothetical protein FLJ20989 | 2.60 | 2.21 |
| | 421391 | AW304350 | Hs.191958 | immunoglobulin superfamily receptor tran | 2.60 | 3.06 |
| 40 | 406678 | U77534 | | gb:Human clone 1A11 immunoglobulin varia | 2.54 | 3.06 |
| | 430278 | AI673074 | Hs.116567 | ESTs, Weakly similar to T22914 hypotheti | 2.49 | 3.44 |
| | 425970 | AK001500 | Hs.165186 | hypothetical protein FLJ13852 | 2.47 | 3.46 |
| | 407363 | AF035032 | Hs.8997 | gb:Homo sapiens clone MCA1L myosin-react | 2.45 | 3.45 |
| | 408367 | AK001178 | Hs.44424 | homolog of rat orphan transporter v7-3 | 2.44 | 3.52 |
| 45 | 420103 | AA382259 | Hs.95197 | aldehyde dehydrogenase 1 family, member | 2.44 | 6.15 |
| | 418635 | L11329 | Hs.1183 | dual specificity phosphatase 2 | 2.42 | 3.92 |
| | 451558 | NM_001089 | Hs.26630 | ATP-binding cassette, sub-family A (ABC1 | 2.41 | 3.08 |
| | 430354 | AA954810 | Hs.239784 | human homolog of Drosophila Scribble | 2.36 | 3.99 |
| | 405701 | | | ENSP00000004954*:Adseverin (Scinderin). | 2.33 | 4.25 |
| 50 | 433427 | AI816449 | Hs.171889 | cholinephosphotransferase 1 | 2.30 | 3.30 |
| | 401965 | | | CGI-148 protein | 2.29 | 3.45 |
| | 417866 | AW067903 | Hs.82772 | collagen, type XI, alpha 1 | 2.23 | 4.07 |
| | 428142 | NM_001308 | Hs.2245 | carboxypeptidase N, polypeptide 1, 50kD | 2.19 | 3.17 |
| | 422103 | AA984330 | Hs.111676 | protein kinase H11; small stress protein | 2.18 | 4.18 |
| 55 | 425746 | NM_001701 | Hs.159440 | bile acid Coenzyme A: amino acid N-acylt | 2.12 | 3.48 |
| | 404835 | | | NM_018943*:Homo sapiens tubulin, alpha-I | 2.09 | 5.72 |
| | 401127 | | | Target Exon | 2.09 | 4.38 |
| | 406161 | | | Target Exon | 2.08 | 3.22 |
| | 421654 | AW163267 | Hs.106469 | suppressor of var1 (S.cerevisiae) 3-like | 2.08 | 3.03 |
| 60 | 406632 | AB006838 | | gb:Homo sapiens mRNA for HRV Fab N31-VH, | 2.07 | 3.25 |
| | 447940 | D86982 | Hs.20060 | KIAA0229 protein | 2.06 | 4.80 |
| | 411773 | NM_006799 | Hs.72026 | protease, serine, 21 (testisin) | 2.05 | 5.33 |
| | 413211 | AW967107 | Hs.109274 | hypothetical protein MGC4365 | 2.02 | 4.74 |
| | 425722 | AI659076 | Hs.97031 | hypothetical protein MGC13047 | 2.01 | 3.76 |
| 65 | 437044 | AL035864 | Hs.69517 | differentially expressed in Fanconi's an | 1.96 | 5.27 |
| | 436420 | AA443966 | Hs.31595 | ESTs | 1.94 | 3.68 |
| | 414809 | AI434699 | Hs.77356 | transferrin receptor (p90, CD71) | 1.92 | 3.88 |
| | 423420 | AI571364 | Hs.128382 | Homo sapiens mRNA; cDNA DKFZp76111224 (f | 1.90 | 3.63 |
| | 427923 | AW274357 | Hs.301406 | hypothetical protein PP3501 | 1.90 | 3.04 |
| 70 | 406652 | AW150304 | Hs.277477 | major histocompatibility complex, class | 1.88 | 3.00 |
| | 435624 | AF218942 | Hs.24889 | formin 2 | 1.88 | 3.54 |
| | 436552 | NM_014038 | Hs.5216 | HSPC028 protein | 1.86 | 3.29 |
| | 408204 | AA454501 | Hs.43666 | protein tyrosine phosphatase type IVA, m | 1.86 | 3.78 |
| | 402728 | | | C1002541*:gij4758590[ref]NP_004249.1[im | 1.86 | 3.14 |
| 75 | 420932 | AW374605 | Hs.11607 | ESTs, Weakly similar to T21697 hypotheti | 1.84 | 4.72 |
| | 458559 | AW028820 | Hs.283614 | ESTs | 1.78 | 3.06 |
| | 400278 | | | ENSP00000243264:Dolichyl-diphosphooligos | 1.76 | 3.55 |
| | 425751 | T19239 | Hs.1940 | crystallin, alpha B | 1.76 | 5.31 |
| | 420737 | L08095 | Hs.99899 | CD70 ; tumor necrosis factor (ligand) s | 1.74 | 3.00 |
| | 410005 | AW732308 | Hs.57783 | eukaryotic translation initiation factor | 1.74 | 3.79 |
| 80 | 454429 | BE273437 | Hs.301406 | hypothetical protein PP3501 | 1.73 | 3.57 |
| | 426321 | BE046490 | Hs.180677 | zinc finger protein 162 | 1.72 | 3.27 |
| | 402897 | | | NM_023068*:Homo sapiens sialoadhesin (SN | 1.69 | 3.81 |
| | 423639 | AB037826 | Hs.130411 | KIAA1405 protein | 1.67 | 3.31 |

| | | | | | | |
|----|--------|----------|-----------|---|------|------|
| 5 | 448848 | AF131851 | Hs.22241 | hypothetical protein | 1.65 | 4.27 |
| | 414420 | AA043424 | Hs.76095 | immediate early response 3 | 1.60 | 3.02 |
| | 440747 | AW297226 | Hs.137840 | ESTs, Moderately similar to SIX4_HUMAN H | 1.56 | 3.28 |
| | 450635 | AW403954 | Hs.25237 | mesenchymal stem cell protein DSCD75 | 1.55 | 3.73 |
| | 400252 | | | NM_004651*:Homo sapiens ubiquitin specif | 1.55 | 3.26 |
| | 411825 | AK000334 | | hypothetical protein FLJ20327 | 1.55 | 3.18 |
| | 414328 | Z21666 | Hs.300463 | aconitase 2, mitochondrial | 1.52 | 4.03 |
| | 400263 | | | Eos Control | 1.51 | 3.42 |
| 10 | 421552 | AF026692 | Hs.105700 | secreted frizzled-related protein 4 | 1.50 | 3.19 |
| | 436673 | AF201931 | Hs.5258 | hypothetical protein FLJ10479 | 1.49 | 3.33 |
| | 404739 | | | Target Exon | 1.49 | 3.10 |
| | 438344 | BE387726 | Hs.343411 | DEAD/H (Asp-Glu-Ala-Asp/His) box polypep | 1.46 | 3.42 |
| | 421696 | AF035306 | Hs.106890 | Homo sapiens clone Z3771 mRNA sequence | 1.44 | 3.15 |
| 15 | 425240 | AA306495 | Hs.1869 | phosphoglucosylase 1 | 1.44 | 3.04 |
| | 412099 | U64198 | Hs.73165 | interleukin 12 receptor, beta 2 | 1.43 | 3.71 |
| | 434642 | W25739 | | chromobox homolog 5 (Drosophila HP 1 alph | 1.42 | 3.07 |
| | 404406 | | | Target Exon | 1.42 | 3.87 |
| 20 | 433320 | D60647 | Hs.250879 | ESTs, Highly similar to CTXN RAT CORTEXI | 1.41 | 3.80 |
| | 447697 | W52125 | | tubulin alpha 1 | 1.40 | 4.45 |
| | 415780 | U75898 | Hs.78846 | heat shock 27kD protein 2 | 1.40 | 3.28 |
| | 447216 | R75812 | Hs.169248 | p7NTR-associated cell death executor, o | 1.39 | 3.77 |
| | 401772 | | | NM_014520:Homo sapiens MYB binding prote | 1.39 | 3.67 |
| 25 | 413031 | BE515051 | Hs.75160 | phosphofructokinase, muscle | 1.38 | 3.31 |
| | 435604 | AA625279 | Hs.26892 | uncharacterized bone marrow protein BM04 | 1.37 | 3.17 |
| | 428011 | BE387514 | Hs.181418 | KIAA0152 gene product | 1.37 | 3.05 |
| | 445580 | AF167572 | Hs.12912 | stb1 (S. pombe) homolog | 1.35 | 3.11 |
| | 436703 | AW880614 | Hs.146381 | RNA binding motif protein, X chromosome | 1.34 | 3.05 |
| | 438277 | AL022326 | Hs.6139 | synaptogyrin 1 | 1.34 | 3.09 |
| 30 | 451481 | AA300228 | Hs.295866 | hypothetical protein DKFZp434N1923 | 1.32 | 3.23 |
| | 421818 | AW992976 | Hs.50098 | NM_002489:Homo sapiens NADH dehydrogenas | 1.31 | 3.01 |
| | 412968 | AW500508 | Hs.75102 | alanyl-tRNA synthetase | 1.28 | 3.58 |
| | 452378 | AA025855 | Hs.19597 | KIAA1694 protein | 1.25 | 3.08 |
| | 447455 | H38335 | Hs.6750 | Homo sapiens mRNA for FLJ00058 protein, | 1.24 | 3.45 |
| 35 | 402212 | | | KIAA0430 gene product | 1.21 | 3.03 |
| | 428773 | BE256238 | Hs.193163 | bridging integrator 1 | 1.20 | 3.20 |
| | 430067 | U79458 | Hs.231840 | VW domain binding protein 2 | 1.18 | 3.03 |
| | 418289 | AW403103 | Hs.83951 | Hermansky-Pudlak syndrome | 1.17 | 3.32 |
| 40 | 405752 | | | Target Exon | 1.00 | 3.40 |
| | 422836 | AL037365 | Hs.194093 | AKAP-binding sperm protein ropparin | 1.00 | 3.00 |

TABLE 58B:
Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

| | | | |
|----|--------|------------|---|
| 45 | Pkey | CAT Number | Accession |
| | 400275 | 18707_1 | NM_006513 BC009390 X91257 BC000716 BM450041 BI771139 AV710955 AU120415 AU141179 AU121081 BE409287 AU141397 AU122238 BI256788 BE386217 AU143368 AU133780 AU139704 BG531086 BE268235 BE545230 AU143414 AV761720 AU129842 AU143343 BE270064 BG473378 BE298813 BI772360 BE617354 AU140124 BE277005 BG746716 BE814960 AW161287 AV762084 BG898985 AW674875 AA313975 AV749916 AA374328 BM011248 AU098465 AW238888 BG940091 BG284599 AW410037 AA378483 D49914 AL573323 AL549819 AL572282 AL572871 AL568117 AL571945 AL547790 AL581217 AL514659 AL573926 AL540816 AW410038 BI262249 BG284713 AI659394 AI093582 AW965846 AA652206 AI686014 AA654357 AU146982 AW273447 AW157715 AW574750 BG683509 AW887824 AI818522 AA703770 BE542873 AA515504 AU154982 AA831254 AA828521 AI088602 AA854654 AA190869 BF062816 AA464944 BG261335 AI003584 BG402620 AA932098 W68695 AW182900 W37334 AI073864 C17924 C18528 AI299318 BF154399 BG319570 BF764242 BF764209 AI820320 T06029 BF447193 F29285 AL548949 BI333775 BE743602 BE618230 BE268139 BF036434 BE562718 BG774381 AA659833 AA297649 AA010945 BG105512 BE269205 T32623 BG015679 AL518518 AL517118 AL538396 AI049861 AL581976 AV752041 W26586 BE181609 AI963016 BG057603 AI720256 AA844560 AA055570 BE619606 C17428 AI042174 N93945 N69743 BF795208 AW057940 BI091399 AW975179 AA909936 H28712 W65445 AL515439 W37117 H66514 T85737 W37369 AW862589 AW860959 |
| 50 | | | NM_033445 BC001193 AI885781 BF794032 AA476620 AA810906 AA810905 AI291244 AI885097 AI359708 AI335629 H97396 AI344589 AA300377 AA457566 AW771833 BE465621 AI364068 AI364452 AI648505 AI918342 AI928670 AA886580 AL531029 AA886344 AI186419 BG329096 BM045465 AI531028 BG437151 BE868021 AA179427 |
| 55 | | | BC014122 M95627 NM_001087 BC020244 BC008809 AL542809 AL522027 AL517616 AL539615 AL555640 AL546094 AL528959 AL555071 BI858518 BI600907 AU120890 BE257146 AV707965 BI911155 BG557776 BE302876 BE277469 BE389232 AL533354 BE389814 BG829179 BE384687 BE276341 BG746912 BG425149 AL047913 BE250277 BG116066 AW410799 BG478074 BG471558 BF813165 AA016192 BG334833 BE383857 AA218784 AL517615 BI822297 BE677910 AW169102 AW410800 AU144298 AI215124 AW275306 AU147438 BE205773 AI343920 AI972200 AA666173 AI568496 AA742466 AI075003 BE858669 BI789274 BI964722 AI310312 AI928567 F28593 BI962793 AA053407 AA603722 AI419246 AA705597 BF445723 AA441804 AA774757 BG152609 AI301244 BF058147 AI879460 AI470194 D80510 AA923557 W69781 AI301243 AI880348 AL517973 AL542808 BE300552 AA143563 AL567123 AA553412 AA547999 AW262497 AW027349 AW469464 BE300553 AI687352 BG222276 AU146833 AA847176 AA724639 AI858270 AL330431 AI583619 AL563298 BI857771 C00178 AW130086 AI312650 AI470187 AL577668 BF816236 BF815492 BE221500 W48859 T54102 AI828100 AW190156 AI961278 AL565165 BF966475 BM013215 BG109077 BF793617 AA381776 AA381486 BF916382 BE745391 AA330239 BG117939 BF337403 BG770295 AL567952 AL571817 BE832508 BF032720 |
| 60 | 411763 | 1103041_1 | |
| | 424036 | 6226_1 | |
| 65 | | | AI245210 AI245212 AI245211 AI245213 |
| | | | BC022413 BE395396 BF754175 AA506621 BE706665 BE706678 AA723159 BE153169 BE706729 BE706558 BE153312 BE706706 AW371853 AW371849 BE153241 BC017410 AI337912 AI090244 AW090300 BE219837 AI623661 BE501576 BE501734 AI742232 AI023964 AI458424 AA975373 AI288904 AI984583 AA890325 N32562 AI358102 AW241694 AI038448 AI672071 AI018389 AA576391 AA977874 AW189392 W37448 AA612894 AI277548 H89551 AI699774 H89365 AA315805 AW579186 BC014584 BC014581 AW780125 AW672414 BE328145 AW600919 BF031306 AW172758 BE708322 AA345675 BE875779 H28241 H25318 BF540913 BG179688 BF110202 AA528775 W37573 BE041644 AW366504 BM129522 BM129822 AI122760 BE718200 AW887496 AA149420 BE706307 BE539395 BE748765 AI373653 R75904 BF979185 BF691393 BG495595 BI094458 BE706702 BG495559 BF248373 BG494800 |
| 70 | | | N92481 AW674508 AA593748 AW974058 AI475594 |
| | 406642 | 0_0 | |
| | 441623 | 3362_1 | |
| 75 | | | BG402852 BG545066 AA150252 AL036760 AA452480 AI033256 W68776 W93372 N31248 AI052219 AI367635 W69374 N88610 R58194 BI524854 BI497111 BF940043 AI29268 AI359798 AI056480 AA121421 AI042150 AW449003 AI418180 AI419420 AI356058 BF832243 AI349330 AI359448 W76647 BF477170 AA099163 BF994549 AW608256 AA045418 H03770 AL574791 AW069455 BE302148 AW022281 AW960273 AA121268 AI336371 |
| 80 | 433464 | 1015899_1 | |
| | 410295 | 2817_1 | |

| | | | |
|----|--------------|---|---|
| | | | A1989381 A1131425 A1147483 A1311537 AW338638 A1141649 AA709414 A187177 AA780884 A1333805 AA045312 A1623918 A1349421 W63753 W70299 AA557276 AA299007 N98212 W74064 N24823 T54892 AA054724 W73059 A1869152 N93462 N71889 A1537432 R71628 AA303089 A1498550 T60941 AV706417 AW057848 A1150677 AW338118 A1336313 AA826256 A1139518 AA662948 AA902723 A1970175 W68682 A1089380 A1148372 H99951 AW183001 A1270317 AA532767 AA044727 AA931652 R82469 AA150261 W67788 H67495 R80715 AW149812 N78914 A1862034 W61122 AW023118 W69375 T88917 T47984 N21531 R35646 AA055544 H15534 AA688295 AA090585 AA044764 BF994641 R79547 N21313 BF674610 H02874 AW975323 R16904 AA328030 AA054671 R79546 BF832310 A1249109 U77534 U77537 AB006838 AB006837 AB006836 AB006834 AB006835 Y00281 NM_002950 BC010839 BC007995 BG675232 BM468552 AL555484 BG831516 BF035300 BG677277 BF852972 BE314901 BF850656 A1371816 AA292474 AA375747 AA308414 BM454544 B1333370 BM049921 B1461428 B1465007 B1223401 BE856245 AW821164 BF914775 BF914761 A1125835 B1222678 B1091137 BF340536 BM462798 B1224452 BG707915 AL569160 AA443815 AW572867 AW363410 BF739268 BG010283 B1013120 BF818845 BF763468 AA305165 A1630370 AA039826 R24906 H02046 T96891 BF981330 AW936510 AA478169 H04587 BG166574 B1869342 BE562482 BE539637 AA165089 AL579118 AL553699 BE044054 AW117440 A1520674 BF435417 AW245648 A1952404 T29534 AU153459 AU152168 AW591591 AU146918 A1393187 AA478013 AU148143 A1224471 A1640728 A1871537 AW264752 N93787 A1189357 AV756134 A1471659 AU147466 AA779206 AU149419 AU149104 AU159135 AA312221 AW445119 AW021912 A1799771 F04407 A1285530 A1914643 AW068751 AA513325 AA164627 AA639285 AA569644 T96892 A1923594 BF439180 B1770936 BF032438 AU154884 AA682793 AW072992 AU158815 A1884444 AL048031 AU158922 AU152546 A1695187 AL048033 A1245650 AU148507 AW467451 BE536868 BF913001 BF062707 AL573082 AW067993 AA523354 BE886727 A1890705 AU159092 A1982683 A1817553 AA236729 A1687858 BG163767 A1524675 A1678155 AA127100 A1762661 AU159718 A1469720 AA483627 AW131696 R26868 A1198885 AW875614 AW938694 AW578974 B1763988 BG819168 BE874767 BG978292 BE162948 AL555483 AW189719 T56783 A1018819 A176552 B1492837 A1824440 BG996262 AA932887 A1380726 R79530 AA622108 A1262575 T56782 R27437 BE784153 AW129649 A1675567 A1866759 BG987935 400252 2656_2 U44839 NM_004651 BC000350 B1458316 AU117940 BG759024 BG749694 BE799505 BG831537 A1816335 AA325352 AL547005 AW157038 A1859331 A1816186 AU150786 AL043549 AW162880 AU159233 A143169 T03478 BE727648 AA764725 BE206603 A1369814 A1984369 AW157545 BE221485 H99016 AU159025 A1074496 A1494516 BE245950 AA704385 AA280862 A1479595 A1369776 BE671398 T05538 AA682249 B1677303 BE645335 A1359434 H92868 D52599 D53609 D54715 T06015 BE222174 A1954706 D53218 D53787 R69889 W68896 A1497670 R07771 BF309414 BE620147 BG910597 AW964968 BE836120 AL579715 H56512 D55956 B1044097 AL555239 BF220278 AA081991 A1819544 AW001573 AW131600 A1858764 D52367 W22034 BG818979 BG024561 BE702779 B1458863 B1910399 BG707755 BF348284 H10055 B1086315 BE620574 H41088 BG119517 W23267 W21941 AA328817 411825 7891_1 AK000695 AK000489 BC001688 BG235988 AW006329 A1887644 A1207230 A1148213 A1304333 A1634653 AW662636 A1281247 AA946921 AA424487 BE272330 A1830588 AA159183 AA977141 BG231801 AA631793 AA975194 BF817537 AA477798 B1906631 AW083424 AA625199 NM_017767 AK000334 BF984048 AW815634 AL573992 AA430612 AA928390 AA644447 AW340827 AA424290 A1927759 BG951502 AW881353 B1765535 Z11692 X51466 NM_001961 M19997 B1224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 B1868669 BG337216 AW629935 BM016525 A1560409 AL562866 A1909178 BF849556 AA317135 BF038841 BF727115 BC006547 BG757526 AL555664 B1261304 BG770095 B1033486 B1517580 BG876485 B1011828 A1313235 BG831724 BF869862 BG988348 B1011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 B1859287 BM016990 BG332369 BE933685 BE166758 BM452445 A1937808 AW026128 N23684 AW006041 A1337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 BE772007 B1199487 BF761700 B1261519 BF944452 BF898506 A1038390 BM044934 AW381142 BG743618 BE769206 BE893973 B1015047 BF886479 BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 B1000274 BG255503 BG674499 BG774174 B1015084 434642 15461_1 AF147443 BM471094 AA948055 AA973157 AA284289 W25739 B1021926 BF898367 W02720 BF798341 BF378312 AA427766 BG955568 BF899591 BF884215 447697 MH497_6 BE742621 AL528391 AA328484 W52125 AA321596 AA022458 AW971024 A1052029 A1761638 AA628498 BE619513 AA412069 A1027538 AW514954 A1884599 A1097362 A1499259 A1419408 AW469200 A1992152 A1142045 A1066572 A1275439 AA581877 A1347308 A1016726 A1127541 AW002064 A1141786 AW051842 A1355329 A1198198 A1347858 A1027870 A1039163 AA576695 A1183286 A1362001 A1361994 AA594668 AA459257 AA745778 A1139667 F20651 A1201510 AA832171 BM464599 BM464574 A1972621 A1183887 AW131911 AW771584 BE619828 AA492218 AA025767 AA977354 AA385481 N45137 W73596 A1864400 A1200026 A1270953 F18139 W46301 H55825 A1039867 A457570 A1928639 A1824685 A1083898 AW024570 AA285299 AW381097 AW582409 BE964181 |
| 50 | TABLE 58C: | | |
| | Pkey: | Unique number corresponding to an Eos probeset | |
| | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <u>Nature</u> 402:489-495. | |
| | Strand: | Indicates DNA strand from which exons were predicted. | |
| | Nt_position: | Indicates nucleotide positions of predicted exons. | |
| 55 | Pkey | Ref | Strand Nt_position |
| | 401941 | 4982556 | Plus 112022-112204 |
| | 402007 | 7381786 | Plus 143964-144081 |
| | 401739 | 2982169 | Plus 132194-132404 |
| 60 | 404405 | 7272262 | Plus 83251-83415 |
| | 401512 | 7622346 | Plus 136399-136557 |
| | 404439 | 7139680 | Plus 55316-55585 |
| | 402273 | 2979528 | Plus 28990-29203,32299-32402,32474-32658 |
| | 405441 | 7408124 | Plus 100952-101283 |
| 65 | 401454 | 9186923 | Minus 114659-114832 |
| | 401009 | 8117391 | Minus 83179-83304 |
| | 405268 | 4156151 | Minus 24404-24521 |
| | 405701 | 4263751 | Plus 93243-93364 |
| | 401965 | 3126781 | Minus 18239-18389,19921-20076 |
| 70 | 404835 | 6970743 | Plus 85462-85684,88139-88287,90338-91018,9482 |
| | 401127 | 8699701 | Minus 88327-88458,96150-96266 |
| | 406161 | 7144954 | Plus 16666-16835 |
| | 402728 | 9211639 | Plus 3192-3569,4267-4728 |
| | 402897 | 8570339 | Plus 61939-62241,64304-64615,65140-65391 |
| 75 | 404739 | 8217493 | Plus 42742-43671 |
| | 404406 | 7329316 | Minus 47543-47928 |
| | 401772 | 9966243 | Plus 183917-184042 |
| | 402212 | 7689783 | Minus 69382-69936 |
| 80 | 405752 | 9212305 | Plus 91392-91528 |

Table 59A lists about 201 genes upregulated in melanoma metastases from patients with progressive disease relative to melanoma metastases from patients with limited disease. Genes were selected from 59680 probesets on the Eos/Alfymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

5 Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: 90th percentile of AIs for metastases from patients with progressive disease divided by the 90th percentile of AIs for metastases from patients with limited disease
10 R2: 90th percentile of AIs for metastases from patients with progressive disease divided by the 90th percentile of AIs for metastases from patients with limited disease, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

| Pkey | ExAccn | UnigeneID | Unigene Title | R1 | R2 |
|--------|-----------|-----------|--|------|-------|
| 422168 | AA586894 | Hs.112408 | S100 calcium-binding protein A7 (psorias | 8.58 | 13.77 |
| 448966 | AW372914 | Hs.86149 | phosphoinositid 3-phosphate-binding prot | 7.43 | 5.91 |
| 440099 | AL080058 | Hs.6909 | DKFZP564G202 protein | 7.07 | 4.56 |
| 431211 | M86849 | Hs.323733 | gap junction protein, beta 2, 26kD (corn | 6.91 | 3.51 |
| 420859 | AW468397 | Hs.100000 | S100 calcium-binding protein A8 (calgran | 6.90 | 6.44 |
| 418067 | AI127958 | Hs.83393 | cystatin E/M | 6.62 | 10.34 |
| 422166 | W72424 | Hs.112405 | S100 calcium-binding protein A9 (calgran | 6.47 | 13.26 |
| 409632 | W74001 | Hs.55279 | serine (or cysteine) proteinase inhibito | 6.25 | 3.41 |
| 401780 | | | NM_005557:Homo sapiens keratin 16 (foca | 6.10 | 4.24 |
| 437191 | NM_006846 | Hs.331555 | serine protease inhibitor, Kazal type, 5 | 5.97 | 6.60 |
| 422511 | AU078442 | Hs.117938 | collagen, type XVII, alpha 1 | 5.89 | 3.57 |
| 412636 | NM_004415 | | desmoplakin (DPI, DPII) | 5.82 | 3.51 |
| 417124 | BE122762 | Hs.25338 | ESTs | 5.16 | 3.16 |
| 430686 | NM_001942 | Hs.2633 | desmoglein 1 | 5.03 | 3.57 |
| 421733 | AL119671 | Hs.1420 | fibroblast growth factor receptor 3 (ach | 4.84 | 4.15 |
| 422192 | AA305159 | Hs.113019 | fts485 | 4.79 | 4.59 |
| 407366 | AF026942 | Hs.17518 | gb:Homo sapiens cig33 mRNA, partial sequ | 4.33 | 2.37 |
| 429493 | AL134708 | Hs.145998 | ESTs | 4.28 | 4.79 |
| 456525 | AW468397 | Hs.100000 | S100 calcium-binding protein A8 (calgran | 4.23 | 4.82 |
| 409010 | AI648675 | | Homo sapiens, Similar to RIKEN cDNA 1700 | 4.23 | 3.69 |
| 410748 | BE383816 | Hs.12532 | chromosome 1 open reading frame 21 | 4.11 | 2.33 |
| 409760 | AA302840 | | gb:EST10534 Adipose tissue, white f Homo | 4.06 | 3.65 |
| 424670 | W61215 | Hs.116651 | epithelial V-like antigen 1 | 4.02 | 4.07 |
| 417366 | BE185289 | Hs.1076 | small proline-rich protein 18 (comitin) | 3.97 | 4.71 |
| 418663 | AK001100 | Hs.41690 | desmocollin 3 | 3.95 | 5.08 |
| 402075 | | | ENSP00000251056:Plasma membrane calcium | 3.93 | 5.85 |
| 428330 | L22524 | Hs.2256 | matrix metalloproteinase 7 (matrilysin, | 3.90 | 3.19 |
| 427809 | M26380 | Hs.180878 | lipoprotein lipase | 3.87 | 3.21 |
| 413859 | AW992356 | Hs.8364 | Homo sapiens pyruvate dehydrogenase kina | 3.85 | 5.75 |
| 431048 | RS0253 | Hs.249129 | cell death-inducing DFFA-like effector a | 3.80 | 3.10 |
| 431369 | BE184455 | Hs.251754 | secretory leukocyte protease inhibitor (| 3.79 | 3.36 |
| 421485 | AA243499 | Hs.104800 | hypothetical protein FLJ10134 | 3.67 | 3.35 |
| 429852 | AB010445 | Hs.225948 | small inducible cytokine subfamily A (Cy | 3.65 | 4.14 |
| 418686 | Z36830 | Hs.87268 | annexin A8 | 3.65 | 3.62 |
| 448429 | D17408 | Hs.21223 | calponin 1, basic, smooth muscle | 3.64 | 3.18 |
| 422963 | M79141 | Hs.13234 | ESTs | 3.60 | 4.10 |
| 428874 | W32133 | Hs.194366 | transferrin (prealbumin, amyloidosis t | 3.58 | 3.97 |
| 401785 | | | NM_002275:Homo sapiens keratin 15 (KRT1 | 3.58 | 5.05 |
| 454117 | BE410100 | Hs.40368 | adaptor-related protein complex 1, sigma | 3.56 | 1.92 |
| 419329 | AY007220 | Hs.288998 | S100-type calcium binding protein A14 | 3.54 | 5.62 |
| 424012 | AW368377 | Hs.137569 | tumor protein 63 kDa with strong homolog | 3.53 | 4.70 |
| 417515 | L24203 | Hs.82237 | ataxia-telangiectasia group D-associated | 3.52 | 8.33 |
| 430376 | AW292053 | Hs.12532 | chromosome 1 open reading frame 21 | 3.51 | 2.32 |
| 454229 | AW957744 | Hs.278469 | lacrimal proline rich protein | 3.50 | 3.12 |
| 401781 | | | Target Exon | 3.45 | 3.57 |
| 408000 | L11690 | Hs.198589 | bullous pemphigoid antigen 1 (230/240kD) | 3.45 | 5.07 |
| 431567 | N51357 | Hs.260855 | Homo sapiens cDNA: FLJ21410 fs, clone C | 3.44 | 5.03 |
| 419648 | T73661 | Hs.91877 | thyroid hormone responsive SPOT14 (rat) | 3.42 | 7.72 |
| 414798 | AI286323 | Hs.97411 | hypothetical protein MGC12335 | 3.41 | 2.65 |
| 442315 | AA173992 | Hs.7956 | ESTs, Moderately similar to ZN91_HUMAN Z | 3.41 | 5.03 |
| 442498 | U54617 | Hs.8364 | Homo sapiens pyruvate dehydrogenase kina | 3.32 | 2.86 |
| 410883 | D43767 | Hs.66742 | CCL17 chemokine (TARC) (SCYA17) | 3.28 | 3.18 |
| 418026 | BE379727 | Hs.83213 | fatty acid binding protein 4, adipocyte | 3.26 | 3.10 |
| 453309 | AI791809 | Hs.32949 | defensin, beta 1 | 3.24 | 3.64 |
| 420783 | AI659838 | Hs.99923 | lectin, galactoside-binding, soluble, 7 | 3.21 | 3.64 |
| 409601 | AF237621 | Hs.80828 | keratin 1 (epidermolytic hyperkeratosis) | 3.19 | 4.37 |
| 413163 | Y00815 | Hs.75216 | protein tyrosine phosphatase, receptor t | 3.16 | 5.48 |
| 452101 | T60298 | Hs.10844 | Homo sapiens cDNA FLJ14476 fs, clone MA | 3.15 | 3.60 |
| 412633 | AF001691 | Hs.74304 | periplakin | 3.15 | 3.98 |
| 407839 | AA045144 | Hs.161566 | ESTs | 3.15 | 4.11 |
| 427318 | AF186081 | Hs.175783 | zinc transporter | 3.11 | 3.58 |
| 427899 | AA829286 | Hs.332053 | serum amyloid A1 | 3.10 | 3.53 |
| 421948 | L42583 | Hs.334309 | keratin 6A | 3.08 | 2.75 |
| 452744 | AI267652 | Hs.246107 | Homo sapiens mRNA: cDNA DKFp434E082 (fr | 3.05 | 2.99 |
| 410001 | AB041036 | Hs.57771 | kalikrein 11 | 3.04 | 3.02 |
| 413435 | X51405 | Hs.75360 | carboxypeptidase E | 3.00 | 2.40 |
| 428500 | AI815395 | Hs.184641 | fatty acid desaturase 2 | 2.98 | 5.22 |
| 410099 | AA081630 | | KIAA0036 gene product | 2.97 | 2.05 |
| 437679 | NM_014214 | Hs.5753 | inositol(myo)-1(or 4)-monophosphatase 2 | 2.93 | 3.45 |
| 413835 | AI272727 | Hs.249163 | fatty acid hydroxylase | 2.93 | 4.78 |

| | | | | | | |
|----|--------|-----------|-----------|---|------|------|
| 5 | 446068 | AL049801 | Hs.13649 | Novel human gene mapping to chromosome 13 | 2.89 | 2.93 |
| | 450680 | AF131784 | Hs.25318 | Homo sapiens clone 25194 mRNA sequence | 2.88 | 3.14 |
| | 428398 | AJ249368 | Hs.98558 | ESTs | 2.88 | 2.05 |
| | 417433 | BE270266 | Hs.82128 | ST4 oncofetal trophoblast glycoprotein | 2.86 | 2.12 |
| | 427919 | AA173942 | Hs.326416 | Homo sapiens mRNA; cDNA DKFZp564H1916 (f | 2.84 | 2.98 |
| | 412676 | NM_000165 | Hs.74471 | gap junction protein, alpha 1, 43kD (con | 2.83 | 2.82 |
| | 428695 | AI355647 | Hs.189999 | purinergic receptor (family A group 5) | 2.83 | 2.37 |
| | 446989 | AK001898 | Hs.16740 | hypothetical protein FLJ11036 | 2.82 | 2.73 |
| 10 | 428471 | X57348 | Hs.184510 | stratiferin | 2.79 | 3.31 |
| | 416305 | AJ076628 | Hs.79187 | coxsackie virus and adenovirus receptor | 2.79 | 3.72 |
| | 433147 | AF091434 | Hs.43080 | platelet derived growth factor C | 2.77 | 1.70 |
| | 412326 | R07566 | Hs.73817 | small inducible cytokine A3 (homologous | 2.76 | 2.18 |
| | 425787 | AA363867 | Hs.155029 | ESTs | 2.75 | 2.42 |
| 15 | 450172 | NM_005864 | Hs.24587 | signal transduction protein (SH3 contain | 2.75 | 2.36 |
| | 421773 | W69233 | Hs.112457 | ESTs | 2.73 | 5.59 |
| | 408536 | AW381532 | Hs.135188 | ESTs | 2.73 | 5.17 |
| | 437143 | AW204056 | Hs.8917 | ESTs | 2.72 | 1.84 |
| | 452862 | AW378065 | Hs.8687 | ADAMTS2 (a disintegrin-like and metallo | 2.70 | 1.82 |
| 20 | 418394 | AF132818 | Hs.84728 | Kruppel-like factor 5 (intestinal) | 2.69 | 4.62 |
| | 410325 | AB023154 | Hs.62264 | KIAA0937 protein | 2.69 | 2.32 |
| | 447164 | AF026941 | Hs.17518 | virpin; similar to inflammatory respon | 2.69 | 3.74 |
| | 444984 | H15474 | Hs.132898 | fatty acid desaturase 1 | 2.67 | 2.36 |
| | 434727 | H43374 | Hs.7890 | Homo sapiens mRNA for KIAA1671 protein, | 2.65 | 1.78 |
| 25 | 420876 | AA918425 | Hs.177744 | ESTs | 2.64 | 7.26 |
| | 426106 | AJ678765 | Hs.21812 | ESTs | 2.64 | 2.51 |
| | 419517 | AF052107 | Hs.90797 | Homo sapiens clone Z3620 mRNA sequence | 2.64 | 2.66 |
| | 409509 | AL036923 | Hs.322710 | ESTs | 2.62 | 2.09 |
| | 426354 | NM_004010 | Hs.169470 | dystrophin (muscular dystrophy, Duchenne | 2.62 | 2.68 |
| 30 | 432503 | AA551196 | Hs.188952 | ESTs | 2.62 | 4.64 |
| | 409341 | AJ963376 | Hs.12532 | chromosome 1 open reading frame 21 | 2.62 | 1.74 |
| | 421116 | T19132 | Hs.101850 | retinol-binding protein 1, cellular | 2.62 | 2.90 |
| | 456247 | R09746 | | gb:y127d10.r1 Soares fetal liver spleen | 2.61 | 3.43 |
| | 414217 | AJ309298 | Hs.279898 | Homo sapiens cDNA: FLJ23165 fis, clone L | 2.60 | 3.84 |
| 35 | 439706 | AW872527 | Hs.59761 | ESTs, Weakly similar to DAPI1_HUMAN DEATH | 2.58 | 3.49 |
| | 440659 | AF134160 | Hs.7327 | claudin 1 | 2.57 | 3.97 |
| | 459710 | AJ701596 | Hs.121592 | ESTs | 2.57 | 3.59 |
| | 430937 | X53463 | Hs.2704 | glutathione peroxidase 2 (gastrointestin | 2.56 | 3.35 |
| 40 | 433882 | U90441 | Hs.3622 | procollagen-proline, 2-oxoglutarate 4-di | 2.51 | 3.75 |
| | 427666 | AJ791495 | Hs.180142 | catmodulin-like skin protein (CLSP) | 2.51 | 3.02 |
| | 431103 | M57399 | Hs.44 | pleiotrophin (heparin binding growth fac | 2.47 | 3.53 |
| | 449550 | AA353125 | Hs.184721 | ESTs | 2.43 | 4.22 |
| | 424675 | NM_005512 | Hs.151641 | glycoprotein A repetitions predominant | 2.40 | 6.22 |
| 45 | 442000 | H38671 | Hs.8071 | KIAA0735 gene product, synaptic vesicle | 2.38 | 3.14 |
| | 427122 | AW057736 | Hs.323910 | HER2 receptor tyrosine kinase (c-erb-b2, | 2.36 | 3.59 |
| | 420039 | NM_004605 | Hs.94581 | sulfotransferase family, cytosolic, 2B, | 2.36 | 2.91 |
| | 412477 | AA150864 | | microsomal glutathione S-transferase 1 | 2.34 | 4.15 |
| | 450693 | AW450461 | Hs.203965 | ESTs | 2.32 | 3.93 |
| | 406433 | | | Target Exon | 2.29 | 3.20 |
| 50 | 423017 | AW178761 | Hs.227948 | serine (or cysteine) proteinase inhibito | 2.24 | 4.40 |
| | 422158 | L10343 | Hs.112341 | protease inhibitor 3, skin-derived (SKAL | 2.23 | 4.87 |
| | 421314 | BE440002 | Hs.180324 | Homo sapiens, clone IMAGE:4183312, mRNA, | 2.23 | 4.22 |
| | 422083 | NM_001141 | Hs.111256 | arachidonate 15-lipoxygenase, second typ | 2.22 | 5.71 |
| | 442503 | AF147078 | Hs.150853 | p53-responsive gene 5 | 2.21 | 4.86 |
| 55 | 418007 | M13509 | Hs.83169 | matrix metalloproteinase 1 (interstitial | 2.19 | 3.90 |
| | 442572 | AJ001922 | Hs.135121 | hypothetical protein FLJ22415 | 2.16 | 2.87 |
| | 413278 | BE563085 | Hs.833 | interferon-stimulated protein, 15 kDa | 2.13 | 3.27 |
| | 414521 | D28124 | Hs.76307 | neuroblastoma, suppression of tumorigeni | 2.09 | 5.28 |
| | 428899 | AA744610 | Hs.194431 | palladin | 2.08 | 3.76 |
| 60 | 412079 | U65590 | Hs.81134 | interleukin 1 receptor antagonist | 2.06 | 3.09 |
| | 439496 | BE616501 | Hs.32343 | Homo sapiens, Similar to RIKEN cDNA 1110 | 2.05 | 2.88 |
| | 450423 | AA486735 | Hs.31869 | slitoadhesin | 2.02 | 3.04 |
| | 444105 | AW189097 | | ESTs | 2.01 | 3.05 |
| | 430410 | AF099144 | Hs.347933 | tryptase beta 1 | 2.01 | 3.71 |
| 65 | 409453 | AJ885516 | Hs.95612 | ESTs | 2.01 | 4.34 |
| | 429655 | U48959 | Hs.211582 | myosin, light polypeptide kinase | 2.00 | 5.28 |
| | 432374 | W68815 | Hs.301885 | Homo sapiens cDNA FLJ11346 fis, clone PL | 1.99 | 3.59 |
| | 447990 | BE048821 | Hs.20144 | small inducible cytokine subfamily A (Cy | 1.92 | 4.16 |
| | 451541 | BE279383 | Hs.26557 | plakophilin 3 | 1.89 | 3.90 |
| 70 | 425206 | NM_002153 | Hs.155109 | hydroxysteroid (17-beta) dehydrogenase 2 | 1.89 | 3.29 |
| | 410197 | NM_005518 | Hs.59689 | 3-hydroxy-3-methylglutaryl-Coenzyme A sy | 1.84 | 3.04 |
| | 401760 | | | Target Exon | 1.84 | 3.32 |
| | 427579 | AA366143 | Hs.179669 | hypothetical protein FLJ20637 | 1.83 | 4.69 |
| | 424263 | M77640 | Hs.1757 | L1 cell adhesion molecule (hydrocephalus | 1.83 | 2.96 |
| 75 | 452208 | AA024792 | Hs.31895 | hypothetical protein MGC4093 | 1.82 | 3.70 |
| | 420074 | AA253425 | Hs.190074 | ESTs | 1.81 | 2.90 |
| | 429299 | AJ620463 | Hs.347408 | hypothetical protein MGC13102 | 1.79 | 3.65 |
| | 427540 | R12014 | Hs.20976 | ESTs | 1.77 | 2.92 |
| | 429259 | AA420450 | Hs.292911 | Plakophilin | 1.76 | 3.65 |
| 80 | 422106 | D84239 | Hs.111732 | Fc fragment of IgG binding protein | 1.75 | 4.06 |
| | 453556 | AA425414 | Hs.33287 | nuclear factor I/B | 1.74 | 3.07 |
| | 436895 | AF037335 | Hs.5338 | carbonic anhydrase XII | 1.73 | 3.22 |
| | 406851 | AA609784 | | major histocompatibility complex, class | 1.73 | 3.96 |
| | 444726 | NM_006147 | | interferon regulatory factor 6 | 1.71 | 3.65 |

| | | | | | |
|--------|-----------|-----------|---|------|------|
| 444781 | NM_014400 | Hs.11950 | GPI-anchored metastasis-associated prote | 1.71 | 4.13 |
| 446051 | BE048061 | Hs.37054 | ephrin-A3 | 1.68 | 3.61 |
| 408522 | AI541214 | Hs.46320 | Small proline-rich protein SPRK (human, | 1.67 | 3.00 |
| 450835 | BE262773 | Hs.25584 | hypothetical protein FLJ10767 | 1.66 | 3.11 |
| 432004 | BE018302 | Hs.2894 | placental growth factor, vascular endoth | 1.66 | 3.23 |
| 431179 | AI338644 | Hs.195432 | aldehyde dehydrogenase 2 family (mitocho | 1.64 | 3.29 |
| 415213 | NM_002933 | Hs.78224 | ribonuclease, RNase A family, 1 (pancrea | 1.57 | 3.94 |
| 423184 | NM_004428 | Hs.1624 | ephrin-A1 | 1.56 | 2.88 |
| 414694 | NM_015362 | Hs.76907 | HSPC002 protein | 1.56 | 2.92 |
| 458746 | AJ380797 | Hs.158992 | ESTs | 1.56 | 2.92 |
| 433091 | Y12642 | Hs.3185 | lymphocyte antigen 6 complex, locus D | 1.55 | 3.75 |
| 438367 | N79688 | Hs.204354 | ras homolog gene family, member B | 1.54 | 4.56 |
| 403903 | | | C5001632:gil10645308[gb]AAG21430.1[AC00 | 1.53 | 3.99 |
| 445656 | W22050 | Hs.21299 | ESTs, Weakly similar to AF151840.1 CGI-8 | 1.52 | 3.16 |
| 443604 | C03577 | Hs.9615 | myosin regulatory light chain 2, smooth | 1.50 | 4.25 |
| 429211 | AF052693 | Hs.198249 | gap junction protein, beta 5 (connexin 3 | 1.50 | 3.35 |
| 415274 | AF001548 | Hs.78344 | myosin, heavy polypeptide 11, smooth mus | 1.49 | 3.21 |
| 418226 | AA424202 | Hs.83834 | cytochrome b-5 | 1.49 | 3.90 |
| 454194 | BE141599 | | gb:QV2-HT0083-071299-018-h01 HT0083 Homo | 1.48 | 2.98 |
| 434879 | M34572 | Hs.159263 | collagen, type VI, alpha 2 | 1.46 | 3.26 |
| 418400 | BE243026 | Hs.301989 | KIAA0246 protein | 1.46 | 4.00 |
| 409178 | BE393948 | Hs.50915 | kallikrein 5 | 1.45 | 2.94 |
| 433662 | W07162 | Hs.150826 | RAB25 RAB25, member RAS oncogene family | 1.44 | 3.18 |
| 429002 | AW248439 | Hs.2340 | junction plakoglobin | 1.43 | 3.07 |
| 422087 | X58968 | Hs.111301 | matrix metalloproteinase 2 (gelatinase A | 1.40 | 4.61 |
| 452934 | AA581322 | Hs.4213 | hypothetical protein MGC16207 | 1.38 | 3.11 |
| 417483 | BE549343 | Hs.82208 | acyl-Coenzyme A dehydrogenase, very long | 1.37 | 4.32 |
| 427929 | BE613835 | Hs.181159 | Homo sapiens mRNA; cDNA DKFZp434F0217 (f | 1.37 | 2.99 |
| 425184 | BE278288 | Hs.155048 | Lutheran blood group (Auburger b antigen | 1.36 | 3.17 |
| 407143 | C14076 | Hs.332329 | EST | 1.36 | 2.99 |
| 416950 | AL049798 | Hs.80552 | dermatopontin | 1.35 | 3.39 |
| 406799 | AA085448 | | gb:rog83g12.s1 NC1_CGAP_Ov8 Homo sapiens | 1.34 | 3.17 |
| 442599 | AF078037 | Hs.324051 | RelA-associated inhibitor | 1.33 | 3.30 |
| 413659 | BE155647 | | gb:PM2-HT0353-130100-002-e09 HT0353 Homo | 1.32 | 2.89 |
| 454478 | AW805749 | | superoxide dismutase 2, mitochondrial | 1.30 | 3.50 |
| 404467 | | | Target Exon | 1.29 | 3.57 |
| 452516 | AA058630 | Hs.29759 | RNA POLYMERASE I AND TRANSCRIPT RELEASE | 1.28 | 3.00 |
| 412524 | AA417813 | Hs.44208 | hypothetical protein FLJ23153 | 1.27 | 3.05 |
| 422354 | U20982 | Hs.1516 | insulin-like growth factor-binding prote | 1.24 | 2.86 |
| 406711 | N25514 | Hs.77385 | myosin, light polypeptide 6, alkali, smo | 1.24 | 3.29 |
| 450796 | NM_001988 | Hs.25482 | envoplakin | 1.23 | 3.21 |
| 431526 | Y10129 | Hs.258742 | myosin-binding protein C, cardiac | 1.23 | 3.65 |
| 452791 | AA227581 | Hs.30634 | hypothetical protein FLJ20509 | 1.22 | 2.90 |
| 406742 | AJ468091 | Hs.279860 | tumor protein, translationally-controlled | 1.19 | 3.47 |
| 406712 | M31212 | Hs.77385 | myosin, light polypeptide 6, alkali, smo | 1.18 | 2.91 |
| 443672 | AA323362 | Hs.9667 | butyrobetaine (gamma), 2-oxoglutarate di | 1.10 | 3.50 |
| 413048 | M93221 | Hs.75182 | mannose receptor, C type 1 | 1.00 | 2.99 |
| 453165 | S74727 | Hs.32042 | aspartoacylase (aminoacylase 2, Canavan | 1.00 | 2.91 |

TABLE 598:

Pkey: Unique Eos probeset identifier number
CAT number: Gene cluster number
Accession: Genbank accession numbers

| | | | |
|--------|--------|------------|--|
| 55 | Pkey | CAT Number | Accession |
| 412635 | 1438_1 | | M77830 NM_004415 AF139065 BG681115 BG740377 B1712964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 B175807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG273489 BE819009 BF381184 BE715956 RS8704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 AI951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI467252 AU159919 AI760816 BF082516 AI439101 AA451923 AI304326 AI590975 BI791553 AI700963 AI142882 AA039975 AA946936 AA644381 BM314884 AA702424 AI17612 AW166807 AI346078 W95070 AA149191 AA026864 AI830049 AW780435 AI078449 AI819984 AI858282 BI468588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 AI927207 AI205263 BF082491 AW021347 AI568096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 AI910434 BF082513 AI494069 AI720027 AI635878 AA128330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654 AV745530 BI672796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 AJ571075 BE067786 AV721320 AJ022862 N29754 C03378 NB4767 AA131077 H30146 BE714290 AI686869 AI568892 AI915596 AW105614 AI887258 AJ538577 BE926474 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 BI770853 BG679406 BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040941 AA337270 AW384371 AW847442 BI058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG945393 BE714441 AW996245 BE711801 AI284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H08099 AW365145 W38382 AI498487 |

| | | | |
|----|--------|-----------|--|
| 5 | 409010 | 10331_1 | AL557207 AL551714 BM014781 BG542863 BG771232 AA429722 AJ377511 AJ770155 AA716665 BG003427 AA810811 AA442760 AA128610 AA059411 AJ796263 AJ494075 AJ572127 AA420992 BF436083 AJ648675 AA878813 BI488614 BG700886 AA128609 AV702879 AA731146 AJ580336 AJ373224 AA919169 AJ58175 AA976350 BG701414 BF057794 AW135598 AA062583 BI549631 AJ185077 AA933879 AW024454 AA193289 AA045194 BG928396 BE856883 BF435859 AA196423 AW237471 R99289 D61992 BE856637 BF368270 AA194235 N51319 AA383499 N63065 BG548812 BF027898 BG779448 |
| 10 | 409760 | 855166_1 | AA302840 T93016 T92950 AU184997 AA077551 |
| 15 | 410099 | 16732_1 | AK055674 AW965247 AV751598 AA290926 R53043 AA331387 AK056148 BI917678 BG819395 BG911971 BG820167 AI174254 AA348720 AA364503 BG714279 AW893230 AA081774 H24222 AV727176 BF875715 AA081630 BE000834 AA334880 AL563737 BG029709 W52882 AJ439658 BE551237 AA283724 BF109530 AJ457096 AJ805992 BE467736 AA693467 AI697593 AJ887863 AI167419 AW901980 AW901768 BE702179 AA484549 T23811 BE327043 AA716027 AA917004 AA167714 BF339675 AA084618 AJ18634 T31586 AA436630 AJ366472 AA706191 AJ422304 AJ204899 AJ041169 AA211402 AW827081 AA788593 T32736 AJ767935 AA747914 T03534 AW959843 AL119527 BE327037 AW901982 AW933370 AW901977 AW902071 W60090 N79906 D52685 T07735 BE702069 BE702172 T08671 BE767121 BE767117 BE767113 |
| 20 | 456247 | 2142387_1 | R10170 R09746 |
| 25 | 412477 | 8669_2 | AJ220117 AJ857837 AJ218371 BM091400 AJ304364 AJ198508 AJ400738 AW571549 AW950042 AJ089943 AA437280 AJ150878 BF197070 AJ267984 BF594181 BF196688 AJ433152 AJ338921 AJ620364 AJ280197 AA652531 AJ674938 AJ342447 AJ620350 AJ281295 AJ148621 NS4787 AJ338121 AJ281153 N51899 AJ087072 AA954788 AW069054 AJ346309 BG529629 AJ340135 BF083036 AJ167365 AW819657 AA935468 AJ467868 AW148701 AJ383720 BE047685 AW015498 AA937149 AA708346 AW771478 AW802508 H53334 AW389204 AW798230 AJ553922 AJ560688 AW950043 AJ961682 AV706506 R01853 AA126514 N62757 AJ536893 AJ926052 AJ418720 N99964 AJ568933 AJ915737 AJ080691 AJ185358 N48996 N68575 H82824 H60037 AJ247247 T95664 BF593863 AJ749637 AW088541 AA991294 AA887452 AJ073726 AA633132 AA629674 AA629649 AA629656 AA578595 AJ168758 AA804572 AJ085788 AA994396 AA991209 AA948663 AA929054 AA927952 T87001 AA928210 AA629296 AW802267 AW384129 BF744400 AA194110 AJ382839 AA194837 AA406284 AJ250750 R37035 AJ525585 W01244 |
| 30 | 444105 | 549788_1 | AW189097 AJ123917 AJ123926 |
| 35 | 406851 | 0_0 | AA609784 R97304 |
| 40 | 444726 | 3503_2 | BG285809 BE940673 BG432524 BE157554 BG676980 AU144284 AJ745383 AU159045 AI693500 AW293668 AW371408 BE856107 AJ338042 AW188320 AI698246 BE673290 AW297653 AA156532 AJ017342 AJ916754 AI190644 AI184302 AA857671 BE857018 AJ307420 AJ318157 AW204327 AW664668 AW274339 AA582788 AJ345741 AW301433 AJ873468 AW137388 BF718731 BF718413 AA877495 BF001575 AJ824693 AW849604 AW849405 AW849396 AW849173 BE673179 AJ611327 AA705753 BE715478 AW849414 AW849399 AJ085759 AJ140849 T67412 AJ889885 AW104647 AJ912495 AJ889874 AJ744241 BE717113 BE717108 BE715564 AJ872527 AA029457 C00338 AJ469558 BE715577 AA045413 BF843813 |
| 45 | 454194 | 171445_1 | BE141599 AW845895 AW178095 BE140914 BE140909 AW178107 AW178094 AW845883 BF349267 AW845898 AW845811 AW845814 BF767720 |
| 50 | 406799 | 0_0 | AA908548 |
| 55 | 413659 | 1526081_1 | BE155647 BE155627 |
| 60 | 454478 | 4273_16 | AW796921 AW798102 AW805749 AW805872 BF985060 AW794380 BF380449 AW794466 AW794538 |

TABLE 59C:

| | |
|--------------|---|
| Pkey: | Unique number corresponding to an Eos probeset |
| Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. |
| Strand: | Indicates DNA strand from which exons were predicted. |
| NL_position: | Indicates nucleotide positions of predicted exons. |

| Pkey | Ref | Strand | NL_position |
|--------|---------|--------|--|
| 401780 | 7249190 | Minus | 28397-28617,28920-29045,29135-29296,2941 |
| 402075 | 8117407 | Plus | 121907-122035,122604-122821,124019-12416 |
| 401785 | 7249190 | Minus | 165776-165996,166189-166314,166408-16656 |
| 401781 | 7249190 | Minus | 83215-83435,83531-83656,83740-83901,8423 |
| 406433 | 9256507 | Plus | 58094-58565 |
| 401760 | 9929699 | Plus | 83126-83250,85320-85540,94719-95287 |
| 403903 | 7710671 | Minus | 101165-102597 |
| 404467 | 8077630 | Minus | 24951-25853 |

TABLE 60A: ABOUT 53 GENES UPREGULATED IN BENIGN NEVI RELATIVE TO NORMAL TISSUES

Table 60A lists about 53 genes upregulated in benign nevi relative to normal tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

| | |
|----------------|---|
| Pkey: | Unique Eos probeset identifier number |
| ExAccn: | Exemplar Accession number, Genbank accession number |
| UnigeneID: | Unigene number |
| Unigene Title: | Unigene gene title |
| R1: | average of benign nevi AIs divided by the 90th percentile of normal tissue AIs |
| R2: | average of benign nevi AIs divided by 90th percentile of normal tissue AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator |

| Pkey | ExAccn | UnigeneID | Unigene Title | R1 | R2 |
|--------|-----------|-----------|--|------|-------|
| 430377 | NM_001922 | Hs.301865 | dopachrome tautomerase (dopachrome delta | 8.69 | 5.62 |
| 409601 | AF237621 | Hs.80828 | keratin 1 (epidermolytic hyperkeratosis) | 8.37 | 13.47 |
| 430686 | NM_001942 | Hs.2633 | desmoglein 1 | 7.26 | 4.78 |
| 406964 | M21305 | | FGFES predicted novel secreted protein | 6.50 | 3.73 |
| 426555 | NM_000372 | Hs.2053 | tyrosinase (oculocutaneous albinism 1A) | 6.40 | 7.35 |
| 429852 | AB010445 | Hs.225948 | small inducible cytokine subfamily A (Cy | 6.23 | 8.85 |
| 430822 | AJ005371 | Hs.248017 | glyceraldehyde-3-phosphate dehydrogenase | 5.49 | 4.32 |
| 420208 | BE276055 | Hs.95972 | silver (mouse homolog) like | 5.45 | 9.84 |
| 431360 | NM_000427 | Hs.251680 | loricin | 3.88 | 3.00 |
| 421773 | W69233 | Hs.112457 | ESTs | 3.80 | 9.04 |
| 438380 | T06430 | Hs.6194 | chondroitin sulfate proteoglycan BEHAB/b | 3.74 | 4.23 |
| 431089 | BE041395 | | ESTs, Weakly similar to unknown protein | 3.21 | 2.34 |
| 420798 | W93774 | Hs.99936 | keratin 10 (epidermolytic hyperkeratosis | 3.08 | 3.20 |
| 442503 | AF147078 | Hs.150853 | p53-responsive gene 5 | 2.88 | 5.01 |
| 405451 | | | dihydropyrimidinase-like 3 | 2.88 | 2.85 |
| 452240 | AI591147 | Hs.61232 | ESTs | 2.86 | 1.90 |
| 402525 | | | NM_002699::Homo sapiens POU domain, clas | 2.78 | 2.72 |
| 413171 | AA318325 | Hs.75219 | tyrosinase-related protein 1 | 2.65 | 5.58 |
| 439496 | BE616501 | Hs.32343 | Homo sapiens, Similar to RIKEN cDNA 1110 | 2.55 | 3.18 |
| 422656 | AI870435 | Hs.1569 | LIM homeobox protein 2 | 2.45 | 2.38 |

| | | | | | | |
|----|--|--|--|---|------|------|
| 5 | 453317 | NM_002277 | Hs.41696 | keratin, hair, acidic, 1 | 2.34 | 3.76 |
| | 420783 | A1659838 | Hs.99923 | lectin, galactoside-binding, soluble, 7 | 2.33 | 2.43 |
| | 422511 | AU076442 | Hs.117938 | collagen, type XVII, alpha 1 | 2.28 | 2.00 |
| | 427666 | A1791495 | Hs.180142 | calmodulin-like skin protein (CLSP) | 2.28 | 2.50 |
| | 459702 | A1204995 | | gb:an03c03.x1 Stratagene schizo brain S1 | 2.25 | 1.85 |
| | 451668 | Z43948 | Hs.326444 | cartilage acidic protein 1 | 2.23 | 2.42 |
| | 431703 | AA514264 | Hs.4437 | triosephosphate isomerase 1 | 2.15 | 2.20 |
| | 453511 | AL031224 | Hs.33102 | AP-2 beta transcription factor | 2.13 | 2.20 |
| 10 | 401780 | | | NM_005557: Homo sapiens keratin 16 (foca | 2.13 | 2.02 |
| | 416640 | BE262478 | Hs.79404 | neuron-specific protein | 2.11 | 2.02 |
| | 444105 | AW189097 | | ESTs | 2.11 | 1.46 |
| | 428748 | AW593206 | Hs.98785 | Ksp37 protein | 2.09 | 1.52 |
| | 418067 | A1127958 | Hs.83393 | cystatin E/M | 2.09 | 2.32 |
| 15 | 417017 | AA976064 | Hs.180842 | ribosomal protein L13 | 2.08 | 2.52 |
| | 401781 | | | Target Exon | 2.02 | 2.03 |
| | 407178 | AA195651 | | AP-2 beta transcription factor | 1.88 | 2.17 |
| | 452308 | A1167560 | Hs.61297 | ESTs | 1.84 | 2.38 |
| | 429348 | AJ242859 | Hs.199731 | Langerhans cell specific c-type lectin | 1.83 | 3.26 |
| 20 | 402880 | | | Target Exon | 1.69 | 2.10 |
| | 434276 | AF123659 | Hs.93605 | leucine zipper, putative tumor suppressor | 1.69 | 2.20 |
| | 401963 | | | NM_006311: Homo sapiens nuclear receptor | 1.66 | 2.02 |
| | 424010 | AL080188 | Hs.137556 | Homo sapiens mRNA; cDNA DKFZp434A132 (fr | 1.65 | 2.05 |
| | 432800 | BE391046 | Hs.278962 | AIM-1 protein | 1.61 | 2.83 |
| 25 | 400328 | X87344 | | transporter 2, ATP-binding cassette, sub | 1.57 | 2.27 |
| | 412580 | AA113262 | Hs.17901 | Homo sapiens, clone IMAGE:3937015, mRNA, | 1.55 | 2.42 |
| | 435292 | N20514 | Hs.172965 | ESTs | 1.53 | 2.21 |
| | 408561 | AJ308037 | Hs.84120 | hypothetical protein MGC13016 | 1.52 | 2.01 |
| | 427923 | AW274357 | Hs.301406 | hypothetical protein PP3501 | 1.47 | 2.71 |
| 30 | 447763 | BE619911 | Hs.115803 | hypothetical protein | 1.40 | 2.10 |
| | 454478 | AW805749 | | superoxide dismutase 2, mitochondrial | 1.30 | 2.36 |
| | 427289 | A1097346 | | phosphoserine aminotransferase | 1.24 | 2.02 |
| | 430513 | AJ012008 | Hs.241586 | G6C protein | 1.20 | 2.18 |
| | 411388 | X72925 | Hs.69752 | desmocollin 1 | 1.00 | 2.43 |
| 35 | TABLE 60B: | | | | | |
| | Pkey: | Unique Eos probeset identifier number | | | | |
| | CAT number: | Gene cluster number | | | | |
| | Accession: | Genbank accession numbers | | | | |
| 40 | Pkey | CAT Number | Accession | | | |
| | 431089 | 125941_2 | BG940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826 | | | |
| | 459702 | 539529_1 | BG207209 BE166299 AJ204995 BG199355 AW969908 AA528756 AW440776 BI044354 | | | |
| | 444105 | 649788_1 | AW189097 AJ123917 AJ123926 | | | |
| 45 | 407178 | 683007_1 | AW235123 AA195651 | | | |
| | 454478 | 4273_15 | AW796921 AW798102 AW805749 AW805872 BF985060 AW794380 BF380449 AW794466 AW794538 | | | |
| | 427289 | 1820_2 | BC007350 BG766159 BG769338 BG761999 BG744385 BG770572 AW370610 AW370581 AA978353 AW327973 AW402425 AJ889380 AA868504 | | | |
| | | | AW612968 AA630644 AJ751211 N26980 AJ394506 AA747849 BF154926 BF477185 AA649647 R39135 AJ750216 T35363 W36278 AW079375 | | | |
| | | | AW612240 AA505495 AA515380 BG760793 AW370651 BG766029 AW370595 BF229885 BG762422 BG764907 T50662 AA025671 AW815715 | | | |
| 50 | | | AV703420 H65047 AA485582 R56186 H90385 R55913 BI261497 BI018403 BF376945 T75578 BF933325 BF932653 BG502266 AW868934 AV683504 | | | |
| | | | BI018121 N41953 BF933343 BF932871 H08334 R14012 BF897622 T50816 BG698803 BF340083 Z20199 | | | |
| | TABLE 60C: | | | | | |
| | Pkey: | Unique number corresponding to an Eos probeset | | | | |
| 55 | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA | | | | |
| | Strand: | sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. | | | | |
| | Nt_position: | Indicates DNA strand from which exons were predicted. | | | | |
| | | Indicates nucleotide positions of predicted exons. | | | | |
| 60 | Pkey | Ref | Strand | Nt_position | | |
| | 405451 | 7622517 | Minus | 145949-146227 | | |
| | 402525 | 9800048 | Minus | 19748-20683 | | |
| | 401780 | 7249190 | Minus | 28397-28617, 28920-29045, 29135-29296, 2941 | | |
| | 401781 | 7249190 | Minus | 83215-83435, 83531-83656, 83740-83901, 8423 | | |
| 65 | 402880 | 9926561 | Minus | 41555-41865 | | |
| | 401963 | 3126783 | Plus | 51382-51521 | | |
| | TABLE 61A: ABOUT 72 GENES UPREGULATED IN BENIGN NEVI RELATIVE TO PRIMARY MELANOMAS | | | | | |
| 70 | Table 61A lists about 72 genes upregulated in benign nevi relative to primary melanomas. Genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. | | | | | |
| | Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. | | | | | |
| | Pkey: | Unique Eos probeset identifier number | | | | |
| | ExAccon: | Exemplar Accession number, Genbank accession number | | | | |
| | UnigenetID: | Unigene number | | | | |
| 75 | Unigene Title: | Unigene gene title | | | | |
| | R1 | average of benign nevi AIs divided by the 90th percentile of primary melanoma AIs | | | | |
| | R2 | average of benign nevi AIs divided by the 90th percentile of primary melanoma AIs, where the 15th percentile of normal tissue AIs was subtracted from both the | | | | |
| | | numerator and denominator | | | | |
| 80 | Pkey | ExAccon | UnigenetID | Unigene Title | R1 | R2 |
| | 431103 | M57399 | Hs.44 | pleiotrophin (heparin binding growth fac | 3.80 | 2.50 |
| | 424897 | D63216 | Hs.153684 | frizzled-related protein | 3.40 | 2.69 |
| | 429852 | AB010445 | Hs.225948 | small inducible cytokine subfamily A (Cy | 2.90 | 3.25 |
| | 431089 | BE041395 | | ESTs, Weakly similar to unknown protein | 2.82 | 1.56 |

| | | | | | | | | | |
|----|-------------|--|--|--|------|------|--|--|--|
| | 456034 | AW450979 | | gb:U1-H-B13-ata-a-12-0-UI.s1 NCI_CGAP_Su | 2.73 | 3.00 | | | |
| | 417017 | AA976064 | Hs.180842 | ribosomal protein L13 | 2.71 | 3.73 | | | |
| | 402880 | | | Target Exon | 2.56 | 3.55 | | | |
| 5 | 422656 | AI870435 | Hs.1569 | LIM homeobox protein 2 | 2.45 | 3.38 | | | |
| | 426451 | AI908165 | Hs.169946 | GATA-binding protein 3 (T-cell receptor | 2.41 | 1.91 | | | |
| | 423467 | AK000214 | Hs.129014 | hypothetical protein FLJ20207 | 2.32 | 2.24 | | | |
| | 424797 | AA622394 | Hs.153177 | ribosomal protein S28 | 2.29 | 2.53 | | | |
| | 459702 | AI204995 | | gb:an03c03.x1 Stratagene schizo brain S1 | 2.25 | 2.19 | | | |
| 10 | 406964 | M21305 | | FGENES predicted novel secreted protein | 2.24 | 1.65 | | | |
| | 428748 | AW593206 | Hs.98785 | Ksp37 protein | 2.09 | 1.43 | | | |
| | 402525 | | | NM_002699: Homo sapiens POU domain, clas | 2.06 | 2.03 | | | |
| | 415823 | R81864 | Hs.205103 | ESTs | 2.05 | 1.87 | | | |
| | 412432 | AA126311 | Hs.9879 | ESTs | 2.05 | 2.48 | | | |
| 15 | 421733 | AL119671 | Hs.1420 | fibroblast growth factor receptor 3 (ach | 2.03 | 2.20 | | | |
| | 414876 | AW950925 | Hs.924 | crystallin, mu | 2.02 | 2.30 | | | |
| | 432306 | Y18207 | Hs.303090 | protein phosphatase 1, regulatory (inhib | 2.02 | 2.39 | | | |
| | 424010 | AL080188 | Hs.137556 | Homo sapiens mRNA: cDNA DKFZp434A132 (lr | 1.95 | 2.72 | | | |
| | 453317 | NM_002277 | Hs.41696 | keratin, hair, acidic, 1 | 1.95 | 2.66 | | | |
| 20 | 452887 | AI702223 | Hs.107253 | hypothetical protein DKFZp761F241 | 1.88 | 2.85 | | | |
| | 410545 | U32324 | Hs.64310 | interleukin 11 receptor, alpha | 1.85 | 3.07 | | | |
| | 400496 | | | ENSP00000224716: GTP-binding protein SAR | 1.84 | 2.09 | | | |
| | 406972 | M32053 | | gb:Human H19 RNA gene, complete cds. | 1.83 | 4.14 | | | |
| | 406266 | | | Target Exon | 1.75 | 2.38 | | | |
| 25 | 414309 | AK000639 | Hs.75884 | DKFZP586A011 protein | 1.73 | 2.80 | | | |
| | 416250 | AA581386 | Hs.73452 | hypothetical protein MGC10791 | 1.72 | 2.27 | | | |
| | 451849 | AI199261 | Hs.27191 | hypothetical protein from clone 24796 | 1.70 | 2.09 | | | |
| | 441134 | W29092 | Hs.346950 | cellular retinoic acid-binding protein 1 | 1.68 | 2.37 | | | |
| | 401963 | | | NM_006311: Homo sapiens nuclear receptor | 1.66 | 2.38 | | | |
| 30 | 430947 | U01212 | Hs.248153 | olfactory marker protein | 1.65 | 2.00 | | | |
| | 413391 | AI223328 | Hs.75335 | glycine amidinotransferase (L-arginine:g | 1.63 | 2.18 | | | |
| | 406387 | | | Target Exon | 1.57 | 2.14 | | | |
| | 405776 | | | cytochrome c-1 | 1.55 | 2.23 | | | |
| 35 | 410677 | NM_003278 | Hs.65424 | tetranectin (plasminogen-binding protein | 1.53 | 3.26 | | | |
| | 406807 | AA057605 | Hs.180920 | ribosomal protein S9 | 1.53 | 2.67 | | | |
| | 420438 | AW403621 | Hs.1311 | CD1C antigen, c polypeptide | 1.52 | 2.09 | | | |
| | 422089 | AA523172 | Hs.103135 | ESTs, Weakly similar to SFR4_HUMAN SPLIC | 1.52 | 2.66 | | | |
| | 456898 | NM_001928 | Hs.155597 | D component of complement (adipsin) | 1.48 | 2.57 | | | |
| | 402412 | | | Target Exon | 1.48 | 2.42 | | | |
| 40 | 427795 | BE268268 | Hs.180842 | ribosomal protein L13 | 1.48 | 3.48 | | | |
| | 452547 | AA335295 | Hs.74120 | adipose specific 2 | 1.47 | 3.89 | | | |
| | 414323 | NM_014759 | Hs.334688 | KIAA0273 gene product | 1.46 | 3.14 | | | |
| | 425831 | U46689 | Hs.159608 | aldehyde dehydrogenase 3 family, member | 1.45 | 2.09 | | | |
| | 457090 | AL080243 | Hs.180920 | ribosomal protein S9 | 1.40 | 2.86 | | | |
| 45 | 445431 | AF137386 | Hs.12701 | plasmolipin | 1.39 | 2.00 | | | |
| | 445636 | AW105401 | | ribosomal protein L29 | 1.38 | 2.08 | | | |
| | 414582 | AL021154 | Hs.76884 | inhibitor of DNA binding 3, dominant neg | 1.37 | 3.32 | | | |
| | 406845 | AI567284 | Hs.119598 | ribosomal protein L3 | 1.37 | 2.04 | | | |
| | 406808 | AI690307 | Hs.180920 | ribosomal protein S9 | 1.36 | 3.32 | | | |
| 50 | 403986 | | | Target Exon | 1.34 | 2.09 | | | |
| | 402218 | | | NM_022165: Homo sapiens Lin-7b protein (| 1.31 | 2.16 | | | |
| | 400649 | | | Target Exon | 1.29 | 2.07 | | | |
| | 432647 | AI807481 | Hs.278581 | fibroblast growth factor receptor 2 (bac | 1.28 | 2.40 | | | |
| | 403211 | | | NM_005400: Homo sapiens protein kinase C | 1.26 | 2.13 | | | |
| 55 | 452678 | AJ243131 | Hs.164661 | ESTs, Weakly similar to TGLX_HUMAN PROTE | 1.26 | 2.14 | | | |
| | 406889 | D50310 | Hs.79933 | cyclin I | 1.26 | 2.37 | | | |
| | 447299 | AF043897 | Hs.18075 | chromosome 9 open reading frame 3 | 1.25 | 2.39 | | | |
| | 404406 | | | Target Exon | 1.24 | 2.09 | | | |
| | 432894 | AW167668 | Hs.279772 | brain specific protein | 1.23 | 2.28 | | | |
| 60 | 406757 | T65957 | Hs.77039 | ATP synthase, H transporting, mitochondr | 1.21 | 2.01 | | | |
| | 425883 | AL137708 | Hs.161031 | Homo sapiens mRNA: cDNA DKFZp434K0322 (l | 1.20 | 2.07 | | | |
| | 409726 | AI479341 | Hs.724 | thyroid hormone receptor, alpha (avian e | 1.17 | 2.62 | | | |
| | 436398 | H87136 | Hs.5174 | ribosomal protein S17 | 1.17 | 2.42 | | | |
| | 444674 | BE562200 | Hs.244 | amino-terminal enhancer of split | 1.16 | 2.02 | | | |
| 65 | 402450 | | | Target Exon | 1.16 | 2.08 | | | |
| | 406758 | AA552326 | Hs.77039 | ATP synthase, H transporting, mitochondr | 1.16 | 2.03 | | | |
| | 431243 | U46455 | Hs.252189 | syndecan 4 (amphiglycan, ryudocan) | 1.13 | 2.23 | | | |
| | 407032 | U73799 | | gb:Human dynactin mRNA, partial cds. | 1.10 | 2.01 | | | |
| | 402921 | | | ENSP00000244047: Cadherin-like protein V | 1.00 | 2.00 | | | |
| 70 | TABLE 61B: | | | | | | | | |
| | Pkey: | Unique Eos probeset identifier number | | | | | | | |
| | CAT number: | Gene cluster number | | | | | | | |
| | Accession: | Genbank accession numbers | | | | | | | |
| 75 | Pkey | CAT Number | Accession | | | | | | |
| | 431089 | 125941_2 | BG940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826 | | | | | | |
| | 456034 | 685586_1 | AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945 | | | | | | |
| | 459702 | 539529_1 | BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354 | | | | | | |
| 80 | 445636 | 8561_5 | BF339388 AI345516 BC391657 BE708967 BG026034 BE261703 H56716 H65572 H93801 T48830 R96953 R96989 R39707 BE867593 AA090310 | | | | | | |
| | | | AA090672 | | | | | | |
| | TABLE 61C: | | | | | | | | |
| | Pkey: | Unique number corresponding to an Eos probeset | | | | | | | |

| | | | |
|--------------|---|--------|--|
| Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. | | |
| Strand: | Indicates DNA strand from which exons were predicted. | | |
| NT_position: | Indicates nucleotide positions of predicted exons. | | |
| Pkey | Ref | Strand | NT_position |
| 402880 | 9926561 | Minus | 41555-41865 |
| 402525 | 9800048 | Minus | 19748-20683 |
| 400496 | 9743564 | Plus | 41515-41695 |
| 405266 | 7528342 | Minus | 2365-2518 |
| 401963 | 3126783 | Plus | 51382-51521 |
| 406387 | 9256180 | Plus | 116229-116371,117512-117651 |
| 405776 | 7159748 | Minus | 105911-107251 |
| 402412 | 7408036 | Plus | 75075-75679 |
| 403986 | 8576059 | Plus | 90692-91238 |
| 402218 | 7689783 | Plus | 127677-127886 |
| 400649 | 8117705 | Plus | 93097-93792 |
| 403211 | 7630841 | Minus | 159211-159369 |
| 404406 | 7329316 | Minus | 47543-47928 |
| 402450 | 9796674 | Plus | 137536-137682,137920-138045 |
| 402921 | 7981303 | Minus | 52242-52384,55599-55858,57124-57309,5963 |

TABLE 62A: ABOUT 121 GENES UPREGULATED IN BENIGN NEVI RELATIVE TO NORMAL SKIN

Table 62A lists about 121 genes upregulated in benign nevi relative to normal skin. These genes were selected from 59680 probesets on the Ecs/Alfymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Ecs probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: average of benign nevi AIs divided by the 90th percentile of normal skin AIs
 R2: average of benign nevi AIs divided by the 90th percentile of normal skin AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

| Pkey | ExAccn | UnigenelD | Unigene Title | R1 | R2 |
|--------|-----------|-----------|--|------|------|
| 430377 | NM_001922 | Hs.301865 | dopachrome tautomerase (dopachrome delta | 8.69 | 7.66 |
| 438380 | T06430 | Hs.61194 | chondroitin sulfate proteoglycan BEHAB/b | 6.71 | 8.11 |
| 406964 | M21305 | | FGENES predicted novel secreted protein | 6.50 | 3.35 |
| 426555 | NM_000372 | Hs.2053 | tyrosinase (oculocutaneous albinism IA) | 6.40 | 4.32 |
| 430822 | AJ005371 | Hs.248017 | glyceraldehyde-3-phosphate dehydrogenase | 5.16 | 4.12 |
| 415752 | BE314524 | Hs.78776 | putative transmembrane protein | 4.77 | 3.59 |
| 431103 | M57399 | Hs.44 | pleiotrophin (heparin binding growth fac | 4.63 | 4.99 |
| 451668 | Z43948 | Hs.326444 | cartilage acidic protein 1 | 4.62 | 6.04 |
| 449644 | AW960707 | Hs.148324 | ESTs | 3.97 | 3.41 |
| 435056 | AW023337 | Hs.5422 | glycoprotein M6B | 3.42 | 2.29 |
| 431089 | BE041395 | | ESTs, Weakly similar to unknown protein | 3.21 | 2.57 |
| 452973 | H88409 | Hs.40527 | ESTs | 3.16 | 3.12 |
| 408393 | AW015318 | Hs.23165 | ESTs | 3.12 | 2.00 |
| 417355 | D13168 | Hs.82002 | endothelin receptor type B | 3.11 | 2.45 |
| 415314 | N88802 | Hs.5422 | glycoprotein M6B | 2.86 | 2.39 |
| 417632 | R20855 | Hs.5422 | glycoprotein M6B | 2.78 | 2.16 |
| 457211 | AW972565 | Hs.32399 | ESTs, Weakly similar to S51797 vasodilat | 2.75 | 3.71 |
| 456034 | AW450979 | | gb:U1-H-BI3-ala-a-12-0-U1.s1 NCI_CGAP_Su | 2.73 | 3.00 |
| 404356 | | | Target Exon | 2.63 | 2.69 |
| 414876 | AW950925 | Hs.924 | crystallin, mu | 2.57 | 3.15 |
| 420208 | BE276055 | Hs.95972 | silver (mouse homolog) like | 2.46 | 2.89 |
| 422656 | AJ870435 | Hs.1569 | UIM homeobox protein 2 | 2.45 | 2.20 |
| 439963 | AW247529 | Hs.6793 | platelet-activating factor acetylhydrola | 2.43 | 2.11 |
| 432222 | AI204995 | | gb:an03c03.x1 Stratagene schizo brain S1 | 2.31 | 1.96 |
| 401116 | | | Target Exon | 2.29 | 2.24 |
| 410326 | AI368909 | Hs.47650 | ESTs | 2.27 | 2.77 |
| 459702 | AI204995 | | gb:an03c03.x1 Stratagene schizo brain S1 | 2.25 | 3.49 |
| 435730 | AB020635 | Hs.4984 | KIAA0828 protein | 2.24 | 2.24 |
| 404977 | | | Insulin-like growth factor 2 (somatomedi | 2.24 | 1.99 |
| 414221 | AW450979 | | gb:U1-H-BI3-ala-a-12-0-U1.s1 NCI_CGAP_Su | 2.16 | 2.36 |
| 437862 | AW978107 | Hs.5884 | Homo sapiens mRNA; cDNA DKFZp586C0224 (I | 2.13 | 2.09 |
| 402181 | | | Target Exon | 2.12 | 2.74 |
| 447907 | AI439110 | Hs.170796 | ESTs | 2.05 | 2.02 |
| 434276 | AF123659 | Hs.93605 | leucine zipper, putative tumor suppresso | 2.04 | 3.14 |
| 459246 | NM_006834 | Hs.32217 | RAB32, member RAS oncogene family | 2.02 | 1.83 |
| 405451 | | | dihydropyrimidinase-like 3 | 2.01 | 2.00 |
| 446727 | AB011095 | Hs.16032 | KIAA0523 protein | 2.01 | 2.36 |
| 417017 | AA976064 | Hs.180842 | ribosomal protein L13 | 2.00 | 2.37 |
| 413171 | AA318325 | Hs.75219 | tyrosinase-related protein 1 | 1.94 | 2.77 |
| 408209 | NM_004454 | Hs.43697 | ets variant gene 5 (ets-related molecule | 1.94 | 2.76 |
| 455657 | BE065209 | | gb:RC1-BT0314-310300-015-b12 BT0314 Homo | 1.92 | 2.91 |
| 419200 | AW966405 | | EST | 1.85 | 2.91 |
| 419687 | AI638859 | Hs.227699 | ESTs, Weakly similar to T2D3_HUMAN TRANS | 1.84 | 2.27 |
| 402217 | | | C19001662:gil5753872reflNP_034345.1 i | 1.83 | 2.33 |
| 406040 | | | Target Exon | 1.81 | 2.04 |
| 435292 | N20514 | Hs.172965 | ESTs | 1.81 | 3.41 |
| 430947 | U01212 | Hs.248153 | olfactory marker protein | 1.79 | 2.00 |
| 434574 | AI424458 | Hs.33470 | ESTs | 1.78 | 4.00 |

| | | | | | |
|--------|-----------|-----------|--|------|------|
| 403532 | | | NM_024638:Homo sapiens hypothetical prot | 1.75 | 2.06 |
| 402829 | | | C1002500.gij6754254[ref]NP_034610.1] hea | 1.72 | 2.20 |
| 403828 | | | C4000447.gij7705570[ref]NP_038851.1] KJ | 1.72 | 2.04 |
| 453837 | AL138387 | Hs.256126 | baculoviral IAP repeat-containing 7 (liv | 1.68 | 2.40 |
| 407826 | AA128423 | Hs.40300 | calpain 3, (p94) | 1.67 | 2.13 |
| 441253 | AI632744 | Hs.129501 | ESTs | 1.67 | 2.13 |
| 405776 | | | cytochrome c-1 | 1.66 | 2.36 |
| 430540 | AW245422 | | Homo sapiens cDNA: FLJ22105 fis, clone H | 1.66 | 2.08 |
| 445745 | AB007924 | Hs.13245 | KIAA0455 gene product | 1.66 | 2.34 |
| 401963 | | | NM_006311:Homo sapiens nuclear receptor | 1.66 | 2.97 |
| 402994 | | | NM_002463:Homo sapiens myxovirus (influ | 1.66 | 2.56 |
| 406016 | | | Target Exon | 1.65 | 2.23 |
| 429186 | BE503443 | Hs.112095 | hypothetical protein DKFZp434F1819 | 1.65 | 2.30 |
| 402911 | | | NM_021158:Homo sapiens protein kinase d | 1.63 | 2.46 |
| 412926 | AI879076 | Hs.75061 | macrophage myristoylated alanine-rich C | 1.61 | 2.28 |
| 440437 | AI923201 | Hs.192352 | ESTs | 1.59 | 2.07 |
| 403960 | | | ENSP00000174317:KIAA0303 (FRAGMENT). | 1.59 | 2.41 |
| 406266 | | | Target Exon | 1.56 | 2.16 |
| 424481 | R19453 | Hs.1787 | proteolipid protein 1 (Pelizaeus-Merzbac | 1.55 | 3.14 |
| 403803 | | | C4001432.gij6009515[dbj]BAAB4941.1] (AB | 1.54 | 2.04 |
| 407038 | X00237 | | gb:Human F variable segment 5' to antiH | 1.53 | 2.09 |
| 424412 | H15512 | Hs.10043 | hypothetical protein FLJ13074 | 1.53 | 2.46 |
| 431836 | AF178532 | Hs.271411 | beta-site APP-cleaving enzyme 2 | 1.52 | 2.76 |
| 427923 | AW274357 | Hs.301406 | hypothetical protein PP3501 | 1.52 | 3.04 |
| 419849 | BE041436 | Hs.93379 | eukaryotic translation initiation factor | 1.51 | 3.42 |
| 404790 | | | C12001707.gij7305215[ref]NP_038599.1] k | 1.50 | 2.16 |
| 434596 | T59538 | | gb:yt65g12.s1 Stratagene ovary (937217) | 1.48 | 2.02 |
| 425069 | AA587465 | Hs.298184 | potassium voltage-gated channel, shaker- | 1.47 | 4.05 |
| 438549 | BE386801 | Hs.21858 | trinucleotide repeat containing 3 | 1.46 | 2.48 |
| 427289 | AI097346 | | phosphoserine aminotransferase | 1.44 | 4.46 |
| 425818 | AB021225 | Hs.159581 | matrix metalloproteinase 17 (membrane-in | 1.43 | 2.32 |
| 432800 | BE391046 | Hs.278962 | AIM-1 protein | 1.43 | 2.08 |
| 447763 | BE619911 | Hs.115803 | hypothetical protein | 1.42 | 2.21 |
| 443219 | AI354669 | Hs.187461 | ESTs, Weakly similar to C29149 proline-r | 1.41 | 2.31 |
| 451489 | NM_005503 | Hs.26468 | amyloid beta (A4) precursor protein-bind | 1.41 | 2.35 |
| 459641 | AW064121 | Hs.279175 | ESTs | 1.41 | 2.01 |
| 405318 | | | C7002129.gij3638957[gb]AAC36301.1] (ACO | 1.40 | 2.31 |
| 402343 | | | Target Exon | 1.40 | 2.35 |
| 447108 | AW449602 | Hs.241493 | natural killer-tumor recognition sequenc | 1.40 | 2.11 |
| 431222 | X56777 | Hs.273790 | zona pellucida glycoprotein 3A (sperm re | 1.39 | 2.06 |
| 400263 | | | Eos Control | 1.39 | 2.60 |
| 403986 | | | Target Exon | 1.38 | 2.09 |
| 437912 | BE278594 | Hs.5912 | F-box only protein 7 | 1.36 | 2.27 |
| 426020 | AL110195 | Hs.166017 | microphthalmia-associated transcription | 1.36 | 2.77 |
| 401914 | | | Target Exon | 1.33 | 2.43 |
| 450395 | BE048545 | Hs.161757 | ESTs | 1.29 | 2.01 |
| 425535 | AB007937 | Hs.158287 | KIAA0468 gene product | 1.29 | 2.94 |
| 450358 | AB010098 | Hs.24907 | coronin, actin-binding protein, 2B | 1.28 | 2.84 |
| 427560 | AA405394 | Hs.161851 | ESTs | 1.27 | 2.14 |
| 402450 | | | Target Exon | 1.27 | 2.89 |
| 405885 | D28423 | | gb:Human mRNA for pre-mRNA splicing fact | 1.26 | 3.19 |
| 404067 | | | Target Exon | 1.26 | 2.45 |
| 406368 | | | NM_022355:Homo sapiens putative dipeptid | 1.25 | 2.06 |
| 454429 | BE273437 | Hs.301406 | hypothetical protein PP3501 | 1.23 | 2.07 |
| 414580 | BE386918 | | gb:G01275386F1 NIH_MGC_20 Homo sapiens c | 1.22 | 2.21 |
| 414060 | BE246327 | Hs.123164 | gb:TCBAP1E1967 Pediatric pre-B cell acut | 1.22 | 2.01 |
| 400867 | | | cofilin 1 (non-muscle) | 1.21 | 2.19 |
| 437026 | AW976573 | | ESTs | 1.21 | 2.31 |
| 402605 | | | Target Exon | 1.20 | 2.09 |
| 431008 | H84058 | Hs.25734 | ESTs, Weakly similar to BING1 [H.sapiens | 1.17 | 2.22 |
| 448143 | AF039704 | Hs.20478 | ceroid-lipofuscinosis, neuronal 2, late | 1.17 | 2.25 |
| 416630 | H69392 | Hs.174051 | small nuclear ribonucleoprotein 70kD pol | 1.16 | 2.34 |
| 407239 | AA076350 | Hs.67846 | leukocyte immunoglobulin-like receptor, | 1.14 | 2.58 |
| 419045 | T85693 | | gb:yd60d06.r1 Soares fetal liver spleen | 1.13 | 2.08 |
| 443923 | X60702 | Hs.210 | leukocyte tyrosine kinase | 1.11 | 2.24 |
| 457585 | AB040799 | Hs.278283 | G protein-coupled receptor 27 | 1.08 | 2.04 |
| 452958 | AA883929 | Hs.40527 | ESTs | 1.03 | 2.28 |
| 403969 | | | ENSP00000034663:Zinc finger protein 131 | 1.00 | 2.04 |
| 436878 | BE465204 | Hs.47448 | ESTs | 1.00 | 2.12 |
| 415929 | AA724373 | Hs.49344 | hypothetical protein FLJ11006 | 1.00 | 2.18 |
| 404632 | | | NM_022490:Homo sapiens hypothetical prot | 1.00 | 2.19 |
| 452838 | U65011 | Hs.30743 | preferentially expressed antigen in mela | 1.00 | 2.35 |
| 447937 | AL109716 | Hs.20034 | Homo sapiens mRNA full length insert cDN | 1.00 | 2.41 |

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TABLE 62B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

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| Pkey | CAT Number | Accession |
|--------|------------|---|
| 431089 | 125941_2 | BG940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826 |
| 456034 | 685585_1 | AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945 |
| 432222 | 539529_1 | BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354 |

| | | |
|--------|--|---|
| 459702 | 539529_1 | BG207209 BE166299 AJ204995 BG199355 AW969908 AA528756 AW440776 BI044354 |
| 414221 | 685586_1 | AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945 |
| 455657 | 1490185_1 | BE065209 BE065364 BE065110 BE065111 |
| 419200 | 9531_1 | BF036043 AW190446 BG194731 AW662036 AJ445021 BE937550 AW818972 AW393132 AA834685 BF112058 AV721682 H16423 AI270167 AI857345 |
| 5 | | AA937302 AW818444 BE929780 BG498678 BF155010 BI598271 BI599811 BE161728 AW578737 AW753711 AW379707 AW381918 BG506608 |
| | | AW028637 AW994240 BF887392 BF790073 AW381624 AV727105 BF439618 AA443174 AI018009 N42850 AW573242 AI417258 AA463483 AI676131 |
| | | AI167170 AA836627 AA443828 AW592922 AA235129 AA730278 AW439062 AW474332 BI043239 AW474342 BG708553 AW362423 BF090028 |
| | | BE827256 R16550 R39478 R39479 R94368 BG540916 BM314745 AA251087 D54231 D56274 BF085805 D31589 AW956405 AW994425 D81879 |
| 10 | | BE093545 AW901107 AA383529 BI021552 R56420 N39976 AA573281 H82595 AA234955 BE093539 AW367006 BF358697 BF366318 AA663856 |
| | | BE702099 BF035989 AI267384 AI267232 BE348320 AA621574 AA861212 BF083343 BF083341 AV745131 D53074 AW954476 AW954472 AA376836 |
| | | AV724531 D53063 C14928 AA093287 AA062638 BG483558 BE940050 AA765964 T70171 BE938775 BE940057 D53502 AW373300 AL118798 |
| | | BM128728 AA193411 AW444709 AW952455 AI887612 BF431948 BI496876 AI264159 BM128481 AI624657 AI689301 AI969467 AA861585 AA251595 |
| | | AA625761 AA872090 AI826790 AA328366 BE827416 R75951 D56918 R68122 BE827384 AI118797 AI184164 AI164411 BI495332 BE858113 |
| 15 | 430540 713_2 | AI863860 H00660 T69849 AW780389 C14667 BE934995 BI018652 R92801 AA164410 H00752 AW373305 AW373299 AW373302 |
| | | BC017171 BC012195 NM_007126 AF100752 AL137377 Z70768 BM474865 BG754806 AU124376 BG757203 BG764420 BG775028 BG824418 |
| | | BM045810 AU120387 BG770238 BG686740 BG913323 BI759980 BG395998 BM048875 BE881070 BE313689 BE879144 BM309834 AW245847 |
| | | AI770171 BF196861 BE856897 AA463876 AI375927 AA648810 AA948193 AA490916 AI459893 AI458188 AI240408 AI191843 AI131029 AW768399 |
| 20 | | AI365196 AW337984 AW026150 BE466591 BE674599 AI818438 AA772197 AI651927 AW151143 BI198825 BG819083 BM458764 BE903567 |
| | | BE732715 BM043200 BE900263 BE900706 BE731097 BE390023 BG875384 BF996406 BF988930 BM475542 AW246215 BE501897 BE903610 |
| | | BE561530 BE560537 BE903782 BE732947 BI227204 BG761305 BE262642 BE391848 BE382475 BG008258 BI547991 BI459099 BE391391 BE259420 |
| | | BE298109 AW245422 AI423847 AI914618 H80534 BE301004 AL531791 AI435581 BF793112 AL577303 AA373265 BE746965 BF743630 BE879296 |
| | | AI359493 BM018598 AI689260 AW072450 F20201 AW151405 AW517572 AA773468 BG259694 BE391163 BG621529 AI421728 BG767231 BM462953 |
| 25 | | BG340524 W52648 AA113434 BE785431 BI041981 BG832385 BG253168 BG759470 BF369329 BF981332 BE259418 BE785738 BI091658 N72512 |
| | | W58732 W85690 BG958989 AI205206 H19721 W17051 W77958 BI262010 AA844319 W74143 W72214 N85194 BE734033 BG164099 AA931069 |
| | | F13645 R41394 AK025758 BG180977 BE349455 AA812018 AA740241 AI027722 AI150356 AA886395 AW977627 BE220225 AA884082 AW518114 |
| | | AJ243844 AA809493 AA481029 AA825718 AI347866 AI431670 AA814436 AI251109 R07704 AA765606 AA724593 AI918399 AI537550 AA491103 |
| | | AW008188 R07703 AA989120 AA746235 AW028983 AA789102 AU185751 AW971465 AA489681 AW971893 AW612086 BE077936 BI860809 |
| | | BE002760 BG746251 BE962912 BM454584 AL134894 BF104082 H80591 |
| 30 | 434596 14701_1 427289 1820_2 | AF147374 T59538 T59589 T59598 T59542 |
| | | BC007350 BG766159 BG769338 BG7644385 BG770572 AW370610 AW370581 AA978353 AW372973 AW404225 AI889380 AA868504 |
| | | AW612968 AA630644 AI751211 N26980 AI394506 AA747849 BF154926 BF477185 AA649647 R39135 AI750216 T35363 W36278 AW079375 |
| | | AW612240 AA505495 AA15380 BG760793 AW370651 BG766029 AW370595 BF229885 BG762422 BG764907 T50662 AA025671 AW815715 |
| | | AV703420 H65047 AA85582 R56186 H90385 R55913 BI261497 BI018403 BF376945 T75578 BF933325 BF932853 BG502266 AW868934 AV683504 |
| 35 | 400263 18977_1 | BI018121 N41953 BF933343 BF932871 H08334 R14012 BF897622 T50816 BG698803 BF340083 Z20199 |
| | | Z11692 X51466 NM_001961 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 BI868669 BG337216 AW629935 |
| | | BM016525 AI560409 AI562866 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033486 |
| | | BI517580 BG876486 BI011829 AJ13235 BG831724 BF869862 BG998348 BI011834 BF888337 BF898627 BF092380 AW803215 F01241 BF805719 |
| | | BG876487 AW498536 BF988866 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758 |
| 40 | | BM452445 AI937808 AW026128 N23684 AW06041 AI337621 F33111 BF344301 BG105450 BG387343 BF569547 BF154671 BM007368 BF569385 |
| | | BE772007 BI199487 BF761700 BI261519 BF944452 BF898506 AI038390 BM044934 AW381142 BG743618 BE769206 BE893973 BI015047 BF886479 |
| | | BF761350 BE769769 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 |
| | | BG674499 BG774174 BI015084 |
| | | BG333973 BE385437 BE408833 BE387650 |
| 45 | 414580 623093_1 437026 1240260_1 419045 348516_2 | AW976573 AA742335 AA830000 |
| | | BF981324 BG723297 T85693 T81681 T81909 |

TABLE 62C:

| | |
|--------------|---|
| Pkey: | Unique number corresponding to an Eos probe set |
| Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. |
| Strand: | Indicates DNA strand from which exons were predicted. |
| NL_position: | Indicates nucleotide positions of predicted exons. |

| | | | | |
|----|--------|---------|--------|-------------------------------------|
| 55 | Pkey | Ref | Strand | NL_position |
| | 404356 | 7630858 | Minus | 126433-126623 |
| | 401116 | 9966559 | Plus | 123579-124447 |
| | 404977 | 3738341 | Minus | 43081-43229 |
| | 402181 | 8575912 | Plus | 449746-450040 |
| | 405451 | 7622517 | Minus | 145949-146227 |
| 60 | 402217 | 9795981 | Minus | 21521-21757 |
| | 406040 | 6758938 | Minus | 23063-23599 |
| | 403532 | 8076842 | Minus | 81750-81901 |
| | 402829 | 8918414 | Plus | 101532-101852,102006-102263 |
| | 403828 | 9838214 | Plus | 31755-32148 |
| 65 | 405776 | 7159748 | Minus | 105911-107251 |
| | 401963 | 3126783 | Plus | 51382-51521 |
| | 402994 | 2996643 | Minus | 4727-4969 |
| | 406016 | 8272661 | Plus | 41341-41940 |
| | 402911 | 7263904 | Plus | 142689-142979 |
| 70 | 403960 | 8224409 | Minus | 90999-94843 |
| | 406266 | 7528342 | Minus | 2365-2518 |
| | 403803 | 8112965 | Plus | 55513-55778 |
| | 404790 | 7230958 | Plus | 38611-38761 |
| | 405318 | 3638954 | Plus | 79689-79967 |
| 75 | 402343 | 8099256 | Plus | 4677-6084 |
| | 403986 | 8576059 | Plus | 90692-91238 |
| | 401914 | 9369520 | Plus | 62537-62945,63155-63308 |
| | 402450 | 9796674 | Plus | 137536-137682,137920-138045 |
| | 404067 | 3282162 | Plus | 1415-2071 |
| 80 | 406368 | 9256126 | Minus | 72447-72588,72673-72802,73119-73245 |
| | 400867 | 9838275 | Plus | 34136-34846 |
| | 402605 | 9909420 | Minus | 47680-47973 |
| | 403969 | 8569909 | Plus | 31237-31375,32405-32506 |

404632 9796668 Plus 45096-45229

TABLE 63A: ABOUT 181 GENES UPREGULATED IN BENIGN NEVI RELATIVE TO MELANOMA METASTASES

Table 63A lists about 181 genes upregulated in benign nevi relative to melanoma metastases. Genes were selected from 59680 probesets on the Eos/Altymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number

ExAcn: Exemplar Accession number, Genbank accession number

UnigenelD: Unigene number

Unigene Title: Unigene gene title

R1: average of benign nevi AIs divided by the 90th percentile of melanoma metastasis AIs

R2: average of benign nevi AIs divided by the 90th percentile of melanoma metastasis AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

| Pkey | ExAcn | UnigenelD | Unigene Title | R1 | R2 |
|--------|-----------|-----------|---|-------|-------|
| 401781 | | | Target Exon | 19.33 | 19.21 |
| 422511 | AU076442 | Hs.117938 | collagen, type XVII, alpha 1 | 13.54 | 14.18 |
| 401780 | | | NM_005557: Homo sapiens keratin 16 (foca | 12.97 | 13.63 |
| 409601 | AF237621 | Hs.80828 | keratin 1 (epidermolytic hyperkeratosis) | 12.61 | 31.19 |
| 412636 | NM_004415 | | desmoplakin (DPI, DPL) | 11.73 | 6.91 |
| 420783 | AI659838 | Hs.99923 | lectin, galactoside-binding, soluble, 7 | 10.18 | 14.08 |
| 409632 | W74001 | Hs.55279 | serine (or cysteine) proteinase inhibitor | 8.48 | 6.79 |
| 421733 | AL119671 | Hs.1420 | fibroblast growth factor receptor 3 (ach | 8.28 | 9.62 |
| 430686 | NM_001942 | Hs.2633 | desmoglein 1 | 7.26 | 5.64 |
| 429852 | AB010445 | Hs.225948 | small inducible cytokine subfamily A (Cy | 7.12 | 10.88 |
| 442577 | AA292998 | Hs.163900 | ESTs | 7.01 | 6.59 |
| 406964 | M21305 | | FGENES predicted novel secreted protein | 6.50 | 8.82 |
| 401785 | | | NM_002275: Homo sapiens keratin 15 (KRT1 | 6.40 | 9.77 |
| 410001 | AB041036 | Hs.57771 | kallikrein 11 | 6.18 | 6.16 |
| 417515 | L24203 | Hs.82237 | ataxia-telangiectasia group D-associated | 5.73 | 16.57 |
| 418686 | Z36830 | Hs.87268 | annexin A8 | 5.32 | 5.27 |
| 439496 | BE616501 | Hs.32343 | Homo sapiens, Similar to RIKEN cDNA 1110 | 4.89 | 9.81 |
| 452240 | AI591147 | Hs.61232 | ESTs | 4.89 | 6.67 |
| 402525 | | | NM_002699: Homo sapiens POU domain, clas | 4.74 | 4.80 |
| 431360 | NM_000427 | Hs.251680 | loricrin | 4.66 | 3.98 |
| 431103 | M57399 | Hs.44 | pleiotrophin (heparin binding growth fac | 4.63 | 5.69 |
| 418067 | AI127958 | Hs.83393 | cystatin E/M | 4.56 | 6.78 |
| 424012 | AW368377 | Hs.137569 | tumor protein 63 kDa with strong homolog | 4.56 | 5.73 |
| 418663 | AK001100 | Hs.41690 | desmocollin 3 | 4.44 | 5.23 |
| 419329 | AY007220 | Hs.288998 | S100-type calcium binding protein A14 | 4.24 | 6.49 |
| 439706 | AW872527 | Hs.59761 | ESTs, Weakly similar to DAP1_HUMAN DEATH | 3.95 | 3.37 |
| 421773 | W69233 | Hs.112457 | ESTs | 3.88 | 9.60 |
| 408536 | AW381532 | Hs.135188 | ESTs | 3.82 | 10.18 |
| 418394 | AF132818 | Hs.84728 | Kruppel-like factor 5 (intestinal) | 3.78 | 6.33 |
| 408000 | L11690 | Hs.198689 | bullous pemphigoid antigen 1 (230/240kD) | 3.77 | 4.92 |
| 432374 | W68815 | Hs.301885 | Homo sapiens cDNA FLJ11346 fis, clone PL | 3.70 | 5.30 |
| 424049 | AB014524 | Hs.138380 | KIAA0624 protein | 3.68 | 4.41 |
| 421948 | L42583 | Hs.334309 | keratin 6A | 3.62 | 3.13 |
| 427666 | AI791495 | Hs.180142 | calmodulin-like skin protein (CLSP) | 3.59 | 4.40 |
| 422168 | AA586894 | Hs.112408 | S100 calcium-binding protein A7 (psorias | 3.48 | 6.09 |
| 436895 | AF037335 | Hs.5338 | carbonic anhydrase XII | 3.42 | 3.28 |
| 437191 | NM_006846 | Hs.331555 | serine protease inhibitor, Kazal type, 5 | 3.28 | 3.89 |
| 401760 | | | Target Exon | 3.21 | 7.11 |
| 431089 | BE041395 | | ESTs, Weakly similar to unknown protein | 3.21 | 5.78 |
| 434293 | NM_004445 | Hs.3796 | EphB6 | 3.14 | 3.11 |
| 412432 | AA126311 | Hs.9879 | ESTs | 3.14 | 4.85 |
| 442503 | AF147078 | Hs.150853 | p53-responsive gene 5 | 3.11 | 5.92 |
| 414987 | AA524394 | Hs.294022 | hypothetical protein FLJ14950 | 3.07 | 4.89 |
| 420798 | W93774 | Hs.99936 | keratin 10 (epidermolytic hyperkeratosis | 2.99 | 3.09 |
| 433339 | AF019226 | Hs.8036 | glioblastoma overexpressed | 2.96 | 2.75 |
| 414876 | AW950925 | Hs.924 | crystallin, mu | 2.94 | 3.82 |
| 437233 | D81448 | Hs.339352 | Homo sapiens brother of CDO (BOC) mRNA, | 2.87 | 3.42 |
| 424897 | D63216 | Hs.153684 | frizzled-related protein | 2.87 | 1.96 |
| 456034 | AW450979 | | gb:U1-H-B13-ata-a-12-0-U1.s1 NCL CGAP_Su | 2.73 | 2.54 |
| 424364 | AW383226 | Hs.163834 | ESTs, Weakly similar to G01763 atrophin- | 2.72 | 2.92 |
| 427318 | AF186081 | Hs.175783 | zinc transporter | 2.71 | 2.21 |
| 452887 | AI702223 | Hs.107253 | hypothetical protein DKFZp761F241 | 2.67 | 6.47 |
| 452308 | AI167560 | Hs.61297 | ESTs | 2.67 | 4.61 |
| 407788 | BE514982 | Hs.38991 | S100 calcium-binding protein A2 | 2.64 | 2.68 |
| 431369 | BE184455 | Hs.251754 | secretory leukocyte protease inhibitor (| 2.57 | 3.91 |
| 451541 | BE279383 | Hs.26557 | plakophilin 3 | 2.49 | 5.47 |
| 453317 | NM_002277 | Hs.41696 | keratin, hair, acidic, 1 | 2.45 | 4.17 |
| 412633 | AF001691 | Hs.74304 | periplakin | 2.42 | 4.90 |
| 417233 | W25005 | Hs.24395 | small inducible cytokine subfamily B (Cy | 2.41 | 2.68 |
| 424797 | AA622394 | Hs.153177 | ribosomal protein S28 | 2.39 | 2.67 |
| 424010 | AL080188 | Hs.137556 | Homo sapiens mRNA; cDNA DKFZp434A132 (fr | 2.39 | 4.07 |
| 453241 | H58995 | Hs.37648 | ESTs | 2.39 | 2.34 |
| 426451 | AI908165 | Hs.169946 | GATA-binding protein 3 (T-cell receptor | 2.36 | 1.88 |
| 423467 | AK000214 | Hs.129014 | hypothetical protein FLJ20207 | 2.32 | 2.24 |
| 432222 | AI204995 | | gb:an03c03.x1 Stratagene schizo brain S1 | 2.31 | 1.99 |
| 430168 | AW968343 | Hs.145582 | DKFZP434I1735 protein | 2.30 | 2.60 |
| 457121 | AI743770 | Hs.180513 | ESTs, Weakly similar to KIAA0822 protein | 2.28 | 1.91 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|------|
| 5 | 433091 | Y12642 | Hs.3185 | lymphocyte antigen 6 complex, locus D | 2.27 | 8.50 |
| | 446989 | AK001898 | Hs.16740 | hypothetical protein FLJ11036 | 2.27 | 2.21 |
| | 429365 | AA451798 | Hs.99249 | ESTs | 2.25 | 2.54 |
| | 459702 | AI204995 | | gb:an03c03.x1 Stratagene schizo brain S1 | 2.25 | 2.35 |
| | 420511 | AF052692 | Hs.98485 | gap junction protein, beta 3, 31kD (conn | 2.23 | 2.17 |
| | 444946 | AW139205 | Hs.156457 | hypothetical protein FLJ22408 | 2.23 | 3.23 |
| | 417017 | AA976064 | Hs.180842 | ribosomal protein L13 | 2.21 | 2.74 |
| | 433124 | U51712 | Hs.13775 | hypothetical protein SMAP31 | 2.21 | 1.68 |
| 10 | 430152 | AB001325 | Hs.234642 | aquaporin 3 | 2.20 | 3.32 |
| | 444726 | NM_006147 | | interferon regulatory factor 6 | 2.15 | 5.20 |
| | 454034 | NM_000691 | Hs.575 | aldehyde dehydrogenase 3 family, member | 2.15 | 2.82 |
| | 425483 | AF231022 | Hs.158159 | FAT tumor suppressor (Drosophila) homolo | 2.14 | 2.96 |
| | 419912 | AF249745 | Hs.6066 | Rho guanine nucleotide exchange factor (| 2.14 | 2.25 |
| 15 | 431441 | U81961 | Hs.2794 | sodium channel, nonvoltage-gated 1 alpha | 2.12 | 2.99 |
| | 444105 | AW189097 | | ESTs | 2.11 | 2.98 |
| | 428748 | AW593206 | Hs.98785 | Ksp37 protein | 2.09 | 1.51 |
| | 456826 | AI871742 | Hs.302428 | wingless-type MMTV integration site fami | 2.09 | 3.25 |
| | 413163 | Y00815 | Hs.75216 | protein tyrosine phosphatase, receptor t | 2.09 | 4.97 |
| 20 | 410677 | NM_003278 | Hs.65424 | tetranectin (plasminogen-binding protein | 2.06 | 5.68 |
| | 430285 | AI917602 | Hs.106440 | ESTs | 2.06 | 2.04 |
| | 444781 | NM_014400 | Hs.11950 | GPI-anchored metastasis-associated prote | 2.05 | 5.92 |
| | 451668 | Z43948 | Hs.326444 | cartilage acidic protein 1 | 2.04 | 2.19 |
| | 441134 | W29092 | Hs.346950 | cellular retinoic acid-binding protein 1 | 2.04 | 3.08 |
| 25 | 433428 | T29975 | Hs.33104 | Huntingtin interacting protein C | 2.04 | 1.63 |
| | 425831 | U46689 | Hs.159608 | aldehyde dehydrogenase 3 family, member | 2.03 | 3.92 |
| | 446727 | AB011095 | Hs.16032 | KIAA0523 protein | 2.01 | 2.60 |
| | 431703 | AA514264 | Hs.4437 | triosephosphate isomerase 1 | 2.01 | 2.05 |
| | 452554 | AW452434 | Hs.58006 | ESTs, Weakly similar to ALU5_HUMAN ALU S | 1.99 | 4.04 |
| 30 | 439625 | AF086453 | Hs.58611 | ESTs | 1.99 | 2.31 |
| | 402880 | | | Target Exon | 1.99 | 2.75 |
| | 428471 | X57348 | Hs.184510 | stratfin | 1.98 | 2.10 |
| | 413859 | AW992356 | Hs.8364 | Homo sapiens pyruvate dehydrogenase kina | 1.97 | 3.16 |
| | 452547 | AA335295 | Hs.74120 | adipose specific 2 | 1.95 | 3.89 |
| 35 | 437679 | NM_014214 | Hs.5753 | inositol(myo)-1(or 4)-monophosphatase 2 | 1.94 | 2.06 |
| | 429259 | AA420450 | Hs.292911 | Plakophilin | 1.93 | 2.96 |
| | 406387 | | | Target Exon | 1.92 | 2.97 |
| | 455797 | BE091833 | | gb:IL2-BT0731-260400-076-F04 BT0731 Homo | 1.91 | 3.46 |
| | 437202 | AA326110 | | nuclear transcription factor Y, gamma | 1.89 | 2.00 |
| 40 | 426150 | NM_003658 | Hs.167218 | BarH-like homeobox 2 | 1.86 | 2.60 |
| | 434574 | AI424458 | Hs.33470 | ESTs | 1.85 | 4.61 |
| | 446051 | BE048061 | Hs.37054 | ephrin-A3 | 1.85 | 3.48 |
| | 424471 | AA341329 | Hs.311524 | ESTs | 1.84 | 2.62 |
| | 422106 | D84239 | Hs.111732 | Fc fragment of IgG binding protein | 1.83 | 4.69 |
| 45 | 451721 | NM_005946 | Hs.26915 | spectrin, beta, non-erythrocytic 2 | 1.82 | 2.00 |
| | 451849 | AI199261 | Hs.27191 | hypothetical protein from clone 24796 | 1.81 | 2.31 |
| | 429348 | AJ242859 | Hs.199731 | Langerhans cell specific c-type lectin | 1.79 | 3.07 |
| | 423523 | AW299828 | Hs.193580 | ESTs | 1.77 | 3.37 |
| | 432543 | AA552690 | Hs.152423 | Homo sapiens cDNA: FLJ21274 fis, clone C | 1.76 | 2.46 |
| 50 | 403828 | | | C40004477:gi7705570ref NP_038851.1 KJ | 1.73 | 2.06 |
| | 412446 | AI768015 | | ESTs | 1.68 | 3.16 |
| | 420039 | NM_004605 | Hs.94581 | sulfotransferase family, cytosolic, 2B, | 1.67 | 2.22 |
| | 411274 | NM_002776 | Hs.69423 | kalikrein 10 | 1.66 | 2.26 |
| | 401963 | | | NM_006311:Homo sapiens nuclear receptor | 1.66 | 2.52 |
| 55 | 435016 | AI284219 | Hs.130749 | ESTs, Weakly similar to I38022 hypothe | 1.65 | 2.20 |
| | 437897 | AA770561 | Hs.146170 | hypothetical protein FLJ22969 | 1.64 | 3.21 |
| | 419648 | T73661 | Hs.91877 | thyroid hormone responsive SPOT14 (rat) | 1.63 | 2.94 |
| | 410545 | U32324 | Hs.64310 | interleukin 11 receptor, alpha | 1.62 | 2.58 |
| | 429211 | AF052693 | Hs.198249 | gap junction protein, beta 5 (connexin 3 | 1.62 | 3.92 |
| 60 | 456898 | NM_001928 | Hs.155597 | D component of complement (adipsin) | 1.60 | 3.43 |
| | 423526 | AB011086 | Hs.129739 | KIAA0514 gene product | 1.60 | 2.18 |
| | 416305 | AU076628 | Hs.79187 | coxsaackie virus and adenovirus receptor | 1.60 | 2.47 |
| | 413966 | AA133935 | Hs.173704 | ESTs, Moderately similar to A53959 throm | 1.59 | 2.99 |
| | 414217 | AI309298 | Hs.279898 | Homo sapiens cDNA: FLJ23165 fis, clone L | 1.59 | 2.82 |
| 65 | 429299 | AI620463 | Hs.347408 | hypothetical protein MGC13102 | 1.57 | 2.64 |
| | 432647 | AI807481 | Hs.278581 | fibroblast growth factor receptor 2 (bac | 1.56 | 2.74 |
| | 429002 | AW248439 | Hs.2340 | junction plakoglobin | 1.56 | 2.97 |
| | 430171 | AF086289 | Hs.234766 | skin-specific protein | 1.54 | 2.18 |
| | 422717 | AI557623 | Hs.119475 | cold inducible RNA-binding protein | 1.51 | 2.19 |
| 70 | 414323 | NM_014759 | Hs.334688 | KIAA0273 gene product | 1.51 | 3.73 |
| | 423184 | NM_004428 | Hs.1624 | ephrin-A1 | 1.50 | 2.18 |
| | 433101 | AW572317 | Hs.12082 | Homo sapiens mRNA: cDNA DKFp566L203 (tr | 1.50 | 2.00 |
| | 424362 | AL137646 | | Homo sapiens mRNA: cDNA DKFp586F0824 (f | 1.48 | 2.04 |
| 75 | 433662 | W07162 | Hs.150826 | RAB25 RAB25, member RAS oncogene family | 1.46 | 2.83 |
| | 445431 | AF137386 | Hs.12701 | plasmofipin | 1.46 | 2.00 |
| | 456906 | AF117646 | Hs.156637 | Cas-Br-M (murine) ectropic retroviral tr | 1.44 | 2.04 |
| | 442599 | AF078037 | Hs.324051 | RelA-associated inhibitor | 1.42 | 3.50 |
| | 445656 | W22050 | Hs.21299 | ESTs, Weakly similar to AF151840 1 CGI-8 | 1.42 | 2.53 |
| | 444672 | Z95636 | Hs.11669 | taminin, alpha 5 | 1.40 | 2.36 |
| 80 | 447990 | BE048821 | Hs.20144 | small inducible cytokine subfamily A (Cy | 1.40 | 2.29 |
| | 418462 | BE001596 | Hs.85266 | integrin, beta 4 | 1.39 | 2.86 |
| | 453023 | AW028733 | Hs.31439 | serine protease inhibitor, Kunitz type, | 1.38 | 2.28 |
| | 416340 | N31772 | Hs.79226 | fasciculation and elongation protein zet | 1.38 | 2.24 |
| | 433417 | AA587773 | Hs.8859 | Homo sapiens, Similar to RIKEN cDNA 5830 | 1.38 | 2.14 |

| | | | | | | |
|----|--------|-----------|-----------|---|------|------|
| 5 | 407815 | AW373860 | Hs.183860 | hypothetical protein FLJ20277 | 1.36 | 2.34 |
| | 432894 | AW167668 | Hs.279772 | brain specific protein | 1.36 | 5.09 |
| | 439733 | AL365412 | Hs.107203 | hypothetical protein from EUROMIMAGE 1759 | 1.36 | 2.00 |
| | 454478 | AW805749 | | superoxide dismutase 2, mitochondrial | 1.35 | 2.85 |
| | 423515 | AA327017 | Hs.176594 | ESTs | 1.35 | 2.45 |
| | 436663 | AW410458 | Hs.5258 | chromosome 11 open reading frame2 | 1.35 | 2.07 |
| | 404246 | | | Target Exon | 1.34 | 2.96 |
| | 411939 | AI365585 | Hs.146246 | ESTs | 1.33 | 2.31 |
| | 409178 | BE393948 | Hs.50915 | kallikrein 5 | 1.33 | 2.03 |
| 10 | 427795 | BE268268 | Hs.180842 | ribosomal protein L13 | 1.33 | 2.29 |
| | 447299 | AF043897 | Hs.18075 | chromosome 9 open reading frame 3 | 1.32 | 2.78 |
| | 447330 | BE279949 | Hs.18141 | ladinin 1 | 1.32 | 3.37 |
| | 433399 | N46406 | Hs.84700 | similar to phosphatidylcholine transfer | 1.31 | 2.71 |
| | 403986 | | | Target Exon | 1.31 | 2.09 |
| 15 | 407597 | AA043925 | Hs.339352 | Homo sapiens brother of CDO (BOC) mRNA, | 1.30 | 2.28 |
| | 450796 | NM_001988 | Hs.25482 | envoplakin | 1.30 | 3.45 |
| | 415550 | L13720 | Hs.78501 | growth arrest-specific 6 | 1.29 | 2.76 |
| | 415512 | Y16270 | Hs.78482 | paralemmin | 1.26 | 2.49 |
| | 430513 | AJ012008 | Hs.241586 | G6C protein | 1.26 | 3.07 |
| 20 | 425581 | NM_016339 | Hs.118562 | Link guanine nucleotide exchange factor | 1.23 | 2.04 |
| | 420048 | AW206824 | Hs.25766 | ESTs | 1.23 | 2.01 |
| | 425883 | AL137708 | Hs.161031 | Homo sapiens mRNA; cDNA DKFZp434K0322 (I | 1.23 | 2.22 |
| | 430560 | Z28942 | Hs.243960 | N-myc downstream-regulated gene 2 | 1.23 | 2.42 |
| 25 | 426377 | AK001921 | Hs.169575 | hypothetical protein MGC2550 | 1.23 | 2.20 |
| | 402218 | | | NM_022165*:Homo sapiens Lin-7b protein (| 1.23 | 2.01 |
| | 413944 | AW001579 | Hs.9645 | Homo sapiens mRNA for KIAA1741 protein, | 1.18 | 2.24 |
| | 414186 | U33446 | Hs.75799 | protease, serine, 8 (prostasin) | 1.16 | 2.16 |
| | 426068 | AF029778 | Hs.166154 | jagged 2 | 1.15 | 2.07 |
| 30 | 431243 | U46455 | Hs.252189 | syndecan 4 (amphiglycan, ryudocan) | 1.14 | 2.33 |
| | 411388 | X72925 | Hs.69752 | desmocollin 1 | 1.00 | 2.61 |
| | 443672 | AA323362 | Hs.9567 | butyrobetaine (gamma), 2-oxoglutarate di | 1.00 | 2.63 |

TABLE 63B:

| | |
|-------------|--|
| Pkey: | Unique Eos probe/est identifier number |
| CAT number: | Gene cluster number |
| Accession: | Genbank accession numbers |

| | | | |
|----|--------|------------|---|
| 35 | Pkey | CAT Number | Accession |
| | 412636 | 1438_1 | M77830 NM_004415 AF139065 BG681115 BG740377 BI172964 BG000656 AA128470 BI438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 BI765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 BI060445 BI060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 BI039774 BE713818 BE713548 AW170253 BE160433 BI039775 AW866475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 BI090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 BI036306 BG990973 BI040954 BF919911 AU140155 AI951766 AI434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW955615 BE814264 BI039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF998889 BF368816 BE184924 BE159646 BE714632 BE184948 BG986845 AA131128 AA099891 W39488 C04715 BF096124 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW507238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 BI467252 AU159919 AI760816 BF082516 AI439101 AA451923 AI340326 AI590975 BI791553 AI700963 AI142882 AA039975 AA946936 AA644381 BM314884 AA702424 AI17612 AW190555 AI220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI346078 W95070 AA149191 AA026864 AI830049 AW780435 AI078449 AI819984 AI858282 BI468588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 AI927207 AI205263 BF082491 AW021347 AI568096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 AI910434 BF082513 AI494069 AI270027 AI635878 AA128330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654 AV745530 BI762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087996 BE002273 AW879451 AI571075 BE067786 AV721320 AI022862 N29754 C03378 N84767 AA131077 H30146 BE714290 AI686869 AI568892 AI915596 AW105614 AI887258 AI538577 BE926474 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 BI770853 BG679406 BG740832 BG681087 BG698430 AA455100 T87267 BE896209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040941 AA337270 AW384371 AW847442 BI058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 AI284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H90899 AW365145 W38382 AI498487 BG940189 AW063489 AA715980 BF001091 BF880066 AA666102 AA621946 AA491826 AA136653 AA136656 AW450979 AA984358 AA809054 AW238038 AA492073 BE168945 BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354 BG207209 BE166299 AI204995 BG199355 AW969908 AA528756 AW440776 BI044354 BG285809 BE940673 BG432524 BE157554 BG676980 AU144284 AI745383 AU159045 AI693500 AW293668 AW371408 BE856107 AI338042 AW188320 AI698246 BE673290 AW297653 AA156532 AI017342 AI916754 AI190644 AI184302 AA857671 BE857018 AI307420 AI318157 AW204327 AW664668 AW274339 AA582788 AI345741 AW301433 AI873468 AW137388 BF18731 BF18413 AA877495 BI001575 AI824693 AW849604 AW849405 AW849396 AW849173 BE673179 AI611327 AA705753 BE715478 AW849414 AW849399 AI085759 AI140849 T67412 AI898885 AW104647 AI912495 AI898874 AI744241 BE717113 BE717108 BE715564 AI872527 AA029457 C00338 AI469558 BE715577 AA045413 BF843813 AW189097 AI123917 AI123926 BE091833 BE091874 BE091871 AL110199 AL598719 AA152097 W84430 AI304351 BE670780 BF003019 AI271659 AW338914 AI127763 AI191873 AI922951 AI568416 AI077680 AA358674 AI138802 AI589070 AI088745 AW418696 BF475830 AI144150 AA724257 AA622339 AI375884 AI880453 AW874251 BF941345 AI619746 AI225114 AI801268 AI554474 BM023333 AI093946 AI699306 AI803839 AA496797 AI361531 AI123010 AW169313 BM023082 AI081626 AA513457 AA278720 AW518810 AA361091 AI499891 AI685346 BF436872 AI681496 AL572961 AI334148 AW138291 AI419063 AA278226 AA370719 AA152023 AI401749 AA127464 AL573761 BG913208 T07824 AI346417 H44939 AV721378 N48299 W72005 AA302424 AI611143 AW514684 BE041749 |

| | | | |
|----|--------|---------|--|
| 5 | 412446 | 63467_1 | AW370992 R42918 H10757 R10703 C01061 R27637 A1827230 AW151953 AA651675 AA228006 AA233950 BE858910 R30801 W32704 H39784 BE090279 BG697660 AW877265 B1818938 BF528291 AW953624 R57461 BF969694 BC021735 A1669212 AL120184 A1769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AA151245 BF960659 AA987907 Z41449 BF908059 BF908053 BF908049 BE699424 BF908060 BF962832 BF952020 BF963134 B1035538 BF908052 BF908057 BF090026 BF943158 A1632924 BF512340 BF952021 BF960776 BF943437 BF942847 A1768015 F09778 F04816 F02721 AA102645 A1633838 AA617929 BF947001 B1035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815 AF284421 AL137646 BG542551 A1278088 A1423919 A1274095 BE638965 BE839174 BE839102 BF924520 B1913343 AW238809 AL134380 AW793289 AL534638 T97116 AW855182 C02210 A1783480 AW024874 AW796921 AW798102 AW805749 AW805872 BF985060 AW794380 BF380449 AW794466 AW794538 |
| | 424362 | 2318_7 | |
| 10 | 454478 | 4273_16 | |

TABLE 63C:

Pkey:

Unique number corresponding to an Eos probeset

Ref:

Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) *Nature* 402:489-495.

Strand:

Indicates DNA strand from which exons were predicted.

NL_position:

Indicates nucleotide positions of predicted exons.

| Pkey | Ref | Strand | NL_position |
|--------|---------|--------|--|
| 401781 | 7249190 | Minus | 83215-83435,83531-83656,83740-83901,8423 |
| 401780 | 7249190 | Minus | 28397-28617,28920-29045,29135-29296,2941 |
| 401785 | 7249190 | Minus | 165776-165996,166189-166314,166408-16656 |
| 402525 | 9800048 | Minus | 19748-20683 |
| 401760 | 9929699 | Plus | 83126-83250,85320-85540,94719-95287 |
| 402880 | 9926561 | Minus | 41555-41865 |
| 405387 | 9256180 | Plus | 116229-116371,117512-117651 |
| 403828 | 9838214 | Plus | 31755-32148 |
| 401963 | 3126783 | Plus | 51382-51521 |
| 404246 | 7406725 | Plus | 82477-82628,82721-82817,82910-83071,8314 |
| 403986 | 8576059 | Plus | 90692-91238 |
| 402218 | 7689783 | Plus | 127677-127886 |

TABLE 64A: ABOUT 929 GENES DOWNREGULATED IN PRIMARY MELANOMAS AND/OR MELANOMA METASTASES RELATIVE TO NORMAL SKIN

Table 64A lists about 929 genes downregulated in primary melanomas and/or melanoma metastases relative to normal skin. Genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey:

Unique Eos probeset identifier number

ExAccn:

Exemplar Accession number, Genbank accession number

UnigeneID:

Unigene number

Unigene Title:

Unigene gene title

R1

90th percentile of normal skin AIs divided by the 90th percentile of primary melanoma and melanoma metastasis AIs

R2

90th percentile of normal skin AIs divided by the 90th percentile of primary melanoma and melanoma metastasis AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

| Pkey | ExAccn | UnigeneID | Unigene Title | R1 | R2 |
|--------|-----------|-----------|---|-------|-------|
| 420813 | X51501 | Hs.99949 | prolactin-induced protein | 27.72 | 20.12 |
| 408591 | AF015224 | Hs.46452 | mammaglobin 1 | 26.40 | 24.26 |
| 431360 | NM_000427 | Hs.251680 | loricrin | 26.16 | 20.45 |
| 401781 | | | Target Exon | 19.68 | 19.56 |
| 412636 | NM_004415 | | desmoplakin (DPI, DP11) | 18.12 | 10.36 |
| 429441 | AJ224172 | Hs.204096 | lipophilin B (uteroglobin family member) | 16.61 | 18.06 |
| 418067 | A1127958 | Hs.83393 | cystatin E/M | 16.00 | 25.32 |
| 409632 | W74001 | Hs.55279 | serine (or cysteine) proteinase inhibitor | 15.64 | 11.81 |
| 409601 | AF237621 | Hs.80828 | keratin 1 (epidermolytic hyperkeratosis) | 15.03 | 37.51 |
| 401780 | | | NM_005557: Homo sapiens keratin 16 (foca | 14.20 | 14.86 |
| 422168 | AA586894 | Hs.112408 | S100 calcium-binding protein A7 (psorias | 13.95 | 28.08 |
| 420783 | A1659838 | Hs.99923 | lectin, galactoside-binding, soluble, 7 | 13.52 | 18.85 |
| 422511 | AU076442 | Hs.117938 | collagen, type XVII, alpha 1 | 13.14 | 13.81 |
| 428330 | L22524 | Hs.2256 | matrix metalloproteinase 7 (matrilysin, | 12.78 | 6.35 |
| 421733 | AL119571 | Hs.1420 | fibroblast growth factor receptor 3 (ach | 12.78 | 15.22 |
| 428824 | W23624 | Hs.173059 | ESTs | 12.67 | 13.24 |
| 453309 | A1791809 | Hs.32949 | defensin, beta 1 | 12.02 | 12.42 |
| 446227 | A1281459 | Hs.270114 | ESTs | 11.79 | 12.32 |
| 421948 | L42583 | Hs.334309 | keratin 6A | 11.58 | 9.02 |
| 432877 | AW974111 | Hs.292477 | ESTs | 11.18 | 11.30 |
| 412047 | AA934589 | Hs.49696 | ESTs | 11.04 | 11.07 |
| 407230 | AA157857 | Hs.182265 | keratin 19 | 10.79 | 11.40 |
| 421296 | NM_002666 | Hs.103253 | perilipin | 10.73 | 7.94 |
| 410001 | AB041036 | Hs.57771 | kalikrein 11 | 10.72 | 10.70 |
| 418026 | BE379727 | Hs.83213 | fatty acid binding protein 4, adipocyte | 10.33 | 7.16 |
| 447966 | AA340605 | Hs.105887 | ESTs, Weakly similar to Homolog of rat Z | 10.09 | 9.67 |
| 401203 | | | Target Exon | 9.95 | 7.37 |
| 452308 | A1167560 | Hs.61297 | ESTs | 9.71 | 20.05 |
| 425580 | L11144 | Hs.1907 | galanin | 9.66 | 8.41 |
| 433124 | U51712 | Hs.13775 | hypothetical protein SMAP31 | 9.50 | 4.96 |
| 420919 | M57892 | Hs.100322 | carbonic anhydrase VI | 9.41 | 6.34 |
| 443162 | T49951 | Hs.9029 | DKFZP434G032 protein | 9.36 | 10.58 |
| 427666 | A1791495 | Hs.180142 | calmodulin-like skin protein (CLSP) | 9.19 | 11.73 |
| 431369 | BE184455 | Hs.251754 | secretory leukocyte protease inhibitor (| 8.85 | 17.76 |
| 408536 | AW381532 | Hs.135188 | ESTs | 8.82 | 26.43 |
| 430686 | NM_001942 | Hs.2633 | desmoglein 1 | 8.73 | 6.58 |
| 436895 | AF037335 | Hs.5338 | carbonic anhydrase XII | 8.69 | 6.81 |
| 418663 | AK001100 | Hs.41690 | desmocollin 3 | 8.61 | 9.15 |

| | | | | | | |
|----|--------|-----------|-----------|---|------|-------|
| | 429852 | AB010445 | Hs.225948 | small inducible cytokine subfamily A (Cy | 8.51 | 13.13 |
| | 424012 | AW368377 | Hs.137569 | tumor protein 63 kDa with strong homolog | 8.44 | 9.61 |
| | 430130 | AL137311 | Hs.234074 | Homo sapiens mRNA: cDNA DKFZp761G02121 (| 8.39 | 5.13 |
| | 442577 | AA292998 | Hs.163900 | ESTs | 8.34 | 7.92 |
| 5 | 437191 | NM_006846 | Hs.331555 | serine protease inhibitor, Kazal type, 5 | 8.16 | 10.08 |
| | 420859 | AW468397 | Hs.100000 | S100 calcium-binding protein A8 (calgran | 8.04 | 7.55 |
| | 413859 | AW992356 | Hs.8364 | Homo sapiens pyruvate dehydrogenase kina | 7.68 | 7.81 |
| | 452240 | AI591147 | Hs.61232 | ESTs | 7.63 | 9.39 |
| | 442757 | AI739528 | Hs.28345 | ESTs | 7.62 | 7.31 |
| 10 | 450680 | AF131784 | Hs.25318 | Homo sapiens clone 25194 mRNA sequence | 7.51 | 6.17 |
| | 456525 | AW468397 | Hs.100000 | S100 calcium-binding protein A8 (calgran | 7.49 | 7.12 |
| | 407328 | AA508857 | | ESTs, Weakly similar to ALU1_HUMAN ALU S | 7.35 | 7.20 |
| | 414217 | AI309298 | Hs.279898 | Homo sapiens cDNA: FLJ23165 fs, clone L | 7.16 | 8.39 |
| | 417240 | N57568 | Hs.48028 | EST | 7.13 | 15.05 |
| 15 | 410052 | AA525225 | Hs.334630 | Homo sapiens cDNA FLJ14462 fs, clone MA | 7.13 | 7.28 |
| | 431842 | NM_005764 | Hs.271473 | epithelial protein up-regulated in carci | 7.06 | 6.93 |
| | 426488 | X03350 | Hs.4 | alcohol dehydrogenase 1B (class I), beta | 7.03 | 7.85 |
| | 439394 | AA149250 | Hs.56105 | ESTs | 7.00 | 4.53 |
| | 422963 | M79141 | Hs.13234 | ESTs | 6.99 | 5.30 |
| 20 | 417515 | L24203 | Hs.82237 | ataxia-telangiectasia group D-associated | 6.97 | 20.68 |
| | 410530 | M25809 | Hs.64173 | ATPase, H transporting, lysosomal (vacuo | 6.96 | 7.04 |
| | 446989 | AK001898 | Hs.16740 | hypothetical protein FLJ11036 | 6.96 | 6.68 |
| | 427890 | AA435761 | | ESTs | 6.94 | 6.68 |
| | 432374 | W68815 | Hs.301885 | Homo sapiens cDNA FLJ11346 fs, clone PL | 6.84 | 8.44 |
| 25 | 429624 | AA458648 | Hs.99476 | ESTs, Weakly similar to 1313184B alpha1 | 6.83 | 6.37 |
| | 451029 | AA852097 | Hs.25829 | ras-related protein | 6.81 | 8.96 |
| | 408000 | L11690 | Hs.198689 | bulbous pemphigoid antigen 1 (230/240kD) | 6.80 | 7.68 |
| | 439496 | BE616501 | Hs.32343 | Homo sapiens, Similar to RIKEN cDNA 1110 | 6.77 | 14.06 |
| | 431713 | AK000388 | Hs.267997 | EHM2 gene | 6.72 | 7.11 |
| 30 | 451253 | H48299 | Hs.26126 | claudin 10 | 6.71 | 7.17 |
| | 414987 | AA524394 | Hs.294022 | hypothetical protein FLJ14950 | 6.67 | 11.68 |
| | 400304 | AF005082 | Hs.113261 | Homo sapiens skin-specific protein (xp33 | 6.64 | 7.90 |
| | 408063 | BE086548 | Hs.42346 | calcineurin-binding protein calcarscin-1 | 6.60 | 7.29 |
| | 424364 | AW383226 | Hs.163834 | ESTs, Weakly similar to G01763 atrophin- | 6.58 | 6.78 |
| 35 | 421773 | W69233 | Hs.112457 | ESTs | 6.55 | 17.59 |
| | 425280 | U31519 | Hs.1872 | phosphoenolpyruvate carboxykinase 1 (sol | 6.55 | 6.79 |
| | 411388 | X72925 | Hs.69752 | desmocollin 1 | 6.55 | 8.97 |
| | 401785 | | | NM_002275*:Homo sapiens keratin 15 (KRT1 | 6.51 | 9.94 |
| | 406867 | AA157857 | Hs.182265 | keratin 19 | 6.50 | 6.23 |
| 40 | 429504 | X99133 | Hs.204238 | lipocatin 2 (oncogene 24p3) (NGAL) | 6.43 | 6.79 |
| | 426106 | AI678765 | Hs.21812 | ESTs | 6.41 | 7.69 |
| | 413172 | M38180 | Hs.38586 | hydroxy-delta-5-steroid dehydrogenase, 3 | 6.39 | 7.09 |
| | 407395 | AF005082 | | gb:Homo sapiens skin-specific protein (x | 6.39 | 7.71 |
| | 422166 | W72424 | Hs.112405 | S100 calcium-binding protein A9 (calgran | 6.36 | 9.23 |
| 45 | 437176 | AW176909 | Hs.42346 | calcineurin-binding protein calcarscin-1 | 6.30 | 5.45 |
| | 440383 | AA884208 | Hs.30484 | ESTs | 6.26 | 6.25 |
| | 419329 | AY007220 | Hs.288998 | S100-type calcium binding protein A14 | 6.22 | 10.13 |
| | 418686 | Z36830 | Hs.87268 | annexin A8 | 6.19 | 6.14 |
| | 440116 | AI798851 | | hemoglobin, gamma G | 6.18 | 4.28 |
| 50 | 424049 | AB014524 | Hs.138380 | KIAA0624 protein | 6.18 | 6.91 |
| | 417366 | BE185289 | Hs.1076 | small proline-rich protein 1B (cornifin) | 6.17 | 7.42 |
| | 432543 | AA552690 | Hs.152423 | Homo sapiens cDNA: FLJ21274 fs, clone C | 6.16 | 6.86 |
| | 414449 | AA557660 | Hs.76152 | decorin | 6.15 | 3.93 |
| | 441188 | AW292830 | Hs.255609 | ESTs | 6.12 | 6.68 |
| 55 | 424008 | R02740 | Hs.137555 | putative chemokine receptor; GTP-binding | 6.12 | 5.33 |
| | 431319 | AA873350 | Hs.302232 | ESTs | 6.11 | 6.84 |
| | 444105 | AW189097 | | ESTs | 5.97 | 6.20 |
| | 428358 | AA993222 | Hs.101915 | Stargardt disease 3 (autosomal dominant) | 5.94 | 5.15 |
| | 407788 | BE514982 | Hs.38991 | S100 calcium-binding protein A2 | 5.71 | 5.83 |
| 60 | 439706 | AW872527 | Hs.59761 | ESTs, Weakly similar to DAP1_HUMAN DEATH | 5.69 | 4.49 |
| | 428566 | AL080190 | Hs.189242 | Homo sapiens mRNA: cDNA DKFZp434A202 (fr | 5.65 | 5.16 |
| | 410541 | AA065003 | Hs.64179 | syntenin-2 protein | 5.62 | 5.84 |
| | 431926 | AW972724 | | gb:EST384816 IMAGE resequences, MAGL Homo | 5.61 | 5.75 |
| | 430332 | RS1790 | Hs.239483 | Human clone 23933 mRNA sequence | 5.60 | 5.76 |
| 65 | 444946 | AW139205 | Hs.156457 | hypothetical protein FLJ22408 | 5.53 | 9.25 |
| | 430714 | AA484757 | Hs.287601 | Homo sapiens cDNA FLJ13830 fs, clone TH | 5.48 | 5.38 |
| | 435538 | AB011540 | Hs.4930 | low density lipoprotein receptor-related | 5.46 | 3.19 |
| | 414407 | AA147026 | Hs.76704 | ESTs | 5.43 | 5.29 |
| | 417035 | AA192455 | Hs.22968 | Homo sapiens clone IMAGE:451939, mRNA se | 5.40 | 5.40 |
| 70 | 442315 | AA173992 | Hs.7956 | ESTs, Moderately similar to ZN91_HUMAN Z | 5.40 | 3.87 |
| | 416931 | D45371 | Hs.80485 | adipose most abundant gene transcript 1 | 5.39 | 9.12 |
| | 431048 | R50253 | Hs.249129 | cell death-inducing DFFA-like effector a | 5.39 | 6.06 |
| | 436090 | AI640635 | Hs.332879 | EST | 5.37 | 5.33 |
| | 411274 | NM_002776 | Hs.69423 | kallikrein 10 | 5.37 | 5.97 |
| 75 | 418394 | AF132818 | Hs.84728 | Kruppel-like factor 5 (intestinal) | 5.36 | 9.35 |
| | 406706 | X03740 | Hs.231581 | myosin, heavy polypeptide 1, skeletal mu | 5.34 | 4.08 |
| | 430171 | AF086289 | Hs.234766 | skin-specific protein | 5.32 | 10.40 |
| | 452747 | BE153855 | Hs.61460 | Ig superfamily receptor LNIR | 5.31 | 6.01 |
| | 426451 | AI908165 | Hs.169946 | GATA-binding protein 3 (T-cell receptor | 5.31 | 3.81 |
| 80 | 414602 | AW630088 | Hs.76550 | Homo sapiens mRNA: cDNA DKFZp564B1264 (f | 5.26 | 5.92 |
| | 424399 | AI905687 | | AI905687:IL-BT095-190199-019 BT095 Homo | 5.25 | 16.94 |
| | 430071 | AA355986 | Hs.232068 | transcription factor 8 (represses interl | 5.20 | 5.01 |
| | 431416 | AA532718 | Hs.178604 | ESTs | 5.18 | 5.38 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|-------|
| | 420039 | NM_004605 | Hs.94581 | sulfotransferase family, cytosolic, 2B, | | |
| | 446082 | AI274139 | Hs.156452 | ESTs | 5.17 | 5.72 |
| | 430699 | AW969847 | Hs.292718 | ESTs, Weakly similar to RET2_HUMAN RETIN | 5.16 | 5.14 |
| 5 | 434625 | W01370 | Hs.46824 | ESTs | 5.14 | 4.97 |
| | 426101 | AL049987 | | Homo sapiens mRNA; cDNA DKFZp564F112 (fr | 5.12 | 6.18 |
| | 419648 | T73661 | Hs.91877 | thyroid hormone responsive SPOT14 (rat) | 5.11 | 3.79 |
| | 438962 | BE046594 | | gb:hn41c11.x1 NCI_CGAP_RDF2 Homo sapiens | 5.08 | 13.64 |
| | 419912 | AF249745 | Hs.6066 | Rho guanine nucleotide exchange factor (| 5.08 | 4.09 |
| 10 | 420583 | H77859 | Hs.65450 | reticulon 4 | 5.08 | 4.77 |
| | 432125 | AW972667 | Hs.183006 | Homo sapiens cDNA FLJ12300 fis, clone MA | 5.06 | 5.56 |
| | 445263 | H57646 | Hs.42586 | KIAA1560 protein | 5.05 | 6.32 |
| | 407839 | AA045144 | Hs.161566 | ESTs | 5.03 | 5.22 |
| | 434293 | NM_004445 | Hs.3796 | Eph86 | 5.03 | 5.27 |
| 15 | 427850 | AA416756 | Hs.161051 | ESTs, Moderately similar to ALU6_HUMAN A | 5.03 | 4.91 |
| | 414657 | AA424074 | Hs.76780 | protein phosphatase 1, regulatory (inhib | 4.99 | 16.04 |
| | 445493 | AI915771 | | metallothionein 1E (functional) | 4.94 | 8.14 |
| | 429365 | AA451798 | Hs.99249 | ESTs | 4.93 | 4.33 |
| | 412633 | AF001691 | Hs.74304 | periplakin | 4.90 | 5.19 |
| 20 | 448490 | AI523897 | Hs.271692 | ESTs, Weakly similar to I38022 hypotheti | 4.90 | 11.71 |
| | 408491 | AI08063 | Hs.7882 | ESTs | 4.85 | 4.88 |
| | 430168 | AW968343 | Hs.145582 | DKFZP434I1735 protein | 4.80 | 4.39 |
| | 407102 | AA007629 | | glycerol-3-phosphate dehydrogenase 1 (so | 4.80 | 6.05 |
| | 421998 | R74441 | | poly(A)-binding protein, nuclear 1 | 4.78 | 7.23 |
| 25 | 422633 | X56832 | Hs.118804 | enolase 3, (beta, muscle) | 4.77 | 4.78 |
| | 444930 | BE185536 | Hs.301183 | molecule possessing ankyrin repeats indu | 4.72 | 6.24 |
| | 439652 | W67826 | Hs.55412 | ESTs, Weakly similar to K1CJ_HUMAN KERAT | 4.71 | 3.72 |
| | 450626 | AW190989 | Hs.1508 | insulin-degrading enzyme | 4.70 | 3.60 |
| | 456898 | NM_001928 | Hs.155597 | D component of complement (adipsin) | 4.68 | 5.14 |
| 30 | 408239 | AA053401 | | ESTs, Moderately similar to ALU7_HUMAN A | 4.68 | 15.83 |
| | 415192 | D17793 | Hs.78183 | aldo-keto reductase family 1, member C3 | 4.67 | 6.17 |
| | 443827 | AI087867 | Hs.134667 | ESTs | 4.64 | 4.48 |
| | 431441 | U81961 | Hs.2794 | sodium channel, nonvoltage-gated 1 alpha | 4.63 | 5.06 |
| | 408741 | M73720 | Hs.646 | carboxypeptidase A3 (mast cell) | 4.63 | 8.48 |
| 35 | 427318 | AF186081 | Hs.175783 | zinc transporter | 4.63 | 3.19 |
| | 453767 | AB011792 | Hs.35094 | extracellular matrix protein 2, female o | 4.62 | 3.57 |
| | 424046 | AF027866 | Hs.138202 | serine (or cysteine) proteinase inhibito | 4.62 | 5.14 |
| | 437233 | D81448 | Hs.339352 | Homo sapiens brother of CDO (BOC) mRNA, | 4.61 | 6.80 |
| | 446525 | AW967069 | Hs.211556 | hypothetical protein MGC5487 | 4.60 | 6.19 |
| 40 | 402294 | | | Target Exon | 4.59 | 2.45 |
| | 424098 | AF077374 | Hs.139322 | small proline-rich protein 3 | 4.57 | 5.47 |
| | 420798 | W93774 | Hs.99936 | keratin 10 (epidermolytic hyperkeratosis | 4.57 | 5.12 |
| | 418021 | M15881 | Hs.1137 | uromodulin (uromucoid, Tamm-Horsfall gly | 4.57 | 4.76 |
| | 422068 | AI807519 | Hs.104520 | Homo sapiens cDNA FLJ13694 fis, clone PL | 4.54 | 4.49 |
| 45 | 414798 | AI286323 | Hs.97411 | hypothetical protein MGC12335 | 4.54 | 4.32 |
| | 410132 | NM_003480 | Hs.300946 | Microfibril-associated glycoprotein-2 | 4.53 | 3.04 |
| | 400109 | | | Eos Control | 4.53 | 2.91 |
| | 407242 | M18728 | | gb:Human nonspecific crossreacting antig | 4.52 | 3.94 |
| | 431901 | AW295050 | Hs.272023 | transforming, acidic coiled-coil contain | 4.51 | 4.07 |
| 50 | 435992 | AI033259 | Hs.118317 | Homo sapiens cDNA FLJ12088 fis, clone HE | 4.50 | 4.16 |
| | 447365 | BE383676 | Hs.334 | Rho guanine nucleotide exchange factor (| 4.50 | 4.77 |
| | 449765 | AI225235 | Hs.288300 | hypothetical protein FLJ23231 | 4.50 | 3.99 |
| | 424620 | AA101043 | Hs.151254 | kallikrein 7 (chymotryptic, stratum com | 4.49 | 4.02 |
| | 432559 | AW452948 | Hs.257631 | ESTs | 4.47 | 5.43 |
| 55 | 459290 | NM_001546 | Hs.34853 | inhibitor of DNA binding 4, dominant neg | 4.47 | 3.10 |
| | 422313 | AF045941 | Hs.115166 | scielin | 4.45 | 3.17 |
| | 416305 | AU076628 | Hs.79187 | coxackievirus and adenovirus receptor | 4.45 | 5.07 |
| | 432314 | AA533447 | Hs.312989 | ESTs | 4.44 | 5.25 |
| | 441633 | AW958544 | Hs.112242 | normal mucosa of esophagus specific 1 | 4.44 | 3.52 |
| 60 | 424670 | W61215 | Hs.116651 | epithelial V-like antigen 1 | 4.43 | 2.64 |
| | 414489 | AI620677 | Hs.73105 | ESTs | 4.42 | 4.27 |
| | 413040 | AA193338 | Hs.12321 | sodium calcium exchanger | 4.41 | 3.77 |
| | 426974 | AB002298 | Hs.173035 | KIAA0300 protein | 4.36 | 4.58 |
| | 448249 | AW855331 | Hs.337124 | ESTs | 4.35 | 4.97 |
| 65 | 451743 | AW074266 | Hs.23071 | ESTs | 4.35 | 4.49 |
| | 427919 | AA173942 | Hs.326416 | Homo sapiens mRNA; cDNA DKFZp564H1916 (f | 4.34 | 4.52 |
| | 422305 | AI928242 | Hs.293438 | ESTs, Highly similar to AF198488 1 trans | 4.33 | 3.94 |
| | 408104 | AW972927 | Hs.293968 | ESTs | 4.32 | 7.20 |
| | 447945 | AI922838 | Hs.9670 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 4.31 | 3.53 |
| 70 | 439349 | AI660898 | Hs.6834 | ESTs | 4.30 | 3.72 |
| | 433339 | AF019226 | Hs.8036 | glioblastoma overexpressed | 4.29 | 4.16 |
| | 427074 | AA527435 | Hs.178589 | hepatocellular carcinoma antigen gene 52 | 4.29 | 3.94 |
| | 453574 | AI767947 | Hs.50841 | ESTs | 4.28 | 4.97 |
| | 410677 | NM_003278 | Hs.65424 | tetranectin (plasminogen-binding protein | 4.25 | 3.66 |
| 75 | 424833 | NM_003894 | Hs.153405 | period (Drosophila) homolog 2 | 4.25 | 17.64 |
| | 426248 | T18988 | Hs.293668 | ESTs | 4.22 | 3.13 |
| | 410480 | R97457 | Hs.63984 | cadherin 13, H-cadherin (heart) | 4.21 | 4.09 |
| | 406805 | AI686003 | Hs.296031 | ESTs | 4.19 | 2.76 |
| | 438533 | AI440266 | Hs.170673 | ESTs, Weakly similar to T24832 hypotheti | 4.19 | 3.87 |
| 80 | 451831 | NM_001674 | Hs.460 | activating transcription factor 3 | 4.18 | 5.93 |
| | 431211 | M86849 | Hs.323733 | gap junction protein, beta 2, 26kD (conn | 4.18 | 4.74 |
| | 434936 | AI285970 | Hs.183817 | ESTs | 4.17 | 2.83 |
| | 430361 | AI033965 | Hs.239926 | sterol-C4-methyl oxidase-like | 4.17 | 4.39 |
| | 448429 | D17408 | Hs.21223 | calponin 1, basic, smooth muscle | 4.17 | 2.38 |
| | | | | | 4.16 | 5.15 |

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|----|--------|-----------|-----------|---|------|-------|
| 5 | 421978 | AJ243662 | Hs.110196 | NICE-1 protein | 4.15 | 8.07 |
| | 437135 | AL038624 | Hs.208752 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 4.14 | 4.92 |
| | 442554 | AW467376 | Hs.129640 | ESTs | 4.12 | 4.00 |
| | 451814 | AA847992 | Hs.137003 | ESTs | 4.11 | 4.58 |
| | 410023 | AB017169 | Hs.57929 | slit (Drosophila) homolog 3 | 4.10 | 3.92 |
| 10 | 457121 | AJ743770 | Hs.180513 | ESTs, Weakly similar to KIAA0822 protein | 4.09 | 3.19 |
| | 426539 | AB011155 | Hs.170290 | discs, large (Drosophila) homolog 5 | 4.09 | 3.69 |
| | 430191 | AI149880 | Hs.188809 | ESTs | 4.07 | 4.49 |
| | 430433 | AA478883 | Hs.273766 | ESTs | 4.07 | 3.74 |
| | 425992 | AA367069 | Hs.100636 | ESTs | 4.06 | 4.37 |
| 15 | 428931 | AA994979 | Hs.98967 | ATPase, H(+)-transporting, lysosomal, non | 4.05 | 4.15 |
| | 452392 | L20815 | Hs.507 | comeodesmosin | 4.04 | 11.00 |
| | 402845 | | | ENSP00000246267-KIAA0444 PROTEIN (FRAGME | 4.03 | 4.18 |
| | 439873 | BE159253 | Hs.300638 | ESTs | 4.03 | 3.86 |
| | 432305 | M62402 | Hs.274313 | insulin-like growth factor binding prote | 4.02 | 8.79 |
| 20 | 420789 | AJ670057 | Hs.199882 | ESTs | 4.02 | 4.34 |
| | 453560 | AA348626 | Hs.5890 | hypothetical protein FLJ23306 | 4.02 | 5.13 |
| | 428957 | NM_003881 | Hs.194679 | WNT1 inducible signaling pathway protein | 4.01 | 4.29 |
| | 429556 | AW139399 | Hs.98988 | ESTs | 4.01 | 4.59 |
| | 448585 | AB020676 | Hs.21543 | KIAA0869 protein | 4.01 | 4.52 |
| 25 | 403710 | | | C4000160.gi12735793.ref XP_011926.1 pr | 4.00 | 3.31 |
| | 423634 | AW959908 | Hs.1690 | heparin-binding growth factor binding pr | 3.98 | 6.61 |
| | 421485 | AA243499 | Hs.104800 | hypothetical protein FLJ10134 | 3.98 | 3.79 |
| | 437611 | AA897108 | | gb:am08a06.s1 Soares_NFL_T_GBC_S1 Homo s | 3.97 | 4.24 |
| | 426500 | NM_014638 | Hs.170156 | KIAA0450 gene product | 3.96 | 4.93 |
| 30 | 448710 | T62926 | Hs.304184 | ESTs | 3.96 | 4.54 |
| | 408199 | AA132637 | Hs.15396 | Homo sapiens, clone IMAGE:3948909, mRNA, | 3.95 | 5.57 |
| | 428340 | AF261088 | Hs.154721 | aconitase 1, soluble | 3.94 | 3.24 |
| | 410197 | NM_005518 | Hs.59889 | 3-hydroxy-3-methylglutaryl-Coenzyme A sy | 3.94 | 9.16 |
| | 456972 | AJ054347 | Hs.2017 | ribosomal protein L38 | 3.93 | 4.37 |
| 35 | 418381 | AA682393 | Hs.119237 | ESTs | 3.93 | 3.45 |
| | 444781 | NM_014400 | Hs.11950 | GPI-anchored metastasis-associated prote | 3.92 | 15.00 |
| | 456332 | AA228357 | | gb:nc39d05.r1 NCL_CGAP_Pr2 Homo sapiens | 3.91 | 4.88 |
| | 445607 | AA488107 | Hs.30156 | ESTs, Weakly similar to unnamed protein | 3.91 | 3.19 |
| | 426411 | AK000708 | Hs.169764 | hypothetical protein FLJ20701 | 3.90 | 4.50 |
| 40 | 446733 | AA863360 | Hs.26040 | ESTs, Weakly similar to fatty acid omega | 3.90 | 3.89 |
| | 442498 | U54617 | Hs.8364 | Homo sapiens pyruvate dehydrogenase kina | 3.89 | 5.11 |
| | 452894 | AI598065 | Hs.61558 | ESTs | 3.88 | 3.73 |
| | 430570 | AJ417881 | Hs.292464 | ESTs | 3.87 | 4.47 |
| | 439625 | AF086453 | Hs.58611 | ESTs | 3.86 | 4.81 |
| 45 | 418793 | AW382987 | Hs.88474 | prostaglandin-endoperoxide synthase 1 (p | 3.85 | 3.01 |
| | 431247 | AL021578 | Hs.278489 | matrilin 4 | 3.85 | 3.35 |
| | 426350 | NM_003245 | Hs.2022 | transglutaminase 3 (E polypeptide, prote | 3.85 | 5.15 |
| | 441319 | AJ354869 | Hs.133081 | ESTs, Weakly similar to T08700 hypothei | 3.84 | 5.03 |
| | 452877 | AJ250789 | Hs.32478 | ESTs | 3.84 | 3.26 |
| 50 | 444252 | R21135 | Hs.54985 | ESTs | 3.83 | 5.58 |
| | 416265 | AA177088 | Hs.190065 | ESTs | 3.82 | 3.87 |
| | 418875 | W19971 | Hs.233459 | ESTs | 3.80 | 2.92 |
| | 440509 | BE410132 | Hs.134202 | ESTs, Weakly similar to T17279 hypothei | 3.80 | 4.36 |
| | 442503 | AF147078 | Hs.150853 | p53-responsive gene 5 | 3.80 | 7.53 |
| 55 | 427081 | AJ474533 | Hs.170528 | ESTs, Moderately similar to ALUC_HUMAN ! | 3.77 | 4.81 |
| | 458222 | AW139592 | | hypothetical protein DKFZp434K1421 | 3.77 | 3.56 |
| | 445107 | AJ208121 | Hs.147313 | ESTs, Weakly similar to I38022 hypothei | 3.77 | 3.20 |
| | 436283 | AI480319 | Hs.120058 | ESTs | 3.76 | 3.76 |
| | 436557 | W15573 | Hs.5027 | ESTs, Weakly similar to A47582 B-cell gr | 3.76 | 2.65 |
| 60 | 448988 | Y09763 | Hs.22785 | gamma-aminobutyric acid (GABA) A recepto | 3.75 | 7.59 |
| | 434206 | AW136973 | | ESTs, Weakly similar to S69890 mitogen i | 3.72 | 3.96 |
| | 424824 | AI217440 | Hs.143873 | ESTs | 3.72 | 3.52 |
| | 457411 | AW085961 | Hs.130093 | iroquis-class homeobox protein IRX2 | 3.71 | 3.05 |
| | 452241 | AL050204 | Hs.28540 | Homo sapiens mRNA: cDNA DKFZp586F1223 (f | 3.70 | 4.84 |
| 65 | 421845 | AW021631 | Hs.16515 | ESTs | 3.69 | 3.59 |
| | 413922 | AJ535895 | Hs.221024 | ESTs | 3.68 | 4.22 |
| | 422746 | NM_004484 | Hs.119651 | glypican 3 | 3.68 | 4.29 |
| | 433934 | AW273261 | Hs.216292 | ESTs | 3.68 | 4.39 |
| | 452547 | AA335295 | Hs.74120 | adipose specific 2 | 3.66 | 12.23 |
| 70 | 400295 | W72838 | | AI905687:IL-BT095-190199-019 BT095 Homo | 3.66 | 9.25 |
| | 419098 | AA234041 | Hs.87271 | ESTs | 3.66 | 4.94 |
| | 417054 | AF017060 | | aldehyde oxidase 1 | 3.65 | 4.51 |
| | 423974 | AL118754 | | gb:DKFZp761P1910_r1 761 (synonym: hamy2) | 3.65 | 4.32 |
| | 431362 | AJ874223 | Hs.293560 | ESTs | 3.65 | 3.73 |
| 75 | 420506 | AW977779 | Hs.194613 | ESTs | 3.65 | 3.25 |
| | 448065 | AJ459177 | Hs.172759 | ESTs, Moderately similar to ALU7_HUMAN A | 3.64 | 4.62 |
| | 437457 | AA757900 | Hs.270823 | ESTs, Weakly similar to S65657 alpha-1C- | 3.64 | 4.54 |
| | 451951 | AW082870 | Hs.210954 | ESTs | 3.64 | 3.69 |
| | 436679 | AJ27483 | Hs.120451 | ESTs, Weakly similar to unnamed protein | 3.64 | 3.39 |
| 80 | 412676 | NM_000165 | Hs.74471 | gap junction protein, alpha 1, 43kD (con | 3.62 | 3.62 |
| | 412668 | AA456195 | | hypothetical protein FLJ14621 | 3.62 | 4.22 |
| | 413899 | AF083892 | Hs.75608 | tight junction protein 2 (zona occludens | 3.62 | 3.06 |
| | 444726 | NM_006147 | | interleukin regulatory factor 6 | 3.59 | 10.65 |
| | 428722 | U76456 | Hs.190787 | tissue inhibitor of metalloproteinase 4 | 3.59 | 3.31 |
| | 429973 | AJ423317 | Hs.164680 | ESTs | 3.59 | 3.71 |
| | 452413 | AW082633 | Hs.215030 | ESTs | 3.58 | 4.66 |
| | 416157 | NM_003243 | Hs.342874 | transforming growth factor, beta recepto | 3.58 | 4.44 |

| | | | | | | |
|----|--------|-----------|-----------|---|------|-------|
| | 430397 | AI924533 | Hs.105607 | bicarbonate transporter related protein | 3.57 | 3.74 |
| | 411939 | AI365585 | Hs.146246 | ESTs | 3.57 | 12.42 |
| | 450353 | AI244561 | Hs.103296 | ESTs, Weakly similar to S65657 alpha-1C- | 3.57 | 4.11 |
| 5 | 432406 | AI340571 | Hs.343666 | KIAA0969 protein | 3.57 | 2.84 |
| | 439609 | AW971945 | Hs.293236 | ESTs | 3.56 | 3.14 |
| | 435381 | AW136397 | Hs.175382 | ESTs | 3.56 | 3.48 |
| | 410173 | AA706017 | Hs.119944 | ESTs | 3.56 | 3.37 |
| | 414002 | NM_006732 | Hs.75678 | FBJ murine osteosarcoma viral oncogene h | 3.56 | 9.93 |
| 10 | 413305 | NM_000426 | Hs.323511 | Homo sapiens cDNA: FLJ23176 fis, clone L | 3.55 | 4.24 |
| | 434360 | AW015415 | Hs.127780 | ESTs | 3.55 | 4.77 |
| | 423973 | AF038461 | Hs.136574 | arachidonate 12-lipoxygenase, 12R type | 3.53 | 5.65 |
| | 425681 | AB018297 | Hs.159183 | KIAA0754 protein | 3.52 | 4.79 |
| | 428382 | AF007132 | Hs.184019 | Homo sapiens clone 23551 mRNA sequence | 3.51 | 4.46 |
| 15 | 451184 | T87943 | | transcription factor 7-like 2 (T-cell sp | 3.51 | 3.63 |
| | 448496 | BE379077 | Hs.130849 | ESTs, Weakly similar to I38022 hypothei | 3.51 | 3.30 |
| | 425831 | U46689 | Hs.159608 | aldehyde dehydrogenase 3 family, member | 3.48 | 8.66 |
| | 428232 | BE272452 | Hs.183109 | monoamine oxidase A | 3.48 | 9.54 |
| | 425483 | AF231022 | Hs.158159 | FAT tumor suppressor (Drosophila) homolo | 3.48 | 6.05 |
| 20 | 401760 | | | Target Exon | 3.48 | 7.86 |
| | 427899 | AA829286 | Hs.332053 | serum amyloid A1 | 3.47 | 3.67 |
| | 451767 | AI625014 | Hs.187328 | ESTs | 3.46 | 3.85 |
| | 452849 | AF044924 | Hs.30792 | hook2 protein | 3.45 | 5.66 |
| | 427408 | AA583206 | Hs.2156 | RAR-related orphan receptor A | 3.45 | 5.02 |
| 25 | 447165 | AL042400 | Hs.75668 | Homo sapiens, Similar to RIKEN cDNA 1700 | 3.45 | 3.61 |
| | 422083 | NM_001141 | Hs.111256 | arachidonate 15-lipoxygenase, second typ | 3.45 | 7.71 |
| | 420876 | AA918425 | Hs.177744 | ESTs | 3.44 | 8.46 |
| | 421114 | AW975051 | Hs.293156 | ESTs, Weakly similar to I78885 serine th | 3.44 | 4.47 |
| | 426233 | AA372796 | Hs.269339 | ESTs, Weakly similar to AF161356 1 HSPC0 | 3.44 | 3.96 |
| 30 | 428221 | U96781 | Hs.183075 | ATPase, Ca transporting, cardiac muscle, | 3.42 | 4.32 |
| | 403593 | | | Target Exon | 3.42 | 6.35 |
| | 423467 | AK000214 | Hs.129014 | hypothetical protein FLJ20207 | 3.42 | 3.34 |
| | 447731 | AA373527 | Hs.19385 | CGI-58 protein | 3.41 | 2.44 |
| | 456327 | H68741 | Hs.38774 | ESTs | 3.40 | 3.46 |
| 35 | 413880 | AI660842 | Hs.110915 | interleukin 22 receptor | 3.37 | 3.61 |
| | 429501 | AI700588 | Hs.293388 | ESTs, Weakly similar to A34612 zinc fing | 3.37 | 3.44 |
| | 437575 | AW954355 | Hs.36529 | hypothetical protein MGC11242 | 3.36 | 4.87 |
| | 420231 | R06866 | Hs.19813 | ESTs | 3.36 | 8.60 |
| | 424010 | AL080188 | Hs.137556 | Homo sapiens mRNA; cDNA DKFZp434A132 (fr | 3.36 | 6.20 |
| 40 | 426789 | F06596 | Hs.23837 | Homo sapiens cDNA FLJ11812 fis, clone HE | 3.34 | 3.40 |
| | 434274 | AA628539 | Hs.116252 | ESTs, Moderately similar to ALU1_HUMAN A | 3.34 | 3.35 |
| | 420693 | NM_001972 | Hs.99863 | elastase 2, neutrophil | 3.34 | 4.06 |
| | 418318 | U47732 | Hs.84072 | transmembrane 4 superfamily member 3 | 3.33 | 4.36 |
| | 413163 | Y00815 | Hs.75216 | protein tyrosine phosphatase, receptor t | 3.32 | 9.47 |
| 45 | 428496 | AA769986 | Hs.185802 | ESTs | 3.32 | 3.88 |
| | 416349 | X69089 | Hs.79227 | myomesin (M-protein) 2 (165kD) | 3.31 | 4.01 |
| | 409095 | AW337272 | Hs.293656 | ESTs, Moderately similar to S72481 proba | 3.31 | 3.31 |
| | 443072 | AI937532 | | gb:wp78d02.x1 NCI_CGAP_Bm25 Homo sapien | 3.31 | 4.40 |
| | 437586 | AA761490 | | ESTs, Moderately similar to S65657 alpha | 3.30 | 5.31 |
| 50 | 444094 | AI695764 | Hs.202394 | ESTs | 3.29 | 3.47 |
| | 437150 | R51407 | Hs.77910 | 3-hydroxy-3-methylglutaryl-Coenzyme A sy | 3.29 | 3.76 |
| | 407334 | AA494411 | Hs.296031 | ESTs | 3.28 | 4.30 |
| | 423017 | AW178761 | Hs.227948 | serine (or cysteine) proteinase inhibito | 3.28 | 3.78 |
| | 447875 | R22029 | Hs.13905 | ESTs | 3.28 | 3.44 |
| 55 | 418969 | W33191 | Hs.28907 | hypothetical protein FLJ20258 | 3.27 | 3.71 |
| | 411962 | AA099050 | | gb:zkb85d12.r1 Soares_pregnant_uterus_Nbh | 3.27 | 4.28 |
| | 424395 | AA165082 | Hs.146388 | microtubule-associated protein 7 | 3.27 | 3.82 |
| | 400494 | | | ENSP00000238970*:CIG30 (Fragment), | 3.27 | 2.60 |
| | 430418 | R98852 | Hs.36029 | heart and neural crest derivatives expre | 3.26 | 6.19 |
| 60 | 409231 | AA446644 | Hs.692 | GAT33-2 antigen; epithelial glycoprotein | 3.26 | 4.24 |
| | 434952 | T10269 | Hs.4285 | Homo sapiens cDNA: FLJ22505 fis, clone H | 3.26 | 5.17 |
| | 445234 | AW137636 | Hs.146059 | ESTs | 3.25 | 5.59 |
| | 426150 | NM_003658 | Hs.167218 | BarH-like homeobox 2 | 3.25 | 5.21 |
| | 400076 | | | Eos Control | 3.25 | 3.60 |
| 65 | 421462 | AF016495 | Hs.104624 | aquaporin 9 | 3.25 | 3.93 |
| | 420677 | AW086215 | Hs.245096 | ESTs | 3.25 | 3.53 |
| | 424125 | M31669 | Hs.1735 | inhibin, beta B (activin AB beta polypep | 3.24 | 3.88 |
| | 443672 | AA323362 | Hs.9667 | butyrobetaine (gamma), 2-oxoglutarate di | 3.24 | 5.64 |
| | 420682 | AI380552 | Hs.88602 | ESTs | 3.24 | 4.13 |
| 70 | 423725 | AJ403108 | Hs.132127 | hypothetical protein LOC57822 | 3.23 | 4.90 |
| | 431157 | AI823969 | Hs.132678 | ESTs | 3.23 | 3.97 |
| | 440469 | AA886068 | | gb:ny40e07.s1 NCI_CGAP_Pr12 Homo sapiens | 3.23 | 3.39 |
| | 449961 | AW265634 | Hs.133100 | ESTs | 3.21 | 5.36 |
| | 407948 | AW085161 | Hs.56279 | ICEBERG caspase-1 inhibitor | 3.21 | 4.61 |
| 75 | 400835 | | | chromosome 2 open reading frame 2 | 3.21 | 3.62 |
| | 413329 | AI056885 | Hs.133539 | ESTs | 3.21 | 3.43 |
| | 414825 | X06370 | Hs.77432 | epidermal growth factor receptor (avian | 3.21 | 3.72 |
| | 450860 | AA021007 | | integrin, beta 8 | 3.20 | 5.89 |
| | 444816 | Z48633 | Hs.283742 | H.sapiens mRNA for retrotransposon | 3.19 | 6.84 |
| 80 | 453855 | AA039576 | Hs.37858 | ESTs, Weakly similar to ALUB_HUMAN !!! | 3.19 | 3.59 |
| | 432278 | AL137506 | Hs.274256 | hypothetical protein FLJ23563 | 3.19 | 3.51 |
| | 420074 | AA253425 | Hs.190074 | ESTs | 3.18 | 5.50 |
| | 418481 | M81945 | | CD34 antigen | 3.18 | 3.65 |
| | 408522 | AI541214 | Hs.46320 | Small proline-rich protein SPRK [human, | 3.18 | 7.43 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|-------|
| | 435337 | AI078307 | Hs.134317 | ESTs, Weakly similar to PC4259 ferritin | 3.17 | 3.51 |
| | 445502 | AW379160 | Hs.12813 | DKFZP434J214 protein | 3.17 | 3.62 |
| | 412477 | AA150864 | | microsomal glutathione S-transferase 1 | 3.17 | 5.39 |
| 5 | 421757 | Z20897 | Hs.296259 | paraoxonase 3 | 3.16 | 3.60 |
| | 413835 | AI272727 | Hs.249163 | fatty acid hydroxylase | 3.16 | 5.56 |
| | 420309 | AW043637 | Hs.21766 | ESTs, Weakly similar to ALU5_HUMAN ALU S | 3.15 | 1.99 |
| | 444895 | AI674383 | Hs.22891 | solute carrier family 7 (cationic amino | 3.15 | 4.45 |
| | 414869 | AA157291 | Hs.21479 | ubiquitin 1 | 3.13 | 4.40 |
| | 412947 | AA122277 | | gb:zk97e09.s1 Soares_pregnant_uterus_NbH | 3.13 | 3.30 |
| 10 | 443265 | AI916207 | Hs.9167 | SH3 domain binding glutamic acid-rich pr | 3.12 | 4.62 |
| | 421335 | X99977 | Hs.103505 | ARS component B | 3.11 | 11.54 |
| | 401905 | | | ENSP00000252232::Sterol regulatory eleme | 3.10 | 2.85 |
| | 443514 | BE464288 | Hs.141937 | ESTs | 3.09 | 3.66 |
| | 418817 | AA913229 | Hs.19339 | ESTs | 3.08 | 3.88 |
| 15 | 434727 | H43374 | Hs.7890 | Homo sapiens mRNA for KIAA1671 protein, | 3.08 | 4.18 |
| | 435858 | AF254260 | Hs.283009 | tufetin 1 | 3.08 | 3.96 |
| | 430285 | AI917602 | Hs.106440 | ESTs | 3.07 | 3.30 |
| | 448106 | AI800470 | Hs.171941 | ESTs | 3.07 | 5.19 |
| | 432908 | AI861896 | | ESTs | 3.07 | 3.85 |
| 20 | 450086 | AW016343 | Hs.233301 | ESTs | 3.07 | 3.38 |
| | 451529 | AI917901 | Hs.208641 | ESTs | 3.07 | 3.29 |
| | 418443 | NM_005239 | Hs.85146 | v-els avian erythroblastosis virus E26 o | 3.06 | 4.12 |
| | 426848 | H72531 | Hs.36190 | ESTs | 3.05 | 4.34 |
| | 429506 | D49835 | Hs.171942 | ras responsive element binding protein 1 | 3.05 | 3.97 |
| 25 | 425955 | T96509 | Hs.248549 | ESTs, Moderately similar to S65657 alpha | 3.05 | 3.29 |
| | 413822 | R08950 | Hs.272044 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 3.05 | 3.89 |
| | 434230 | AA551569 | | hypothetical protein PRO2822 | 3.04 | 3.63 |
| | 453655 | AW960427 | Hs.342874 | transforming growth factor, beta recepto | 3.04 | 8.09 |
| | 415696 | AI821552 | Hs.188682 | ESTs | 3.03 | 3.43 |
| 30 | 449618 | AI076459 | Hs.15978 | KIAA1272 protein | 3.01 | 3.29 |
| | 414665 | AA160873 | | serum amyloid A1 | 3.01 | 9.22 |
| | 446682 | AW205632 | Hs.211198 | ESTs | 3.00 | 3.30 |
| | 443801 | AW206942 | Hs.253594 | intron of trichorhinophalangeal syndro | 2.99 | 3.74 |
| | 412446 | AI768015 | | ESTs | 2.99 | 4.47 |
| 35 | 449271 | AW338067 | Hs.7869 | Homo sapiens cDNA FLJ11946 fis, clone HE | 2.99 | 4.35 |
| | 435702 | AI033647 | Hs.121001 | Homo sapiens, clone IMAGE:3460280, mRNA | 2.98 | 3.49 |
| | 403180 | | | Target Exon | 2.98 | 3.92 |
| | 434442 | AA737415 | | ESTs | 2.98 | 3.61 |
| | 439593 | BE073597 | Hs.124863 | ESTs | 2.98 | 3.86 |
| 40 | 410453 | AW749036 | | gb:RC2-BT0318-241199-011-410 BT0318 Homo | 2.98 | 3.49 |
| | 414766 | AW293452 | Hs.16228 | ESTs | 2.97 | 3.63 |
| | 432566 | AW439330 | Hs.256889 | ESTs, Weakly similar to 2109260A B cell | 2.97 | 3.99 |
| | 451541 | BE279383 | Hs.26557 | plakophilin 3 | 2.97 | 6.90 |
| | 452195 | AA994712 | Hs.116878 | ESTs | 2.97 | 3.30 |
| 45 | 401747 | | | Homo sapiens keratin 17 (KRT17) | 2.97 | 4.10 |
| | 431316 | AA502663 | Hs.145037 | ESTs | 2.96 | 3.05 |
| | 445437 | AI224165 | Hs.148725 | ESTs | 2.95 | 7.12 |
| | 421690 | AW162667 | Hs.106857 | catbindin 2, (29kD, catretinin) | 2.95 | 5.68 |
| | 456371 | S76825 | Hs.89695 | insulin receptor | 2.94 | 4.59 |
| 50 | 449543 | AF070632 | Hs.23729 | Homo sapiens clone 24405 mRNA sequence | 2.94 | 4.12 |
| | 436664 | AW197887 | Hs.253353 | ESTs | 2.93 | 3.57 |
| | 406962 | M13485 | | gb:Human metallothionein I-B gene, exon | 2.93 | 2.66 |
| | 422158 | L10343 | Hs.112341 | protease inhibitor 3, skin-derived (SKAL | 2.92 | 7.48 |
| 55 | 428769 | AW207175 | Hs.106771 | ESTs | 2.92 | 3.28 |
| | 414629 | AA345824 | Hs.76688 | carboxylesterase 1 (monocyte/macrophage | 2.92 | 3.48 |
| | 444204 | AI129194 | Hs.143040 | ESTs | 2.92 | 3.92 |
| | 421407 | T82331 | Hs.182278 | ESTs, Weakly similar to CGHU6C collagen | 2.91 | 6.55 |
| | 453180 | N46243 | Hs.110373 | ESTs, Highly similar to T42626 secreted | 2.90 | 3.92 |
| | 429538 | BE182592 | Hs.139322 | small proline-rich protein 2A | 2.88 | 4.75 |
| 60 | 452554 | AW452434 | Hs.58006 | ESTs, Weakly similar to ALU5_HUMAN ALU S | 2.88 | 6.74 |
| | 417184 | N52510 | Hs.268597 | Homo sapiens cDNA: FLJ21498 fis, clone C | 2.87 | 3.97 |
| | 412093 | BE242691 | Hs.14947 | ESTs | 2.86 | 3.48 |
| | 424135 | AW994455 | Hs.140978 | Homo sapiens mRNA; cDNA DKFZp762H106 (lr | 2.86 | 3.32 |
| | 437167 | AL050184 | Hs.21610 | DKFZP434B203 protein | 2.86 | 3.87 |
| 65 | 454065 | BE394588 | | gb:G01311808F1 NIH_MGC_44 Homo sapiens c | 2.86 | 3.43 |
| | 420230 | AL034344 | Hs.284186 | forkhead box C1 | 2.85 | 3.67 |
| | 403108 | | | ENSP00000241415::Hypothetical 67.7 kDa p | 2.85 | 2.62 |
| | 434433 | AW629759 | | gb:hh70e05.y1 NCI_CGAP_GU1 Homo sapiens | 2.84 | 3.35 |
| 70 | 420544 | AA677577 | Hs.98732 | Homo sapiens Chromosome 16 BAC clone CIT | 2.83 | 2.66 |
| | 429429 | AA829725 | Hs.334437 | hypothetical protein MGC4248 | 2.83 | 3.59 |
| | 451721 | NM_006946 | Hs.26915 | spectrin, beta, non-erythrocytic 2 | 2.83 | 3.36 |
| | 424982 | U94777 | | phosphorylase, glycogen; muscle (McArdle | 2.83 | 4.50 |
| | 429259 | AA420450 | Hs.292911 | Plakophilin | 2.81 | 4.81 |
| | 423523 | AW299828 | Hs.193580 | ESTs | 2.80 | 7.08 |
| 75 | 433637 | AW024214 | Hs.102307 | ESTs | 2.80 | 3.39 |
| | 452089 | T97294 | Hs.271492 | ESTs, Weakly similar to PC4211 hepatocel | 2.80 | 3.62 |
| | 441187 | AW195237 | Hs.7734 | hypothetical protein FLJ22174 | 2.80 | 3.52 |
| | 421965 | AA301100 | Hs.346482 | gb:EST14128 Testis tumor Homo sapiens cD | 2.79 | 3.49 |
| | 432098 | AF252297 | Hs.91546 | cytochrome P450 retinoid metabolizing pr | 2.79 | 2.31 |
| 80 | 429128 | AA445869 | Hs.119316 | ESTs | 2.78 | 4.17 |
| | 438913 | AI380429 | Hs.172445 | ESTs | 2.77 | 3.65 |
| | 445029 | AF196481 | | midline 2 | 2.76 | 3.79 |
| | 419923 | AW081455 | Hs.120219 | ESTs | 2.76 | 3.00 |

| | | | | | | |
|----|--------|---------------|-----------|--|------|-------|
| 5 | 416508 | R39769 | Hs.56406 | ESTs, Moderately similar to ALU8_HUMAN A | 2.76 | 3.59 |
| | 412507 | L36645 | Hs.73964 | EphA4 | 2.76 | 3.90 |
| | 446339 | ALD46962 | Hs.14845 | forkhead box O3A | 2.75 | 3.50 |
| | 433710 | AI341867 | Hs.188920 | ESTs | 2.75 | 3.33 |
| | 432375 | BE536089 | Hs.2962 | PTK6 protein tyrosine kinase 6 | 2.74 | 5.77 |
| 10 | 409213 | U61412 | Hs.51133 | S100 calcium-binding protein P | 2.74 | 3.76 |
| | 426653 | AA530892 | Hs.171695 | dual specificity phosphatase 1 | 2.74 | 8.19 |
| | 408839 | AW277084 | | gb:xp61h09.x1 NCL_CGAP_Ov39 Homo sapiens | 2.73 | 3.93 |
| | 433091 | Y12642 | Hs.3185 | lymphocyte antigen 6 complex, locus D | 2.73 | 11.46 |
| | 444026 | AA205759 | Hs.10119 | hypothetical protein FLJ14957 | 2.73 | 6.17 |
| 15 | 433713 | AW976511 | Hs.112592 | ESTs | 2.72 | 3.42 |
| | 453317 | NM_002277 | Hs.41696 | keratin, hair, acidic, 1 | 2.72 | 4.76 |
| | 408493 | BE206854 | Hs.46039 | phosphoglycerate mutase 2 (muscle) | 2.72 | 3.74 |
| | 432947 | AA570710 | Hs.270998 | ESTs, Weakly similar to I38022 hypothe | 2.72 | 3.44 |
| | 421428 | U26726 | Hs.1376 | hydroxysteroid (11-beta) dehydrogenase 2 | 2.72 | 4.95 |
| 20 | 423217 | NM_000094 | Hs.1640 | collagen, type VII, alpha 1 (epidermolys | 2.72 | 4.29 |
| | 435016 | AI284219 | Hs.130749 | ESTs, Weakly similar to I38022 hypothe | 2.71 | 4.45 |
| | 449667 | AB023227 | Hs.23860 | KIAA1010 protein | 2.71 | 3.72 |
| | 407112 | AA070801 | Hs.51615 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 2.70 | 3.82 |
| | 433848 | AF095719 | Hs.93764 | carboxypeptidase A4 | 2.70 | 2.76 |
| 25 | 430152 | AB001325 | Hs.234642 | aquaporin 3 | 2.69 | 4.26 |
| | 456063 | NM_006744 | Hs.76461 | retinol-binding protein 4, interstitial | 2.69 | 6.72 |
| | 424471 | AA341329 | Hs.311524 | ESTs | 2.68 | 4.57 |
| | 453201 | AI432195 | Hs.135098 | ESTs | 2.68 | 3.69 |
| | 450912 | AW939251 | Hs.25647 | v-fos FBJ murine osteosarcoma viral onco | 2.68 | 4.25 |
| 30 | 404996 | | | Target Exon | 2.67 | 4.28 |
| | 409453 | AI885516 | Hs.95612 | ESTs | 2.65 | 6.51 |
| | 430937 | X53463 | Hs.2704 | glutathione peroxidase 2 (gastrointestin | 2.65 | 3.78 |
| | 452887 | AI702223 | Hs.107253 | hypothetical protein DKFZp761F241 | 2.64 | 6.38 |
| | 444169 | AV648170 | Hs.58756 | ESTs | 2.64 | 3.40 |
| 35 | 428500 | AI815395 | Hs.184641 | fatty acid desaturase 2 | 2.64 | 3.47 |
| | 408395 | BE072425 | Hs.44579 | hypothetical protein FLJ20199 | 2.64 | 4.01 |
| | 432093 | H28383 | | gb:y152c03.r1 Soares breast 3NbHBst Homo | 2.63 | 4.08 |
| | 451621 | AI879148 | Hs.26770 | fatty acid binding protein 7, brain | 2.62 | 2.51 |
| | 447335 | BE617695 | Hs.286192 | hypothetical protein FLJ20940 | 2.61 | 3.62 |
| 40 | 429343 | AK000785 | Hs.199480 | Homo sapiens, Similar to epsin 3, clone | 2.61 | 3.68 |
| | 431166 | AW971186 | Hs.293839 | ESTs | 2.61 | 3.33 |
| | 440659 | AF134160 | Hs.7327 | claudin 1 | 2.61 | 3.53 |
| | 413542 | BE295928 | Hs.75424 | inhibitor of DNA binding 1, dominant neg | 2.61 | 4.48 |
| | 413956 | AI821351 | Hs.193133 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 2.60 | 3.51 |
| 45 | 407299 | AA460205 | Hs.289770 | ESTs, Weakly similar to I38022 hypothe | 2.59 | 3.82 |
| | 449539 | W80363 | Hs.58446 | ESTs | 2.58 | 4.05 |
| | 413884 | AI668892 | Hs.239758 | hypothetical protein FLJ12389 similar to | 2.58 | 4.19 |
| | 445620 | AI245225 | Hs.17441 | ESTs | 2.57 | 3.44 |
| | 433688 | AA628467 | Hs.112572 | Homo sapiens cDNA FLJ14130 fis, clone MA | 2.56 | 3.57 |
| 50 | 424834 | AK001432 | Hs.153408 | Homo sapiens cDNA FLJ10570 fis, clone NT | 2.56 | 3.47 |
| | 407083 | Z48511 | | H.sapiens XG mRNA (clone PEP11) | 2.55 | 3.61 |
| | 406790 | AA293303 | | ribosomal protein L27a | 2.54 | 4.36 |
| | 450472 | AI190071 | Hs.55278 | ESTs | 2.54 | 4.30 |
| | 410310 | J02931 | Hs.62192 | coagulation factor III (thromboplastin, | 2.54 | 3.82 |
| 55 | 454034 | NM_000691 | Hs.575 | aldehyde dehydrogenase 3 family, member | 2.54 | 3.44 |
| | 430821 | AA487264 | Hs.154974 | Homo sapiens mRNA: cDNA DKFZp667N064 (fr | 2.54 | 4.55 |
| | 402575 | | | Rho GTPase activating protein 1 | 2.53 | 5.47 |
| | 429554 | NM_012275 | Hs.207224 | interleukin 1, delta | 2.53 | 2.40 |
| | 431631 | AA548906 | Hs.122244 | ESTs | 2.52 | 3.79 |
| 60 | 408806 | AW847814 | Hs.75608 | Homo sapiens cDNA: FLJ21532 fis, clone C | 2.52 | 4.51 |
| | 420235 | AA256756 | Hs.31178 | ESTs | 2.51 | 4.21 |
| | 436314 | AI983409 | | ESTs | 2.51 | 3.11 |
| | 432906 | BE265489 | Hs.3123 | lethal giant larvae (Drosophila) homolog | 2.50 | 5.62 |
| | 429547 | AW009165 | Hs.99376 | FGFENSH predicted novel secreted protein | 2.49 | 2.60 |
| 65 | 410532 | T53088 | Hs.155376 | hemoglobin, beta | 2.49 | 4.73 |
| | 413475 | AW021488 | Hs.26981 | ESTs | 2.49 | 3.90 |
| | 429325 | AW088739 | Hs.243770 | ESTs | 2.48 | 3.71 |
| | 424604 | AW865388 | Hs.151076 | KIAA1243 protein | 2.48 | 4.16 |
| | 414320 | U13616 | Hs.75893 | ankyrin 3, node of Ranvier (ankyrin G) | 2.48 | 3.80 |
| 70 | 423929 | M69136 | Hs.135626 | chymase 1, mast cell | 2.48 | 3.47 |
| | 410275 | U85658 | Hs.61796 | transcription factor AP-2 gamma (activat | 2.47 | 2.09 |
| | 444935 | AA262449 | Hs.223569 | ESTs | 2.47 | 5.96 |
| | 445389 | NM_016831 | Hs.12582 | period (Drosophila) homolog 3 | 2.47 | 3.41 |
| | 437897 | AA770561 | Hs.146170 | hypothetical protein FLJ22969 | 2.47 | 6.80 |
| 75 | 446292 | AF081497 | Hs.279682 | Rh type C glycoprotein | 2.46 | 7.37 |
| | 409178 | BE393948 | Hs.50915 | kallikrein 5 | 2.46 | 5.59 |
| | 452865 | AI924046 | Hs.119567 | ESTs, Weakly similar to A47582 B-cell gr | 2.46 | 6.03 |
| | 447179 | AW015633 | Hs.157299 | CCAAT/enhancer binding protein (C/EBP), | 2.46 | 3.23 |
| | 414459 | Y11525 | Hs.76171 | transglutaminase 1 (K polypeptide epider | 2.45 | 3.94 |
| 80 | 428188 | M98447 | Hs.22 | degenerative spermatocytia (homolog Dros | 2.44 | 2.17 |
| | 428593 | AW207440 | Hs.185973 | ESTs | 2.44 | 2.94 |
| | 436009 | H57130 | Hs.120925 | platelet-derived growth factor receptor, | 2.43 | 3.61 |
| | 412810 | M21574 | Hs.74615 | fibulin 1 | 2.43 | 4.46 |
| | 416749 | AW068550.comp | Hs.79732 | laminin, alpha 5 | 2.42 | 6.39 |
| | 444672 | Z95636 | Hs.11669 | ESTs, Weakly similar to ALU5_HUMAN ALU S | 2.42 | 3.45 |
| | 433143 | BE552155 | Hs.294035 | metallothionein IV | 2.42 | 3.92 |
| | 406997 | U07807 | | | | |

| | | | | | | |
|----|--------|-----------|-----------|---|------|-------|
| 5 | 423184 | NM_004428 | Hs.1624 | ephrin-A1 | 2.41 | 4.34 |
| | 421321 | NM_005309 | Hs.103502 | glutamic-pyruvate transaminase (alanine | 2.41 | 5.08 |
| | 456826 | AJ871742 | Hs.302428 | wingless-type MMTV integration site fami | 2.41 | 3.92 |
| | 428897 | AJ245719 | Hs.194385 | hypothetical protein FLJ20234 | 2.41 | 5.18 |
| | 400232 | | | NM_001895*:Homo sapiens casein kinase 2, | 2.41 | 3.82 |
| 10 | 421481 | AW391972 | Hs.104596 | KIAA1324 protein | 2.40 | 4.03 |
| | 442083 | R50192 | Hs.165062 | ESTs | 2.39 | 4.21 |
| | 422287 | F16365 | Hs.114346 | cytochrome c oxidase subunit VIIa polype | 2.39 | 8.60 |
| | 418004 | U37519 | Hs.87539 | aldehyde dehydrogenase 3 family, member | 2.39 | 2.57 |
| | 457008 | AA410446 | Hs.112011 | ESTs, Weakly similar to unknown (H.sapie | 2.39 | 3.85 |
| 15 | 418355 | L42563 | Hs.1165 | ATPase, H? transporting, nongastric, atp | 2.38 | 3.84 |
| | 431179 | AJ338644 | Hs.195432 | aldehyde dehydrogenase 2 family (mitocho | 2.37 | 7.89 |
| | 432563 | NM_013261 | Hs.198468 | peroxisome proliferative activated recep | 2.37 | 3.77 |
| | 402338 | | | Target Exon | 2.37 | 3.46 |
| | 443725 | AW245680 | Hs.9701 | growth arrest and DNA-damage-inducible, | 2.37 | 4.57 |
| 20 | 436723 | AW975895 | Hs.307486 | ESTs | 2.37 | 6.39 |
| | 452669 | AA216363 | Hs.262958 | hypothetical protein DKFZp434B044 | 2.37 | 3.92 |
| | 409212 | AJ082423 | Hs.141892 | ESTs | 2.36 | 3.79 |
| | 451323 | AJ903313 | Hs.34579 | ESTs, Moderately similar to ALU5_HUMAN A | 2.35 | 3.29 |
| | 400307 | AF005081 | | Homo sapiens skin-specific protein (xp32 | 2.35 | 9.96 |
| 25 | 421993 | R22497 | Hs.110571 | growth arrest and DNA-damage-inducible, | 2.35 | 5.16 |
| | 451092 | AJ207256 | Hs.13766 | Homo sapiens mRNA for FLJ00074 protein, | 2.34 | 5.24 |
| | 446948 | BE409053 | Hs.299629 | peroxisomal long-chain acyl-coA thioeste | 2.34 | 3.77 |
| | 424425 | AB031480 | Hs.146824 | SPR1 protein | 2.34 | 4.43 |
| | 426050 | AF017307 | Hs.166096 | E74-like factor 3 (ets domain transcript | 2.34 | 5.64 |
| 30 | 425180 | U00115 | Hs.155024 | B-cell CLL/lymphoma 6 (zinc finger prote | 2.33 | 3.51 |
| | 422106 | D84239 | Hs.111732 | Fc fragment of IgG binding protein | 2.33 | 6.95 |
| | 423503 | M92843 | Hs.343586 | zinc finger protein homologous to Zfp-36 | 2.33 | 5.57 |
| | 453999 | BE328153 | Hs.240087 | ESTs | 2.32 | 3.40 |
| | 419358 | T78763 | Hs.90063 | neurocalcin delta | 2.32 | 6.72 |
| 35 | 430468 | NM_004673 | Hs.241519 | angiotensin-like 1 | 2.32 | 3.90 |
| | 456876 | AL044870 | Hs.208780 | ESTs, Weakly similar to T29647 hypothesi | 2.32 | 3.27 |
| | 454947 | AW846590 | | gb:QV0-CT0180-011099-025-d07 CT0180 Homo | 2.32 | 4.43 |
| | 429211 | AF052693 | Hs.198249 | gap junction protein, beta 5 (connexin 3 | 2.31 | 7.22 |
| | 438282 | BE268288 | Hs.195432 | aldehyde dehydrogenase 2 family (mitocho | 2.31 | 3.34 |
| 40 | 420202 | AL036557 | Hs.95910 | putative lymphocyte G0/G1 switch gene | 2.31 | 8.47 |
| | 419245 | AJ732742 | Hs.87440 | ESTs | 2.31 | 3.39 |
| | 444920 | AW450967 | Hs.235240 | ESTs | 2.30 | 3.30 |
| | 417314 | N68168 | | gb:za11c01.s1 Soares fetal liver spleen | 2.30 | 3.12 |
| | 409586 | AL050214 | Hs.55044 | DKFZP586H2123 protein | 2.30 | 3.52 |
| 45 | 433662 | V07162 | Hs.150826 | RAB25 RAB25, member RAS oncogene family | 2.29 | 6.11 |
| | 451176 | AA046457 | Hs.60677 | ESTs | 2.29 | 6.59 |
| | 410531 | AW752953 | | gb:QV0-CT0224-261099-035-g02 CT0224 Homo | 2.29 | 3.29 |
| | 425982 | R05327 | Hs.189726 | ESTs | 2.29 | 3.37 |
| | 435684 | NM_001290 | Hs.4980 | LIM domain binding 2 | 2.29 | 4.54 |
| 50 | 453003 | AA808466 | Hs.103395 | hypothetical protein FLJ14146 | 2.28 | 3.70 |
| | 434411 | AA632649 | Hs.201372 | ESTs | 2.28 | 4.40 |
| | 407394 | AF005081 | | gb:Homo sapiens skin-specific protein (x | 2.28 | 10.57 |
| | 411579 | AC005258 | Hs.70830 | U6 snRNA-associated Sm-like protein LSM7 | 2.28 | 4.06 |
| | 401205 | | | Target Exon | 2.27 | 2.71 |
| 55 | 443102 | AJ247472 | Hs.132965 | ESTs | 2.27 | 5.66 |
| | 422109 | S73265 | Hs.1473 | gastrin-releasing peptide | 2.26 | 3.94 |
| | 434987 | AW975114 | | ESTs | 2.26 | 3.72 |
| | 415477 | NM_002228 | Hs.78465 | v-jun avian sarcoma virus 17 oncogene ho | 2.26 | 3.42 |
| | 423515 | AA327017 | Hs.176594 | ESTs | 2.25 | 6.21 |
| 60 | 434903 | AF161369 | Hs.187763 | Homo sapiens HSPC106 mRNA, partial cds | 2.25 | 3.62 |
| | 443049 | AJ028613 | Hs.132343 | ESTs | 2.25 | 3.13 |
| | 444637 | T19101 | Hs.11494 | fibulin 5 | 2.24 | 6.43 |
| | 410026 | AJ912061 | Hs.55016 | hypothetical protein FLJ21935 | 2.23 | 3.31 |
| | 418629 | BE247550 | Hs.86859 | growth factor receptor-bound protein 7 | 2.23 | 4.17 |
| 65 | 429587 | AA283969 | Hs.334706 | Homo sapiens cDNA FLJ11801 fis, clone HE | 2.23 | 3.79 |
| | 431986 | AA536130 | Hs.149018 | Novel human gene mapping to chromosome 20 | 2.22 | 3.54 |
| | 409571 | AA504249 | Hs.187585 | ESTs | 2.22 | 3.87 |
| | 446051 | BE048061 | Hs.37054 | ephrin-A3 | 2.22 | 4.57 |
| | 422418 | AK001383 | Hs.116385 | hypothetical protein FLJ10521 | 2.21 | 4.25 |
| 70 | 453023 | AW028733 | Hs.31439 | serine protease inhibitor, Kunitz type, | 2.21 | 5.07 |
| | 435748 | AA699756 | Hs.117335 | ESTs | 2.20 | 3.35 |
| | 420105 | AW015571 | Hs.32244 | ESTs, Weakly similar to FMOD_HUMAN FIBRO | 2.19 | 6.55 |
| | 444922 | AJ921750 | Hs.144871 | Homo sapiens cDNA FLJ13752 fis, clone PL | 2.19 | 3.51 |
| | 433052 | AW971983 | Hs.293003 | ESTs, Weakly similar to PC4259 femiun | 2.19 | 3.32 |
| 75 | 430310 | U60115 | Hs.239069 | four and a half LIM domains 1 | 2.19 | 3.83 |
| | 447205 | BE617015 | Hs.11006 | ESTs, Moderately similar to T17372 plasm | 2.19 | 15.65 |
| | 449967 | R40978 | Hs.271498 | ESTs, Moderately similar to ALU1_HUMAN A | 2.18 | 3.54 |
| | 452689 | F33868 | Hs.284176 | transferrin | 2.18 | 3.30 |
| | 417061 | AJ675944 | Hs.188591 | Homo sapiens cDNA FLJ12033 fis, clone HE | 2.18 | 3.77 |
| 80 | 432647 | AJ807481 | Hs.278581 | fibroblast growth factor receptor 2 (bac | 2.18 | 5.64 |
| | 401192 | | | Target Exon | 2.17 | 3.33 |
| | 421752 | AK001521 | Hs.107882 | hypothetical protein FLJ10659 | 2.16 | 3.44 |
| | 456646 | AJ243662 | Hs.110196 | NICE-1 protein | 2.16 | 2.39 |
| | 421263 | AB020638 | Hs.103000 | KIAA0831 protein | 2.16 | 3.37 |
| | 445656 | W22050 | Hs.21299 | ESTs, Weakly similar to AF151840 1 CGI-8 | 2.16 | 5.17 |
| | 450624 | AL043983 | Hs.125063 | Homo sapiens cDNA FLJ13825 fis, clone TH | 2.15 | 3.87 |
| | 429350 | AJ754634 | Hs.131987 | ESTs | 2.15 | 3.90 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|------|
| | 448144 | AW169230 | | ESTs, Moderately similar to PC4259 ferri | 2.14 | 3.28 |
| | 429002 | AW248439 | Hs.2340 | junction plakoglobin | 2.14 | 5.05 |
| | 429297 | X82494 | Hs.198862 | fibulin 2 | 2.14 | 4.32 |
| 5 | 452093 | AA447453 | Hs.27860 | Homo sapiens mRNA; cDNA DKFZp586M0723 (f | 2.14 | 3.99 |
| | 428848 | NM_000230 | Hs.194236 | leptin (murine obesity homolog) | 2.14 | 3.39 |
| | 407584 | W25945 | Hs.8173 | hypothetical protein FLJ10803 | 2.14 | 3.38 |
| | 453155 | AF052126 | Hs.552 | steroid-5-alpha-reductase, alpha polypep | 2.14 | 2.51 |
| | 453283 | AA694386 | Hs.290914 | ESTs | 2.13 | 3.28 |
| 10 | 456906 | AF117646 | Hs.156637 | Cas-Br-M (murine) ectropic retroviral tr | 2.13 | 3.76 |
| | 414815 | AW292140 | Hs.130286 | ESTs | 2.13 | 4.16 |
| | 417155 | T75125 | Hs.299148 | hypothetical protein FLJ21801 | 2.13 | 3.57 |
| | 416673 | T77052 | Hs.14039 | ESTs | 2.13 | 3.43 |
| | 452208 | AA024792 | Hs.31895 | hypothetical protein MGC4093 | 2.12 | 5.67 |
| 15 | 413966 | AA133935 | Hs.173704 | ESTs, Moderately similar to A53959 throm | 2.12 | 4.76 |
| | 430967 | H16791 | Hs.100895 | ESTs | 2.12 | 2.64 |
| | 429015 | BE168484 | Hs.194737 | KIAA0453 protein | 2.12 | 3.30 |
| | 439518 | W76326 | | gb:zd60d04.r1 Soares_fetal_heart_NbHH19W | 2.11 | 2.59 |
| | 426468 | AA379306 | Hs.117558 | ESTs | 2.10 | 3.56 |
| 20 | 407555 | Z48511 | | gb:H.sapiens XG mRNA (clone PEP11). | 2.10 | 3.66 |
| | 418226 | AA424202 | Hs.83834 | cytochrome b-5 | 2.10 | 5.14 |
| | 423441 | R68649 | Hs.278359 | absent in melanoma 1 like | 2.10 | 3.64 |
| | 436961 | AW375974 | Hs.156704 | ESTs | 2.10 | 3.21 |
| | 432633 | A1796390 | Hs.210667 | ESTs | 2.10 | 2.58 |
| 25 | 426102 | AF200496 | Hs.166371 | interleukin 1, zeta | 2.09 | 3.77 |
| | 445467 | AJ239832 | Hs.15617 | ESTs, Weakly similar to ALU4_HUMAN ALU S | 2.09 | 3.85 |
| | 437124 | AA554458 | | KIAA0666 protein | 2.09 | 3.35 |
| | 407757 | BE048414 | Hs.165215 | hypothetical protein MGC5395 | 2.08 | 4.41 |
| | 407815 | AW373860 | Hs.183860 | hypothetical protein FLJ20277 | 2.08 | 5.01 |
| 30 | 443906 | AA348031 | Hs.7913 | ESTs | 2.08 | 3.40 |
| | 423887 | AL080207 | Hs.134585 | DKFZP434G232 protein | 2.08 | 3.92 |
| | 406400 | | | kallikrein 8 (neurosin/ovasin) (KLK8) | 2.08 | 4.19 |
| | 437704 | AA766142 | Hs.131810 | ESTs, Moderately similar to ALU1_HUMAN A | 2.07 | 3.30 |
| | 412533 | AA679863 | Hs.69606 | ESTs | 2.07 | 3.39 |
| 35 | 426310 | NM_000909 | Hs.169256 | neuropeptide Y receptor Y1 | 2.06 | 3.55 |
| | 411821 | BE299339 | Hs.72249 | three-PDZ containing protein similar to | 2.06 | 4.98 |
| | 442599 | AF078037 | Hs.324051 | RelA-associated inhibitor | 2.06 | 7.23 |
| | 432212 | AW137742 | | ESTs | 2.04 | 3.52 |
| | 453469 | AB014533 | Hs.33010 | KIAA0633 protein | 2.04 | 4.01 |
| 40 | 443652 | AJ080692 | Hs.134229 | ESTs, Weakly similar to I54401 hypertens | 2.04 | 3.36 |
| | 452955 | AW390282 | Hs.31130 | transmembrane 7 superfamily member 2 | 2.03 | 3.64 |
| | 424464 | R68537 | Hs.17962 | ESTs | 2.03 | 4.36 |
| | 408702 | AW959893 | Hs.27099 | hypothetical protein FLJ23293 similar to | 2.03 | 3.31 |
| | 439908 | A1168031 | Hs.155507 | ESTs | 2.03 | 3.83 |
| 45 | 412825 | AW167439 | Hs.190651 | Homo sapiens cDNA FLJ13625 fis, clone PL | 2.02 | 5.56 |
| | 406784 | A1144297 | Hs.169401 | apolipoprotein E | 2.02 | 3.40 |
| | 427309 | NM_005714 | Hs.175218 | potassium channel, subfamily K, member 7 | 2.02 | 4.58 |
| | 453195 | BE241876 | Hs.32352 | hypothetical protein DKFZp434K1210 | 2.02 | 3.57 |
| | 404246 | | | Target Exon | 2.01 | 7.30 |
| 50 | 443679 | AK001810 | Hs.9670 | hypothetical protein FLJ10948 | 2.01 | 5.81 |
| | 410669 | AW805749 | | superoxide dismutase 2, mitochondrial | 2.01 | 3.05 |
| | 446193 | AJ279390 | Hs.144658 | ESTs, Weakly similar to T17257 hypothi | 2.01 | 2.32 |
| | 449228 | AJ403107 | Hs.148590 | protein related with psoriasis | 2.00 | 5.10 |
| 55 | 434346 | AA630445 | | ESTs | 2.00 | 3.51 |
| | 456098 | AW747800 | Hs.55016 | hypothetical protein FLJ21935 | 2.00 | 4.96 |
| | 452467 | AW500815 | | ESTs | 2.00 | 4.66 |
| | 442866 | AJ743317 | Hs.283622 | ESTs, Weakly similar to ALU5_HUMAN ALU S | 1.98 | 3.72 |
| | 434699 | AA643687 | Hs.149425 | Homo sapiens cDNA FLJ11980 fis, clone HE | 1.98 | 3.11 |
| | 417553 | L09190 | | trichohyalin | 1.98 | 2.09 |
| 60 | 449142 | R15913 | Hs.194987 | ESTs | 1.98 | 3.50 |
| | 407597 | AA043925 | Hs.339352 | Homo sapiens brother of CDO (BOC) mRNA, | 1.98 | 6.25 |
| | 429299 | A1620463 | Hs.347408 | hypothetical protein MGC13102 | 1.97 | 3.77 |
| | 423031 | AJ278995 | | ESTs | 1.97 | 3.62 |
| | 433495 | AW373784 | Hs.71 | alpha-2-glycoprotein 1, zinc | 1.96 | 4.57 |
| 65 | 430420 | AW140027 | Hs.26373 | Homo sapiens cDNA: FLJ23449 fis, clone H | 1.96 | 6.09 |
| | 420139 | NM_005357 | Hs.95351 | lipase, hormone-sensitive | 1.95 | 5.77 |
| | 418462 | BE001596 | Hs.85266 | integrin, beta 4 | 1.95 | 6.09 |
| | 447261 | NM_006691 | Hs.17917 | extracellular link domain-containing 1 | 1.95 | 3.33 |
| 70 | 437220 | AL117542 | Hs.334305 | GS1999full | 1.94 | 3.45 |
| | 407601 | AC002300 | Hs.37129 | sodium channel, nonvoltage-gated 1, beta | 1.94 | 5.46 |
| | 443595 | AF169312 | Hs.9613 | PPAR(gamma) angiotensin related protein | 1.94 | 4.67 |
| | 409007 | AL122107 | Hs.49599 | Homo sapiens mRNA; cDNA DKFZp434G0827 (f | 1.94 | 3.59 |
| | 408717 | AF045458 | Hs.47061 | unc-51 (C. elegans)-like kinase 1 | 1.94 | 4.29 |
| | 420055 | NM_001487 | Hs.94672 | GCN5 (general control of amino-acid synt | 1.94 | 3.38 |
| 75 | 430392 | NM_000627 | Hs.241257 | latent transforming growth factor beta b | 1.93 | 3.75 |
| | 425078 | NM_002599 | Hs.154437 | phosphodiesterase 2A, cGMP-stimulated | 1.93 | 4.06 |
| | 423527 | AJ206965 | Hs.105861 | hypothetical protein FLJ13824 | 1.93 | 4.70 |
| | 447151 | AJ022813 | Hs.92679 | Homo sapiens clone CDABP0014 mRNA sequen | 1.91 | 3.77 |
| 80 | 422101 | AW404176 | Hs.111611 | ribosomal protein L27 | 1.91 | 3.18 |
| | 456653 | AJ807519 | Hs.104520 | Homo sapiens cDNA FLJ13694 fis, clone PL | 1.91 | 3.41 |
| | 443444 | AW952619 | Hs.17235 | Homo sapiens clone TCCIA00176 mRNA sequ | 1.91 | 3.52 |
| | 420924 | R01026 | Hs.245321 | ESTs | 1.91 | 3.22 |
| | 426048 | AJ768853 | Hs.134478 | ESTs | 1.90 | 3.56 |
| | 414092 | Z14244 | Hs.75752 | cytochrome c oxidase subunit VIIb | 1.90 | 4.15 |

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|----|--------|-----------|-----------|--|------|------|
| 5 | 415274 | AF001548 | Hs.78344 | myosin, heavy polypeptide 11, smooth mus | 1.90 | 5.88 |
| | 428368 | BE440042 | Hs.83326 | matrix metalloproteinase 3 (stromelysin | 1.90 | 2.28 |
| | 418418 | R61527 | Hs.237517 | ESTs | 1.90 | 3.56 |
| | 449372 | AA001266 | Hs.133521 | ESTs | 1.89 | 3.90 |
| | 438752 | AW238673 | Hs.146038 | ESTs | 1.89 | 5.24 |
| 10 | 428193 | NM_004235 | | Kruppel-like factor 4 (gut) | 1.89 | 5.21 |
| | 433251 | AB040955 | Hs.322735 | KIAA1522 protein | 1.89 | 5.00 |
| | 430560 | Z28942 | Hs.243960 | N-myc downstream-regulated gene 2 | 1.89 | 7.09 |
| | 427795 | BE268268 | Hs.180842 | ribosomal protein L13 | 1.89 | 4.51 |
| | 410209 | AI583661 | Hs.60548 | hypothetical protein PRO1635 | 1.89 | 3.35 |
| 15 | 449243 | AW295031 | Hs.198671 | ESTs | 1.89 | 4.26 |
| | 420225 | AW243046 | Hs.282076 | Homo sapiens mRNA for KIAA1650 protein, | 1.88 | 6.20 |
| | 443932 | AW888222 | Hs.9973 | tensin | 1.88 | 9.28 |
| | 427929 | BE613835 | Hs.181159 | Homo sapiens mRNA; cDNA DKFZp434F0217 (f | 1.87 | 4.25 |
| | 400078 | | | Eos Control | 1.87 | 6.73 |
| 20 | 422639 | AI929377 | Hs.173724 | creatine kinase, brain | 1.87 | 5.51 |
| | 447374 | AF263462 | Hs.18376 | KIAA1319 protein | 1.87 | 3.42 |
| | 430346 | AK000331 | Hs.297641 | KIAA0462 protein | 1.87 | 4.15 |
| | 428223 | AA424313 | Hs.98402 | ESTs | 1.87 | 3.70 |
| | 408792 | L29433 | Hs.47913 | coagulation factor X | 1.87 | 4.08 |
| 25 | 433855 | AA834082 | Hs.307559 | ESTs | 1.87 | 4.16 |
| | 451583 | AI653797 | Hs.24133 | ESTs | 1.87 | 3.81 |
| | 426377 | AK001921 | Hs.169575 | hypothetical protein MGC2550 | 1.86 | 5.55 |
| | 431647 | AL138578 | Hs.266738 | hypothetical protein dJ796117.1 | 1.86 | 3.74 |
| | 422055 | NM_014320 | Hs.111029 | putative heme-binding protein | 1.86 | 4.68 |
| 30 | 425750 | AL050276 | Hs.42400 | zinc finger protein 288 | 1.86 | 4.04 |
| | 422491 | AA338548 | Hs.117546 | neuronatin | 1.86 | 4.37 |
| | 438942 | AW875398 | Hs.6451 | PRO0659 protein | 1.85 | 5.06 |
| | 400198 | | | Eos Control | 1.85 | 5.22 |
| | 427136 | AL117415 | Hs.173716 | a disintegrin and metalloproteinase doma | 1.85 | 3.41 |
| 35 | 427605 | NM_000997 | Hs.337445 | ribosomal protein L37 | 1.85 | 4.73 |
| | 418253 | AA215539 | Hs.283643 | Homo sapiens cDNA FLJ11606 fs, clone HE | 1.84 | 5.94 |
| | 441912 | AA971484 | Hs.159938 | ESTs | 1.84 | 3.73 |
| | 421632 | AA825426 | Hs.334689 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 1.83 | 3.62 |
| | 440602 | AI743491 | Hs.292692 | ESTs | 1.83 | 2.39 |
| 40 | 431882 | NM_001426 | Hs.271977 | engrailed homolog 1 | 1.83 | 3.30 |
| | 420772 | AW752656 | Hs.222707 | KIAA1718 protein | 1.83 | 3.73 |
| | 429197 | H24471 | Hs.26930 | ESTs, Weakly similar to T20272 hypotheti | 1.82 | 3.41 |
| | 450796 | NM_001988 | Hs.25482 | envoplakin | 1.82 | 7.73 |
| | 426928 | AF037062 | Hs.172914 | retinol dehydrogenase 5 (11-cis and 9-c | 1.82 | 3.38 |
| 45 | 415409 | AW993701 | | NS1-associated protein 1 | 1.82 | 3.60 |
| | 401131 | | | NM_001651*:Homo sapiens aquaporin 5 (AQP | 1.82 | 5.53 |
| | 421324 | BE257515 | Hs.103503 | deoxyribonuclease I-like 2 | 1.81 | 5.53 |
| | 400079 | | | Eos Control | 1.81 | 6.79 |
| | 430513 | AJ012008 | Hs.241586 | G6C protein | 1.81 | 7.49 |
| 50 | 426508 | W23184 | Hs.170171 | glutamate-ammonia ligase (glutamine synt | 1.81 | 3.55 |
| | 425883 | AL137708 | Hs.161031 | Homo sapiens mRNA; cDNA DKFZp434K0322 (f | 1.80 | 5.43 |
| | 429191 | AF065215 | Hs.198161 | phospholipase A2, group IVB (cytosolic) | 1.79 | 5.90 |
| | 432417 | AL040360 | Hs.162203 | ESTs, Weakly similar to alternatively sp | 1.79 | 3.63 |
| | 406467 | | | Target Exon | 1.79 | 4.16 |
| 55 | 444135 | AK000374 | Hs.10346 | hypothetical protein FLJ20154 | 1.79 | 3.32 |
| | 426402 | BE387327 | Hs.80475 | polymerase (RNA) II (DNA directed) polyp | 1.78 | 3.51 |
| | 412524 | AA417813 | Hs.44208 | hypothetical protein FLJ23153 | 1.78 | 3.72 |
| | 425880 | X01630 | Hs.160786 | argininosuccinate synthetase | 1.78 | 3.29 |
| | 400300 | X03363 | | HER2 receptor tyrosine kinase (c-erb-b2, | 1.78 | 3.44 |
| 60 | 451304 | M92642 | Hs.26208 | collagen, type XVI, alpha 1 | 1.78 | 3.57 |
| | 400082 | | | Eos Control | 1.78 | 3.82 |
| | 446603 | NM_014835 | Hs.15519 | oxysterol-binding protein-related protei | 1.77 | 3.48 |
| | 425415 | M13903 | Hs.157091 | involucrin | 1.77 | 4.64 |
| | 400083 | | | Eos Control | 1.77 | 6.31 |
| 65 | 427620 | NM_003705 | Hs.179866 | solute carrier family 25 (mitochondrial | 1.76 | 3.47 |
| | 446971 | AI652143 | Hs.288382 | hypothetical protein FLJ13111 | 1.76 | 4.21 |
| | 429807 | AK002138 | Hs.306227 | Homo sapiens cDNA FLJ11276 fs, clone PL | 1.76 | 2.63 |
| | 446560 | AK001567 | Hs.311002 | Homo sapiens cDNA FLJ10705 fs, clone NT | 1.76 | 3.82 |
| | 412824 | AW958075 | Hs.11261 | small proline-rich protein 2A | 1.76 | 4.31 |
| 70 | 439927 | AA854650 | Hs.124597 | ESTs | 1.75 | 3.63 |
| | 410223 | S73775 | Hs.60708 | calsequestrin 1 (fast-twitch, skeletal m | 1.75 | 3.79 |
| | 414500 | W24087 | Hs.76285 | DKFZP5648167 protein | 1.75 | 3.55 |
| | 448182 | AF244137 | Hs.20597 | host cell factor homolog | 1.75 | 3.40 |
| | 439651 | AF086480 | Hs.56255 | ESTs | 1.75 | 2.55 |
| 75 | 430486 | BE062109 | Hs.241551 | chloride channel, calcium activated, fam | 1.75 | 3.54 |
| | 424389 | AA339786 | | lymphocyte-specific protein 1 | 1.75 | 4.48 |
| | 450837 | D58463 | Hs.85969 | hypothetical protein FLJ12270 | 1.74 | 3.40 |
| | 425920 | AL049977 | Hs.162209 | claudin 8 | 1.74 | 3.33 |
| | 435680 | HS0946 | Hs.284183 | Homo sapiens galectin-related inhibitor | 1.74 | 3.47 |
| 80 | 439639 | AA370045 | Hs.6607 | AXIN1 up-regulated | 1.73 | 5.22 |
| | 416950 | AL049798 | Hs.80552 | dermatopontin | 1.73 | 4.99 |
| | 400199 | | | Eos Control | 1.73 | 6.25 |
| | 409737 | AB011539 | Hs.56186 | EGF-like-domain, multiple 3 | 1.73 | 4.28 |
| | 424420 | BE614743 | Hs.146688 | prostaglandin E synthase | 1.72 | 3.42 |
| | 421545 | AA292810 | Hs.90034 | hypothetical protein FLJ21916 | 1.72 | 2.12 |
| | 414323 | NM_014759 | Hs.334688 | KIAA0273 gene product | 1.71 | 4.82 |
| | 407228 | M25079 | Hs.155376 | hemoglobin, beta | 1.70 | 7.02 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|------|
| 5 | 406643 | N77976 | Hs.347939 | hemoglobin, alpha 2 | 1.70 | 3.60 |
| | 447299 | AF043897 | Hs.18075 | chromosome 9 open reading frame 3 | 1.70 | 5.10 |
| | 439733 | AL365412 | Hs.107203 | hypothetical protein from EUROIIMAGE 1759 | 1.69 | 2.92 |
| | 415512 | Y16270 | Hs.78482 | parafemin | 1.69 | 4.92 |
| | 407100 | R29657 | | gb:F1-1179D 22 week old human fetal live | 1.69 | 3.96 |
| | 425503 | W92517 | Hs.158203 | actin binding LIM protein 1 | 1.68 | 5.97 |
| | 433738 | A1584802 | | ESTs | 1.68 | 2.88 |
| | 406791 | A1220684 | Hs.347939 | hemoglobin, alpha 2 | 1.68 | 3.44 |
| 10 | 428975 | NM_004672 | Hs.194694 | mitogen-activated protein kinase kinase | 1.68 | 2.74 |
| | 435661 | AF220263 | Hs.193920 | MOST2 protein | 1.67 | 3.56 |
| | 459317 | BRCA1b | | Eos Control | 1.67 | 3.34 |
| | 426923 | AF112977 | Hs.172887 | phytanoyl-CoA hydroxylase (Refsum disease) | 1.67 | 4.53 |
| | 426682 | AV660038 | Hs.2056 | UDP glycosyltransferase 1 family, polypeptide | 1.67 | 3.36 |
| 15 | 417029 | AW952192 | Hs.273385 | guanine nucleotide binding protein (G protein) | 1.67 | 5.22 |
| | 437201 | F29279 | Hs.171625 | hypothetical protein MGC14697 | 1.67 | 5.75 |
| | 454478 | AW805749 | | superoxide dismutase 2, mitochondrial | 1.67 | 4.55 |
| | 406710 | A1708347 | Hs.184014 | ribosomal protein L31 | 1.66 | 3.80 |
| | 431593 | NM_002108 | Hs.276590 | ESTs | 1.66 | 2.45 |
| 20 | 457820 | AA341497 | Hs.31408 | RAR (RAS like GTPASE) | 1.66 | 2.44 |
| | 441899 | A1372588 | Hs.8022 | TU3A protein | 1.66 | 4.06 |
| | 414186 | U33446 | Hs.75799 | protease, serine, 8 (prostasin) | 1.65 | 6.52 |
| | 418116 | AA252457 | Hs.86543 | ESTs, Moderately similar to T00256 hypot | 1.65 | 3.44 |
| | 403105 | | | Target Exon | 1.64 | 4.12 |
| 25 | 450014 | N41322 | Hs.18441 | ESTs | 1.64 | 2.90 |
| | 436685 | W28661 | Hs.5288 | Homo sapiens mRNA: cDNA DKFZp434M245 (fr | 1.64 | 4.49 |
| | 401429 | | | C14001067:gi4126465 dbj BAA36581.1 (AB | 1.64 | 3.82 |
| | 420983 | W95228 | Hs.100764 | cathepsin G | 1.64 | 3.64 |
| | 433126 | AB021262 | Hs.99816 | beta-catenin-interacting protein ICAT | 1.63 | 3.29 |
| 30 | 428150 | AW950547 | Hs.70312 | cytochrome c oxidase subunit VIIa polypeptide | 1.63 | 7.05 |
| | 412295 | AW088826 | | poly(A)-binding protein, nuclear 1 | 1.63 | 4.01 |
| | 430831 | AA703239 | Hs.269804 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 1.63 | 3.60 |
| | 429348 | AJ242859 | Hs.199731 | Langerhans cell specific c-type lectin | 1.62 | 2.64 |
| | 407082 | Z47055 | | gb:Human partial cDNA sequence, farnesyl | 1.62 | 2.13 |
| 35 | 452556 | H78517 | Hs.33905 | ESTs | 1.62 | 4.64 |
| | 415688 | AA166963 | | hypothetical protein DKFZp566i133 | 1.62 | 3.33 |
| | 446515 | AL048875 | | hypothetical protein MGC14141 | 1.62 | 3.66 |
| | 445919 | TS3519 | Hs.334692 | laminin 1 | 1.62 | 5.65 |
| 40 | 447330 | BE279949 | Hs.18141 | apolipoprotein C-III | 1.61 | 5.61 |
| | 412374 | X01388 | Hs.73849 | NM_021724: Homo sapiens nuclear receptor | 1.61 | 5.18 |
| | 400229 | | | farnesyl diphosphate synthase (farnesyl | 1.61 | 3.57 |
| | 414814 | D14697 | Hs.77393 | gb:wp08d10.x1 NCI_CGAP_Kd12 Homo sapien | 1.61 | 2.08 |
| | 424397 | A1950320 | | imidazole receptor candidate | 1.60 | 3.59 |
| 45 | 451335 | AB023192 | Hs.26285 | natriuretic peptide receptor A/guanylate | 1.60 | 5.54 |
| | 426156 | BE244537 | Hs.167382 | cystatin E/M | 1.60 | 4.79 |
| | 456267 | A1127958 | Hs.83393 | epoxide hydrolase 2, cytoplasmic | 1.60 | 2.50 |
| | 436950 | L05779 | Hs.113 | gamma-aminobutyric acid (GABA) A recepto | 1.60 | 3.98 |
| | 421397 | S67368 | Hs.103998 | mucin 1, transmembrane | 1.60 | 3.28 |
| 50 | 419092 | J05581 | Hs.89603 | NPD002 protein | 1.60 | 3.69 |
| | 440160 | BE560269 | Hs.7010 | ESTs | 1.59 | 2.49 |
| | 417481 | AA203281 | Hs.6191 | Homo sapiens mRNA: cDNA DKFZp434C107 (fr | 1.59 | 3.60 |
| | 406778 | H06273 | Hs.101651 | Target Exon | 1.58 | 3.98 |
| | 402991 | | | ESTs | 1.58 | 3.36 |
| 55 | 425169 | AW292500 | Hs.128514 | ESTs | 1.58 | 4.00 |
| | 446429 | A1681807 | Hs.201391 | ESTs | 1.58 | 3.20 |
| | 426445 | AA378739 | Hs.187711 | carbonic anhydrase II | 1.57 | 3.63 |
| | 425196 | AL037915 | Hs.155097 | Link guanine nucleotide exchange factor | 1.57 | 3.44 |
| | 422581 | NM_016339 | Hs.118562 | splicing factor, arginine/serine-rich 6 | 1.57 | 3.55 |
| 60 | 440054 | AW661947 | Hs.6891 | bleomycin hydrolase | 1.56 | 3.39 |
| | 415988 | BE407713 | Hs.78943 | hypothetical protein FLJ20262 | 1.56 | 2.43 |
| | 441860 | AW451330 | Hs.348198 | ESTs | 1.55 | 3.38 |
| | 428462 | A1571486 | Hs.30258 | ESTs | 1.55 | 3.65 |
| | 449518 | BE395253 | Hs.30861 | TEA domain family member 3 | 1.55 | 3.80 |
| | 420075 | AF142482 | Hs.203846 | gb:og83g12.s1 NCI_CGAP_Ov8 Homo sapiens | 1.55 | 3.81 |
| 65 | 406799 | AA908548 | | aquaporin 7 | 1.54 | 3.87 |
| | 450787 | AB006190 | Hs.25475 | Leman coiled-coil protein | 1.54 | 4.06 |
| | 419659 | AB023206 | Hs.92186 | ESTs | 1.54 | 3.82 |
| | 408543 | N78098 | Hs.44289 | hypothetical protein MGC3047 | 1.54 | 3.10 |
| | 410169 | A1373741 | Hs.59384 | jagged 2 | 1.54 | 4.73 |
| 70 | 426068 | AF029778 | Hs.166154 | hypothetical protein, clone Telethon11a | 1.54 | 4.82 |
| | 432191 | AA043193 | Hs.273186 | carboxypeptidase Z | 1.54 | 5.83 |
| | 415166 | NM_003652 | Hs.78068 | proline oxidase homolog | 1.54 | 4.58 |
| | 410048 | W76467 | Hs.343874 | ESTs, Weakly similar to JC5314 CDC28/tcd | 1.54 | 4.66 |
| 75 | 430502 | A1123657 | Hs.127264 | Homo sapiens cDNA: FLJ23538 fs, clone L | 1.53 | 3.41 |
| | 433640 | AW390125 | Hs.240443 | eukaryotic translation elongation factor | 1.53 | 4.57 |
| | 413353 | AW293542 | Hs.75309 | thiosulfate sulfurtransferase (rhodanese) | 1.53 | 3.59 |
| | 431021 | A1869664 | | syndecan 4 (amphiglycan, ryudocan) | 1.53 | 3.73 |
| | 431243 | U46455 | Hs.252189 | translocase of inner mitochondrial membr | 1.52 | 6.09 |
| 80 | 433019 | A1208513 | Hs.279915 | ribosomal protein L9 | 1.52 | 4.49 |
| | 406801 | AW242054 | Hs.190813 | hypothetical protein MGC13010 | 1.51 | 5.56 |
| | 427451 | AA531527 | Hs.332040 | brain specific protein | 1.51 | 3.77 |
| | 432894 | AW167668 | Hs.279772 | growth arrest-specific 6 | 1.51 | 6.72 |
| | 415550 | L13720 | Hs.78501 | Homo sapiens cDNA FLJ14476 fs, clone MA | 1.50 | 4.02 |
| | 424707 | BE061914 | Hs.10844 | | 1.49 | 4.21 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|------|
| 5 | 445624 | AW140103 | Hs.78880 | ilvB (bacterial acetolactate synthase)-I | 1.48 | 3.61 |
| | 445071 | AI280246 | Hs.149504 | ESTs | 1.48 | 3.39 |
| | 40763 | A8028988 | Hs.7407 | KIAA1065 protein | 1.48 | 4.03 |
| | 451988 | AF263928 | Hs.27410 | papillomavirus regulatory factor PRF-1 | 1.47 | 3.58 |
| | 427841 | AW883367 | | hypothetical protein MGC5306 | 1.47 | 3.61 |
| | 426335 | AI054347 | Hs.2017 | ribosomal protein L38 | 1.47 | 3.76 |
| | 454098 | W27953 | Hs.292911 | Plakophilin | 1.46 | 2.95 |
| | 456766 | R87310 | Hs.7740 | oxysterol binding protein-like 1 | 1.46 | 3.40 |
| 10 | 440526 | AI832243 | | ESTs | 1.46 | 3.38 |
| | 452586 | AW958479 | Hs.289043 | spindlin | 1.45 | 3.48 |
| | 433399 | N46406 | Hs.84700 | similar to phosphatidylcholine transfer | 1.45 | 3.44 |
| | 430238 | N72519 | Hs.236545 | hydroxyacid oxidase 2 (long chain) | 1.45 | 4.00 |
| | 425456 | T70445 | Hs.157850 | ribosomal protein L9 | 1.45 | 4.79 |
| 15 | 411085 | AF022991 | Hs.68398 | period (Drosophila) homolog 1 | 1.45 | 4.43 |
| | 433638 | AW872507 | Hs.3462 | cytochrome c oxidase subunit VIc | 1.44 | 3.89 |
| | 445156 | N89367 | Hs.12373 | adenylate cyclase 6 | 1.44 | 3.60 |
| | 446576 | AI659477 | | dystroglycan 1 (dystrophin-associated gl | 1.44 | 3.07 |
| | 440433 | AA252452 | Hs.7187 | hypothetical protein FLJ10707 | 1.43 | 3.67 |
| 20 | 434536 | H14486 | Hs.3903 | Cdc42 effector protein 4; binder of Rho | 1.42 | 3.35 |
| | 423513 | AF035960 | Hs.129719 | transglutaminase 5 | 1.42 | 3.18 |
| | 418681 | AA287786 | Hs.23449 | insulin receptor tyrosine kinase substra | 1.42 | 3.38 |
| | 421935 | AA131632 | Hs.109672 | CMP-NeuAC:(beta)-N-acetylglactosaminide | 1.41 | 4.04 |
| | 406712 | M31212 | Hs.77385 | myosin, light polypeptide 6, alkali, smo | 1.41 | 4.27 |
| 25 | 413944 | AW001579 | Hs.9645 | Homo sapiens mRNA for KIAA1741 protein, | 1.41 | 3.80 |
| | 435879 | AW084463 | Hs.30002 | SH3-containing protein SH3GLB2; KIAA1848 | 1.41 | 3.55 |
| | 417967 | BE244373 | Hs.1119 | nuclear receptor subfamily 4, group A, m | 1.40 | 4.07 |
| | 412669 | AW880841 | Hs.96908 | p53-induced protein | 1.40 | 3.59 |
| | 415523 | AL042003 | Hs.296847 | cell matrix adhesion regulator | 1.40 | 4.38 |
| 30 | 406713 | U02629 | Hs.77385 | myosin, light polypeptide 6, alkali, smo | 1.39 | 4.03 |
| | 439606 | W79123 | Hs.58561 | G protein-coupled receptor 87 | 1.39 | 3.65 |
| | 430135 | NM_000035 | Hs.234234 | aldolase B, fructose-bisphosphate | 1.37 | 3.99 |
| | 422682 | W05238 | Hs.94316 | ESTs, Weakly similar to T31613 hypotheli | 1.36 | 3.30 |
| | 408198 | AA131111 | | gbzo16b06.r1 Stratagene colon (537204) | 1.36 | 3.33 |
| 35 | 419600 | AA448958 | Hs.91481 | NEU1 protein | 1.35 | 3.49 |
| | 437141 | BE304917 | Hs.31097 | hypothetical protein FLJ21478 | 1.34 | 3.47 |
| | 408250 | R92918 | Hs.19597 | KIAA1694 protein | 1.34 | 3.89 |
| | 430012 | NM_015373 | Hs.227637 | chromosome 22 open reading frame 2 | 1.32 | 4.24 |
| | 425183 | W76098 | Hs.19223 | HCCA2 protein | 1.32 | 3.52 |
| 40 | 427706 | AW971225 | Hs.293800 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 1.32 | 3.50 |
| | 438303 | A8028998 | Hs.6147 | KIAA1075 protein | 1.32 | 3.71 |
| | 406800 | AA505535 | | gb:nh84h10.s1 NCI_CGAP_Br1.1 Homo sapien | 1.32 | 3.65 |
| | 442533 | AA161224 | Hs.8372 | ubiquinol-cytochrome c reductase (6.4kD) | 1.32 | 4.14 |
| | 428475 | AF172940 | Hs.184542 | CGI-127 protein | 1.31 | 3.43 |
| 45 | 406742 | AI468091 | Hs.279860 | tumor protein, translationally-controlle | 1.30 | 3.34 |
| | 432295 | BE091049 | Hs.343665 | ribosomal protein S15a | 1.30 | 3.29 |
| | 422959 | AV647015 | | paired immunoglobulin-like receptor beta | 1.28 | 3.53 |
| | 402956 | | | ENSP00000244002: KIAA1335 protein (Fragm | 1.24 | 3.38 |
| 50 | 406743 | AA911568 | Hs.279860 | tumor protein, translationally-controlle | 1.24 | 3.70 |
| | 437142 | AI791617 | Hs.145068 | ESTs, Moderately similar to A46010 X-lin | 1.23 | 3.48 |
| | 424372 | AW952803 | Hs.21732 | Homo sapiens cDNA FLJ11780 fis, clone HE | 1.18 | 2.44 |
| | 414716 | AF199598 | Hs.97044 | Kv channel-interacting protein 2 | 1.18 | 3.43 |
| | 431931 | AB035302 | Hs.272212 | cadherin 9, type 2 (T1-cadherin) | 1.15 | 2.49 |
| | 406587 | | | C15000544: gij5454148refjNP_006368.1[U | 1.06 | 2.25 |
| 55 | 409574 | AW419080 | Hs.250645 | ESTs | 1.00 | 3.60 |
| | 417435 | NM_005181 | Hs.82129 | carbonic anhydrase III, muscle specific | 1.00 | 3.44 |
| | 402075 | | | ENSP00000251056: Plasma membrane calcium | 1.00 | 3.37 |
| | 422330 | D30783 | Hs.115263 | epiregulin | 1.00 | 3.35 |
| | 418986 | AI123555 | Hs.81796 | ESTs | 1.00 | 3.28 |
| | 404175 | | | Target Exon | 1.00 | 3.08 |
| 60 | 452640 | AA027115 | Hs.100206 | ESTs, Weakly similar to A53856 aryl-acyl | 1.00 | 2.82 |
| | 443564 | AI921685 | Hs.199713 | ESTs | 1.00 | 2.51 |

TABLE 64B:

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

| | | | |
|----|--------|------------|---|
| 70 | Pkey | CAT Number | Accession |
| | 412636 | 1438_1 | M77830 NM_004415 AF139065 BG681115 BG740377 B1712964 BG000656 AA128470 B1438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG698865 BG740734 BG680618 BG739778 B1765807 BM353403 BM353248 AW177784 AW205789 AW951576 AW848592 BE182164 BF149266 BE940187 B1060445 B1060444 BF350983 BE720095 BE720069 BE715154 BE082584 BE082576 BE004047 AA857316 B1039774 BE713818 BE713548 AW170253 BE160433 B1039775 AW886475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 AU127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 B1090358 BF087707 BE819046 BE819005 AA377127 BE073467 BE819069 BE819048 B1036306 BG990973 B1040954 BF919911 AU140155 AI951766 AJ434518 AW804674 BF752969 BE837009 BE925826 BF149265 AW995615 BE814264 B1039782 AU140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476866 BF086994 BF592276 BE082507 BE082514 BE082505 BF873693 AW068840 AW847678 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF839562 BE184933 BF842254 BE865341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705968 AW848723 AW376699 AW376817 AW376697 BG005097 BF751115 BE696084 AW848371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE865474 BE185187 BE156621 BE715089 BE713297 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 AI190590 AI554403 AI392926 AU158477 B1467252 AU159919 AI760816 BF082516 AI439101 AA451923 AI340326 AI590975 B1791553 AI700963 |

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| 5 | | | AI142882 AA039975 AA946936 AA644381 BM314884 AA702424 AM17612 AW190555 AJ220573 AI304772 AI270345 AI627383 AA552300 AI911702 AW166807 AI364078 W95070 AA149191 AA026864 AI830049 AW780435 AI078449 AI819984 AI858282 BI468588 AI860584 AI025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 AI927207 AI205263 BF082491 AW021347 AI568096 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 AI910434 BF082513 AI494069 AI270027 AI635878 AA128330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654 AV745530 BI762796 BG287391 AW798780 BE706045 BE925470 AW799118 BF087996 BE002273 AW879451 AI571075 BE067786 AV721320 AI022862 N29754 C03378 N84767 AA131077 H30146 BE714290 AI686869 AI568892 AI915596 AW105614 AI887258 AI538577 BE925474 BE067737 BG319486 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG950164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 AI905927 BF992780 AW853812 BG954443 B770853 BG679406 BG740832 BG681087 BG698430 AA455100 T87267 BE695209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705999 BG677157 BE009090 BG681378 BE712291 BG691498 BG678984 BI040941 AA337270 AW384371 AW847442 BI058659 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 AI284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW506653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H08999 AW365145 W38382 AI498487 AI673735 AA978066 |
| 10 | | | AA417099 AA435761 AA972917 AI660387 R69942 BG655457 BF111453 AI149320 N23160 AI464631 AI758316 AV741781 BI791950 BM055014 AI798851 AA865357 AI417230 N67277 T55592 T52179 |
| 15 | 407328 427890 440116 | 534268_1 1373988_1 454673_1 | AW189097 AI123917 AI123926 AW972724 AA877998 AA522631 AU185388 NM_058173 AF414087 W72837 BF742809 AW070916 BE092421 AI905687 AA340069 BE074512 AI905623 AI905633 BG202312 W72838 AI139456 BG218084 BE926938 BE186013 AW176044 AW291950 BG185269 BG197186 BG192597 BG183176 BG207535 AI127172 BE815819 AI905624 R75793 BG202313 AI905837 BE815853 |
| 20 | 444105 431926 424399 | 649788_1 1237041_1 2196_1 | AL049987 BG620667 BG571984 AW362842 BE150456 BE326465 AW872412 AA688553 AI024689 AA442638 AA813604 AA442648 AA663108 AA442379 AA229448 N56349 AA460220 AW971193 AA453725 AI742087 AI860142 AW769479 AI917507 AI860141 BE045272 AW277065 AI921333 AI354470 BE466760 AI827987 AI005467 AA833517 AA563934 AA522837 AA812876 AW020895 AA600372 AA663178 AI187977 AA229164 AW2770324 AA703066 T79891 AA632986 BE708493 R31132 AI253986 AI916737 T84795 T84294 AW961515 AI459289 BF109829 BI491853 AI084517 AW103830 BE835233 AI472712 AV741009 AA551512 N28268 AA436880 AA447794 BE835410 BE835385 BE818352 BE818350 R64648 BE646467 AA493776 AA437299 BE818343 R95914 R31089 BF576826 AU186065 BF802058 AI217018 AA247541 AI191725 BE766918 |
| 25 | 426101 | 3211_1 | AI207343 BF813684 BF928775 AA828585 AV711317 AI809938 AI808768 AI240593 AI915771 AW945170 BF930905 F33652 BG057818 AI368018 AI421485 AI300352 AI378525 AI264177 AI276281 AI245302 AI281050 AI190036 AW451438 AW242903 AA910870 F22289 F19647 F22375 AW473816 BF445785 AA774528 F33447 C01077 AW772227 F17759 H42812 R09701 AA340906 R48772 H42892 H42537 R47898 N28263 H25721 F32386 H43971 R48205 F21390 H45809 AA007629 R47897 R83734 H45844 AW983653 H43970 H42536 H24495 R48875 H42961 H22079 R86018 |
| 30 | 438962 445493 407102 | 195763_1 423456_1 7177_2 | BI757233 BG911321 BF351759 AW244016 AW026834 AW024260 AI420138 AA779354 AI093360 AI934858 AW151292 AI373133 AI335587 AI969728 AA101632 BE218525 AI802114 AI783721 AA845265 AW088826 AI832852 F03967 AI611148 AI720358 AW293764 N91161 R79192 W85852 AW771263 BG820263 BG012864 R74441 R86080 W04256 BE707244 BF899452 BE327552 BE669500 AI492388 AI241532 BF448184 AI209012 AA886528 N70309 AW582776 BF110563 BF448329 BE326537 AW770471 BF444926 BE674147 AI793266 AI991774 AI807726 AI218667 AA301750 R44328 |
| 35 | 421998 | 133592_1 | AW469418 AA053401 AA053416 H93046 AA897108 AI652046 AA761626 BF882276 N68615 T88896 H93912 T84424 BG740624 AV720262 BG198346 BG215119 AW841716 AA228357 AW841786 AA932742 AW593558 AW139592 BF591031 AW205438 AA933791 AI434866 BF513564 AI191480 AI972330 AI582824 AW779392 AI359970 AI199117 AI910783 BF800971 AA627401 AI799778 BF222639 AI937737 AW136973 |
| 40 | 408239 437611 456332 458222 434206 | 103120_1 240436_1 21353_10 631332_1 185910_1 | NM_058173 AF414087 W72837 BF742809 AW070916 BE092421 AI905687 AA340069 BE074512 AI905623 AI905633 BG202312 W72838 AI139456 BG218084 BE926938 BE186013 AW176044 AW291950 BG185269 BG197186 BG192597 BG183176 BG207535 AI127172 BE815819 AI905624 R75793 BG202313 AI905837 BE815853 |
| 45 | 400295 | 2196_1 | BC533564 BG618564 AW296119 AI269233 BF508328 AW364777 AW292258 AA371049 AI452471 AI092522 BG618376 AL049080 AA631068 BG564643 T53833 AV702544 BG533452 AV705004 AA588281 T28665 BG569026 AV646874 AV647253 AV647455 AV647749 BI759444 AV652457 AV695354 AV696010 AV697248 BG617586 AV722549 AI435836 AI950676 AI245019 AW338243 AA530898 D52191 AI435352 D57473 BG566952 AI420505 AA035245 AV704972 BG564113 AI439237 AI287456 AV695686 AA349017 |
| 50 | 417054 | 12405_2 | AL118754 AA333202 H38001 AK057749 AI701055 AA115476 AI633570 AI435607 AW173392 AI092468 AI989318 AA833891 AW295964 AI804107 AI767415 AI473818 AI076758 AA278949 AA428547 N31385 H82560 AA464804 AA809073 AA832476 AW295298 BF108690 AI492243 N22394 AA487175 AA431891 AW070941 AA278823 AA707840 AI346067 AI184307 AA936342 AI288633 AA425697 AI435960 AI301433 AA939334 AI917652 AA487234 AA490964 AA937925 AI301378 AI783840 AI093652 AA723864 BF001378 BI818971 BI762256 AW957064 BG720359 BI821176 BI906440 AI472868 AL523506 BF962934 BF960650 BI837618 BF956256 AA487349 BF961475 AA354431 AA115452 AA491157 N75632 BF962141 AL562216 BI754640 N24091 R00062 AI963686 T56529 AU185624 T56460 H97658 BI752843 BI819132 AA210796 |
| 55 | 423974 412668 | 888155_1 33230_1 | BG285809 BE940673 BG432524 BE157554 BG676980 AU144284 AI745383 AU159045 AI693500 AW293668 AW371408 BE856107 AI338042 AW188320 AI698246 BE673290 AW297653 AA156532 AI017342 AI916754 AI190644 AI184302 AA857671 BE857018 AI307420 AI318157 AW204327 AW654668 AW274339 AA582788 AI345741 AW301433 AI873458 AW137388 BF718731 BF718413 AA877495 BF001575 AI824693 AW849604 AW849405 AW849396 AW849173 BE673179 AI611327 AA705753 BE715478 AW849414 AW849399 AI085759 AI140849 T67412 AI889885 AW104647 AI912495 AI889874 AI744241 BE717113 BE717108 BE715564 AI872527 AA029457 C00338 AI469558 BE715577 AA045413 BF843813 Z99386 AV716301 BE222333 AI949687 BF732426 AI494086 AV721430 AW577332 N68315 BE672030 AI084440 AI250908 N50901 AI757364 BF515264 AI186231 BE466036 AW631313 AA935154 N54411 BG057515 AW013895 N77963 AA708723 AI273295 N59093 AA522665 AI871574 AA505521 AA812256 AA553841 AW467057 W68650 AI168772 AA988308 AA910057 AI868258 AA918322 AI335847 AA621494 AA904390 AI760007 AU146694 AV758440 BM142562 N66507 AI674563 AW628584 AI263902 BF223368 AI090490 AI452918 N71423 AA062767 T94332 AA016003 |
| 60 | 444726 | 3503_2 | BG681508 AA082426 AA029451 N71873 BF437845 T54154 AV741757 AV734838 AI937532 AI032318 AW749500 AA091720 BC022398 AV743635 AW976922 AW152652 AA910013 AA834629 BG536317 AW849807 AV713062 AI684337 BE044081 AA761490 AW753257 AA886068 D61974 |
| 65 | 451184 | 1531_4 | AK026697 BE938558 BE843975 BE843962 AW304313 AI735759 AA021055 AI769145 AI188319 BF064105 AI677654 AA723627 AA781580 AI611167 BE162152 R77997 BG059091 AV722360 AA370451 AA033786 AV729790 AW953851 AW953855 BE504303 AI765853 BF059302 AA410685 AI978745 AA399236 BG149495 BE670366 AI694777 BE503109 AA633474 AI700568 AI432181 AI637714 AW302164 AA196790 AI928519 BE673464 BF437523 AI281974 AI306156 AW418884 AA523952 AA683187 AW075563 AA877270 AW204404 AW771341 AI913892 AW770312 AW242851 AU154858 AA021007 AI521932 AA034044 AI760631 R34679 AI915923 AI911609 AW242360 AA059025 AA370450 BF432186 AW862278 AW859976 BE159936 BF514075 BI057841 R34781 R77900 AA011413 |
| 70 | 443072 437596 411962 440469 450860 | 449629_1 2875_1 2307710_1 1030831_1 40397_1 | SS3911 NM_001773 AL572644 AL550179 AI688653 AW025002 AW614285 AU158779 AI017002 AA434387 AI252665 AI262206 AU147582 AI144193 AW952860 AI128776 AI017793 AI160509 AA906021 AI149563 AU154950 AI128488 W74409 AI970362 AI141453 AU158772 W58493 BM148338 R73091 AW020496 BI491517 AA022917 AI432610 AI879448 R69099 AI708954 AW014274 AA483672 AA528783 AA912271 AI262942 BE677587 AI874217 AA152376 AA640408 AI287334 BF830285 AA311473 C18678 AA922603 C00910 AI124073 R38730 AA043439 W94644 W58646 AA664247 |
| 75 | | | |
| 80 | 418481 | 17381_1 | |

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| | | BE061934 H01096 R69613 AI383162 AU133723 AA311526 R67942 H01097 H72113 R72430 R39494 AV744074 AA535925 B1759288 B1052385 BF854687 AW608286 AA043438 R72478 AL513811 R69214 AA188435 AA054965 AI220117 AI857837 AI218371 BM091400 AI304964 AI198508 AI400738 AW571549 AW950042 AI089943 AA437280 AU150878 BF197070 AI267984 BF594181 BF196688 AI433152 AI338921 AI620364 AI280197 AA652531 AI674938 AI342447 AI620350 AI281295 AI148621 N54787 AI338121 AI281153 N51899 AI087072 AA954788 AW069054 AI346309 BG529629 AI340135 BF083036 AI167365 AW819657 AA935468 AI467868 AW148701 AI383720 BE047685 AW015498 AA937149 AA708346 AW771478 AW802508 H53334 AW389204 AW798230 AI553922 AI560688 AW950043 AI961682 AV706506 R01853 AA126514 N62757 AI536893 AI926052 AI418720 N99964 AI568933 AI915737 AI080691 AI185358 N48996 N68575 H82824 H60037 AI247247 T95664 BF593863 AI749637 AW088541 AA991294 AA887452 AI073726 AA633132 AA629674 AA629649 AA629656 AA578595 AI168758 AA804572 AI085786 AA994396 AA991209 AA948663 AA929054 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BE175745 T64217 BE394588 AW024754 BE183167 BE183166 BE378353 AA633408 AW749955 AW629759 AI651005 AK057547 BG181248 AA883756 F25670 AA778128 F27657 F18914 F25171 AA178844 F21556 F25872 F20457 F27617 F36059 F34817 F26967 F25922 F31278 F34666 F01176 F36333 F01226 F27406 F27130 F28742 F24126 F29891 AA195955 AA086351 W69291 F25880 F32791 F31311 F32380 F25216 F19679 F18656 F29700 F24954 F32741 F30404 F35470 F33989 F33141 F36382 F34118 F17714 AA176345 F24700 AA550940 F18617 F16859 F15633 F34675 F16528 F17281 AA086388 F30859 F21852 C02644 F29425 F25286 C03553 F35259 W80691 F16457 F24094 F16783 AA180319 F28443 F17763 F17448 F00542 AA197179 AA193012 BG566720 AA010276 W92098 BE837833 BF541660 AW889587 AI651246 AI339033 AI078183 AI686504 AA813616 BF056955 R43664 BF509917 AW563717 W95054 AI382907 AI399929 F10511 AA427819 AW269408 BE825398 BG654856 AA037082 AI203007 AW593522 H65211 AA010218 AI355222 BF378422 AA366587 BF874552 AW277084 R26970 D79194 R27662 AW972670 AA525808 H28359 H28383 AA293303 AA492458 AA948195 AI341912 AI436673 AA708982 AI095911 AI983409 NA AL581381 BE220341 AI695121 BG149299 AI205526 AI968389 B1752979 AI291204 AI954763 AA344460 AA344581 BF082319 AU125758 BE825566 AA954549 AI286069 AA948280 BG149854 BI862122 AU024440 AI090013 NM_001895 M55265 BC002615 BC011668 BM452475 AL560958 AU125134 BE408670 AL134963 AI589577 AI952244 AW972197 AW403214 AW069872 AI804464 AU123365 AI342226 H50982 AV738572 R94284 BG536938 AI970166 AI585205 J02853 AU131772 BE841258 AW867858 AA19595 AL597675 BF361319 AW877122 AW877060 AW876962 AU126276 AA279620 AA805295 AU132198 AU130091 AI375524 AW183031 AU129003 AI373257 H92896 BE244655 AW028253 AW571546 BI258630 AI807134 AW672915 AW893438 BF035080 AW054815 AW963200 AI797895 AA604241 AI014611 BE092080 BE092076 AA639870 AA714906 N39594 AA173857 AW951102 AW951101 BG823603 AI478558 R32009 AW149282 BG818283 R69507 T29481 BE766560 AI693579 H06201 AF005081 BG193848 AW846590 AW846615 AW846584 AW846592 AW846621 AW846610 N68168 N69188 N90450 H88044 BE156092 AW752953 AF005081 BG193848 AW975114 AI096634 AI767001 AA658364 AW517542 BC015871 AI521618 AI471709 AW169230 BG539605 BI058963 BI058949 BG548398 BG952412 AW842037 AW842040 AW890573 AF086341 W76326 W72300 AL050013 BG939500 AW969191 AA769925 AI377973 AI625545 AA811365 AA521114 N24705 AI379579 AA424899 AI684671 AA829715 AI453010 N35401 AA677452 AA504340 AI209149 AA883574 AI379062 AI084455 AI280147 AA644327 BF432508 N27873 N47364 N34880 AI147024 T86860 AI219716 AA960926 H25544 BI857123 AW960489 AA599099 AA765246 AA328537 BG434703 AA890373 AA424765 AI292318 AA829886 N95742 AI218758 H25588 N36282 AA024987 N36687 BI919187 AI49471 AA889970 AW166152 AA468546 AI262504 AI452782 AA554458 AA807080 AA724542 AW102730 AA909978 AW118134 AW827241 W56431 BM127381 BF436987 AI016509 AW663972 BM127686 C15552 N63435 N51744 T98800 N56980 BG108636 N49381 R49886 D61278 BI756612 AA508234 R49885 BF850422 AW972351 AW182936 AI478370 AA528309 BG997292 AW137742 AI632006 AA775020 AA961625 W86628 BF112014 AI275423 AI680786 AW796921 AW798102 AW805749 AW805872 BF985060 AW794380 BF380449 AW794466 AW794538 AK056896 AI924216 AI660493 AI984141 AI991272 AA593860 AI983793 AI346155 AI274929 AI281211 AI821178 BC020841 BF352476 BF843140 BF917041 W80832 AA630445 BF350167 BE162052 BE931808 AI572329 BG536379 AA026381 AW500815 AI806691 AW502933 AW303573 BE328059 AI201422 BE673566 AW182125 H13705 AL545411 AI096369 BF431750 AI130946 W60065 W80663 AA258580 W73279 W76156 W80662 AW058658 AI204699 W60115 N56751 N30878 AI769345 R71250 AI363766 R22777 R17009 R27985 R28243 AI278995 AW964552 AI885189 AI571775 AI660803 AI293327 AI719401 Z39652 H25636 BF091855 AI218354 AI928704 AI817774 AI885495 AI695453 BF340929 AV749610 AF105036 U70663 NM_004235 AF022184 AU141767 AU141110 AL040569 D44830 BI011351 AL575805 AI290876 AI014784 AI393429 AI265211 AW074303 AA620711 BF197792 AW008766 D25944 AI687397 AA621680 AV714408 BF446905 BM314505 BF514079 BM314197 AA845201 AW874084 BE720622 AI127241 AA236239 AI679709 AI679135 AI572470 AA573434 AI568487 BE049325 AA687950 BG925989 AI338031 AI365073 AI024576 AA298805 H04001 H45668 BG682146 AL552388 BI462361 BG547513 BG896863 BI256661 AK056188 BM455117 BG527027 AA480032 AW993701 AA164703 AL537682 AA836491 AA515961 AL537681 BF437856 AA683484 AW152367 AV691022 AA025156 AI624297 AW071132 BG951486 AI907206 BF348688 AI904222 BG954414 AI590133 AW080151 AA480116 BF360696 AI689419 N75837 AW373844 BF991704 BG222449 BI030443 BE698057 BG954850 AI905836 BF984111 AU123871 BF834727 AI904283 AI909847 BF757857 BF923905 BG283493 AA299475 R80150 BG987145 BF837559 BG469759 AA496412 BF758339 BG957192 AW373869 BG952345 BF229957 BE697472 BE697475 AA011005 BG005000 T56558 AA908196 AA716585 |
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[illegible]

TABLE 65A: ABOUT 838 GENES DOWNREGULATED IN BENIGN NEVI RELATIVE TO NORMAL SKIN
Table 65A lists about 838 genes downregulated in benign nevi relative to normal skin.

Table 65A lists about 838 genes downregulated in benign nevus relative to normal skin. Genes were selected from 59680 probesets on the Eos/Affymetrix Hu30 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: 90th percentile of normal skin AIs divided by the average of benign nevi AIs
 R2: 90th percentile of normal skin AIs divided by the average of benign nevi AIs, where the 15th percentile of normal tissue AIs was subtracted from both the numerator and denominator

| Pkey | ExAccn | UnigenelD | Unigene Title | R1 | R2 | |
|------|--------|-----------|---------------|---|-------|-------|
| 10 | 420813 | X51501 | Hs.99949 | prolactin-induced protein | 27.72 | 28.59 |
| | 408591 | AF015224 | Hs.46452 | mammaglobin 1 | 26.40 | 28.34 |
| | 422166 | W72424 | Hs.112405 | S100 calcium-binding protein A9 (calgran | 21.33 | 21.57 |
| | 418026 | BE379727 | Hs.83213 | fatty acid binding protein 4, adipocyte | 18.06 | 18.96 |
| 15 | 429441 | AJ224172 | Hs.204096 | lipophilin B (uteroglobin family member) | 16.61 | 18.06 |
| | 428087 | AA100573 | Hs.182421 | troponin C2, fast | 14.70 | 14.60 |
| | 407245 | X90568 | Hs.172004 | titin | 13.08 | 13.84 |
| | 428824 | W23624 | Hs.173059 | ESTs | 12.89 | 13.36 |
| | 428330 | L22524 | Hs.22556 | matrix metalloproteinase 7 (matrilysin, | 12.78 | 13.98 |
| | 444816 | Z48633 | Hs.283742 | HLsapiens mRNA for retrotransposon | 12.26 | 9.86 |
| 20 | 453309 | AI791809 | Hs.32949 | defensin, beta 1 | 12.02 | 10.62 |
| | 423024 | AA593731 | Hs.325823 | ESTs, Moderately similar to ALU5_HUMAN A | 11.90 | 10.86 |
| | 446227 | AI281459 | Hs.270114 | ESTs | 11.79 | 12.32 |
| | 413902 | AU076743 | Hs.75613 | CD36 antigen (collagen type I receptor, | 11.19 | 10.82 |
| | 432877 | AW974111 | Hs.292477 | ESTs | 11.18 | 11.30 |
| 25 | 426752 | X69490 | Hs.172004 | titin | 10.97 | 12.63 |
| | 427899 | AA829286 | Hs.332053 | serum amyloid A1 | 10.85 | 13.85 |
| | 407230 | AA157857 | Hs.182265 | keratin 19 | 10.79 | 11.40 |
| | 451029 | AA852097 | Hs.25829 | ras-related protein | 10.78 | 10.35 |
| | 421296 | NM_002666 | Hs.103253 | perilipin | 10.73 | 11.25 |
| 30 | 431211 | M86849 | Hs.323733 | gap junction protein, beta 2, 26kD (conn | 10.66 | 7.24 |
| | 422633 | X56832 | Hs.118804 | enolase 3, (beta, muscle) | 10.57 | 9.92 |
| | 405121 | | | | 10.41 | 10.54 |
| | 450912 | AW939251 | Hs.25647 | mitogen-activated protein kinase 8 inter | 10.26 | 23.20 |
| | 420859 | AW468397 | Hs.100000 | S100 calcium-binding protein A8 (calgran | 10.25 | 9.45 |
| 35 | 410850 | AW362867 | Hs.302738 | Homo sapiens cDNA: FLJ21425 fis, clone C | 10.15 | 9.88 |
| | 416931 | D45371 | Hs.80485 | adipose most abundant gene transcript 1 | 10.13 | 11.58 |
| | 447966 | AA340605 | Hs.105887 | ESTs, Weakly similar to Homolog of rat Z | 10.09 | 5.51 |
| | 401203 | | | Target Exon | 9.95 | 10.74 |
| 40 | 425545 | N98529 | Hs.158295 | Homo sapiens, clone MGC:12401, mRNA, com | 9.94 | 11.47 |
| | 425580 | L11144 | Hs.1907 | galanin | 9.66 | 6.60 |
| | 414092 | Z14244 | Hs.75752 | cytochrome c oxidase subunit VIIb | 9.45 | 6.44 |
| | 420919 | M57892 | Hs.100322 | carbonic anhydrase VI | 9.41 | 10.49 |
| | 443162 | T49951 | Hs.9029 | DKFZP434G032 protein | 9.36 | 10.58 |
| 45 | 430154 | AW583058 | Hs.234726 | serine (or cysteine) proteinase inhibitor | 8.91 | 10.27 |
| | 452322 | BE566343 | Hs.28988 | glutaredoxin (thioltransferase) | 8.90 | 7.26 |
| | 430071 | AA355986 | Hs.232068 | transcription factor 8 (represses interl | 8.86 | 8.94 |
| | 417240 | N57568 | Hs.48028 | EST | 8.81 | 18.90 |
| | 415477 | NM_002228 | Hs.78465 | v-jun avian sarcoma virus 17 oncogene ho | 8.72 | 6.86 |
| | 430130 | AL137311 | Hs.234074 | Homo sapiens mRNA; cDNA DKFZp761G02121 (| 8.39 | 10.26 |
| 50 | 408491 | AI088063 | Hs.7882 | ESTs | 8.00 | 8.20 |
| | 414657 | AA424074 | Hs.76780 | protein phosphatase 1, regulatory (inhib | 7.99 | 8.14 |
| | 409738 | BE222975 | Hs.56205 | insulin induced gene 1 | 7.95 | 7.75 |
| | 428221 | U96781 | Hs.183075 | ATPase, Ca transporting, cardiac muscle, | 7.89 | 8.86 |
| | 451831 | NM_001674 | Hs.460 | activating transcription factor 3 | 7.79 | 7.51 |
| 55 | 410867 | X63556 | Hs.750 | fibrillin 1 (Marfan syndrome) | 7.76 | 7.55 |
| | 444984 | H15474 | Hs.132898 | fatty acid desaturase 1 | 7.75 | 5.64 |
| | 413076 | U10564 | Hs.75188 | wee1 (S. pombe) homolog | 7.68 | 5.65 |
| | 410532 | T53088 | Hs.155376 | hemoglobin, beta | 7.64 | 4.73 |
| | 442757 | AI739528 | Hs.28345 | ESTs | 7.62 | 7.66 |
| 60 | 412047 | AA934589 | Hs.49696 | ESTs | 7.61 | 7.48 |
| | 410052 | AA525225 | Hs.334630 | Homo sapiens cDNA FLJ14462 fis, clone MA | 7.52 | 7.28 |
| | 439394 | AA149250 | Hs.56105 | ESTs | 7.52 | 6.72 |
| | 442941 | AU076728 | Hs.8867 | cysteine-rich, angiogenic inducer, 61 | 7.51 | 6.27 |
| | 450680 | AF131784 | Hs.25318 | Homo sapiens clone 25194 mRNA sequence | 7.51 | 4.10 |
| 65 | 456525 | AW468397 | Hs.100000 | S100 calcium-binding protein A8 (calgran | 7.49 | 8.08 |
| | 407334 | AA494411 | Hs.296031 | ESTs | 7.48 | 6.78 |
| | 414449 | AA557660 | Hs.76152 | decorin | 7.39 | 8.30 |
| | 432305 | M62402 | Hs.274313 | insulin-like growth factor binding prote | 7.38 | 8.79 |
| | 407328 | AA508857 | | ESTs, Weakly similar to ALU1_HUMAN ALU S | 7.35 | 7.20 |
| 70 | 431842 | NM_005764 | Hs.271473 | epithelial protein up-regulated in carci | 7.06 | 6.93 |
| | 426488 | X03350 | Hs.4 | alcohol dehydrogenase 1B (class I), beta | 7.03 | 7.85 |
| | 445502 | AW379160 | Hs.12813 | DKFZP434J214 protein | 7.01 | 6.63 |
| | 419285 | D31887 | Hs.89868 | KIAA0062 protein | 7.01 | 5.82 |
| | 409024 | AW883529 | Hs.173830 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 6.99 | 4.58 |
| | 422963 | M79141 | Hs.13234 | ESTs | 6.99 | 4.08 |
| 75 | 447918 | AI129320 | Hs.115175 | ESTs, Highly similar to JCS818 gamma-act | 6.98 | 6.49 |
| | 410530 | M25809 | Hs.64173 | ATPase, H transporting, lysosomal (vacuo | 6.96 | 7.04 |
| | 444381 | BE387335 | Hs.283713 | ESTs, Weakly similar to S64054 hypothei | 6.95 | 8.08 |
| | 417993 | AW963705 | Hs.301183 | molecule possessing ankyrin repeats indu | 6.94 | 7.12 |
| 80 | 443060 | D78874 | Hs.8944 | procollagen C-endopeptidase enhancer 2 | 6.94 | 6.79 |
| | 427890 | AA435761 | | ESTs | 6.94 | 6.68 |
| | 442207 | AI565004 | | cathepsin D (lysosomal aspartyl protease | 6.93 | 4.66 |
| | 442083 | RS0192 | Hs.165062 | ESTs | 6.92 | 6.92 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|-------|
| 5 | 441633 | AW958544 | Hs.112242 | normal mucosa of esophagus specific 1 | 6.87 | 5.07 |
| | 407722 | BE252241 | Hs.38041 | pyridoxal (pyridoxine, vitamin B6) kinas | 6.87 | 4.99 |
| | 444051 | N48373 | Hs.10247 | activated leucocyte cell adhesion molecu | 6.84 | 5.33 |
| | 414841 | H55601 | Hs.77490 | glutathione S-transferase theta 1 | 6.84 | 3.47 |
| | 430314 | AA369601 | Hs.239138 | pre-B-cell colony-enhancing factor | 6.79 | 7.14 |
| 10 | 427704 | AW971063 | Hs.292882 | ESTs | 6.72 | 7.30 |
| | 431713 | AK000388 | Hs.267997 | EHM2 gene | 6.72 | 7.10 |
| | 451253 | H48299 | Hs.26126 | claudin 10 | 6.71 | 7.20 |
| | 453187 | AI161383 | Hs.34549 | ESTs, Highly similar to S94541 1 clone 4 | 6.68 | 3.02 |
| | 400304 | AF005082 | Hs.113261 | Homo sapiens skin-specific protein (xp33 | 6.64 | 6.08 |
| 15 | 434625 | W01370 | Hs.46824 | ESTs | 6.61 | 6.92 |
| | 408063 | BE086548 | Hs.42346 | calcineurin-binding protein calsarcin-1 | 6.60 | 7.29 |
| | 425280 | U31519 | Hs.1872 | phosphoenolpyruvate carboxykinase 1 (sol | 6.55 | 6.79 |
| | 411388 | X72925 | Hs.69752 | desmocollin 1 | 6.55 | 3.44 |
| | 413731 | BE243845 | Hs.75511 | connective tissue growth factor | 6.52 | 4.86 |
| 20 | 455863 | AA907305 | Hs.36475 | ESTs | 6.50 | 4.24 |
| | 412247 | AF022375 | Hs.73793 | vascular endothelial growth factor | 6.49 | 4.56 |
| | 407102 | AA007629 | | glycerol-3-phosphate dehydrogenase 1 (so | 6.47 | 7.23 |
| | 421407 | T82331 | Hs.182278 | ESTs, Weakly similar to CGH06C collagen | 6.47 | 8.55 |
| | 406867 | AA157857 | Hs.182265 | keratin 19 | 6.44 | 6.23 |
| 25 | 429504 | X99133 | Hs.204238 | lipocalin 2 (oncogene 24p3) (NGAL) | 6.43 | 6.79 |
| | 446945 | AI193115 | Hs.16611 | tumor protein D52-like 1 | 6.43 | 5.66 |
| | 413172 | M38180 | Hs.38586 | hydroxy-delta-5-steroid dehydrogenase, 3 | 6.39 | 7.09 |
| | 407395 | AF005082 | | gb:Homo sapiens skin-specific protein (x | 6.39 | 4.76 |
| | 450626 | AW190989 | Hs.1508 | insulin-degrading enzyme | 6.37 | 6.22 |
| 30 | 450713 | AL133611 | Hs.25362 | Homo sapiens mRNA; cDNA DKFZp43401317 (f | 6.37 | 4.91 |
| | 437596 | AA761490 | | ESTs, Moderately similar to S65657 alpha | 6.35 | 5.31 |
| | 430191 | AI149880 | Hs.188809 | ESTs | 6.34 | 6.15 |
| | 433713 | AW976511 | Hs.112592 | ESTs | 6.34 | 5.67 |
| | 420107 | AL043980 | Hs.7886 | pellino (Drosophila) homolog 1 | 6.33 | 6.39 |
| 35 | 422069 | AJ010063 | Hs.343603 | titin-cap (telethonin) | 6.33 | 5.77 |
| | 437176 | AW176909 | Hs.42346 | calcineurin-binding protein calsarcin-1 | 6.30 | 5.45 |
| | 433412 | AV653729 | Hs.8185 | CGI-44 protein; sulfide dehydrogenase li | 6.29 | 6.68 |
| | 447335 | BE617695 | Hs.286192 | hypothetical protein FLJ20940 | 6.28 | 10.35 |
| | 413063 | AL035737 | Hs.75184 | chitinase 3-like 1 (cartilage glycoprote | 6.21 | 5.98 |
| 40 | 440116 | AI798851 | | hemoglobin, gamma G | 6.18 | 6.86 |
| | 454229 | AW957744 | Hs.278469 | lacrimal proline rich protein | 6.17 | 6.54 |
| | 441188 | AW292830 | Hs.255609 | ESTs | 6.12 | 6.68 |
| | 451144 | AW956103 | Hs.61712 | pyruvate dehydrogenase kinase, isoenzyme | 6.12 | 5.79 |
| | 431319 | AA873350 | Hs.302232 | ESTs | 6.11 | 7.91 |
| 45 | 442498 | U54617 | Hs.8364 | Homo sapiens pyruvate dehydrogenase kina | 6.10 | 5.63 |
| | 414555 | N98569 | Hs.76422 | phospholipase A2, group IIA (platelets, | 6.08 | 6.96 |
| | 418321 | D63477 | Hs.84087 | KIAA0143 protein | 6.08 | 4.71 |
| | 443072 | AI937532 | | gb:wp78d02.x1 NCI_CGAP_Bm25 Homo sapien | 6.07 | 5.48 |
| | 423712 | W46802 | Hs.81988 | disabled (Drosophila) homolog 2 (mitogen | 6.04 | 5.81 |
| 50 | 442679 | R53718 | | hypothetical protein FLJ10659 | 6.03 | 5.67 |
| | 424824 | AI217440 | Hs.143873 | ESTs | 6.02 | 5.46 |
| | 413719 | BE439580 | Hs.75498 | small inducible cytokine subfamily A (Cy | 6.01 | 7.05 |
| | 428358 | AA993222 | Hs.101915 | Stargardt disease 3 (autosomal dominant) | 5.94 | 7.17 |
| | 430821 | AA487264 | Hs.154974 | Homo sapiens mRNA; cDNA DKFZp667N064 (fr | 5.92 | 5.79 |
| 55 | 424670 | W61215 | Hs.116651 | epithelial V-like antigen 1 | 5.92 | 5.63 |
| | 424673 | AA345051 | Hs.294092 | ESTs, Weakly similar to I38022 hypothe | 5.91 | 6.81 |
| | 418205 | L21715 | Hs.83760 | troponin I, skeletal, fast | 5.91 | 6.95 |
| | 400440 | X83957 | Hs.83870 | nebulin | 5.89 | 7.01 |
| | 444239 | R57988 | Hs.10706 | epithelial protein lost in neoplasm beta | 5.89 | 5.49 |
| 60 | 419517 | AF052107 | Hs.90797 | Homo sapiens clone 23620 mRNA sequence | 5.86 | 5.88 |
| | 432626 | AA471098 | Hs.278544 | acetyl-Coenzyme A acetyltransferase 2 (a | 5.85 | 5.58 |
| | 407584 | W25945 | Hs.8173 | hypothetical protein FLJ10803 | 5.81 | 5.09 |
| | 449335 | AW150717 | Hs.345728 | STAT induced STAT inhibitor 3 | 5.79 | 6.33 |
| | 445607 | AA488107 | Hs.30156 | ESTs, Weakly similar to unnamed protein | 5.78 | 5.91 |
| 65 | 424571 | BE379766 | | polymerase (RNA) II (DNA directed) polyp | 5.78 | 3.74 |
| | 412630 | AA738437 | Hs.26226 | Homo sapiens cDNA: FLJ21286 fs, clone C | 5.76 | 4.21 |
| | 408819 | AW163483 | Hs.48320 | double ring-finger protein, Dorfin | 5.71 | 4.59 |
| | 433027 | AF191018 | Hs.279923 | putative nucleotide binding protein, est | 5.70 | 4.71 |
| | 406704 | M21665 | Hs.929 | myosin, heavy polypeptide 7, cardiac mus | 5.68 | 6.12 |
| 70 | 408515 | AI289507 | Hs.299883 | hypothetical protein FLJ23399 | 5.67 | 4.81 |
| | 443827 | AI087867 | Hs.134667 | ESTs | 5.67 | 5.54 |
| | 429693 | BE254962 | Hs.211612 | SEC24 (S. cerevisiae) related gene famil | 5.67 | 4.12 |
| | 427373 | AB007972 | Hs.130760 | myosin phosphatase, target subunit 2 | 5.66 | 4.27 |
| | 428666 | AL080190 | Hs.189242 | Homo sapiens mRNA; cDNA DKFZp434A202 (fr | 5.65 | 5.16 |
| 75 | 421834 | BE543205 | Hs.288771 | DKFZP586A0522 protein | 5.65 | 4.52 |
| | 427081 | AA474533 | Hs.170528 | ESTs, Moderately similar to ALUC_HUMAN ! | 5.65 | 4.81 |
| | 419731 | S47242 | Hs.92909 | SON DNA binding protein | 5.64 | 3.77 |
| | 420787 | AA564248 | | ESTs, Weakly similar to I38022 hypothe | 5.64 | 3.27 |
| | 420682 | AI380552 | Hs.88602 | ESTs | 5.63 | 4.13 |
| 80 | 410541 | AA065003 | Hs.64179 | syntenin-2 protein | 5.62 | 5.84 |
| | 431360 | NM_009427 | Hs.251680 | loricrin | 5.61 | 5.14 |
| | 418127 | BE243982 | Hs.83532 | membrane cofactor protein (CD46, trophob | 5.61 | 4.28 |
| | 430332 | R51790 | Hs.239483 | Human clone 23933 mRNA sequence | 5.60 | 5.76 |
| | 427850 | AA416756 | Hs.161051 | ESTs, Moderately similar to ALU6_HUMAN A | 5.51 | 16.04 |
| 80 | 429679 | NM_006290 | Hs.211600 | tumor necrosis factor, alpha-induced pro | 5.49 | 5.28 |
| | 422082 | AA016188 | Hs.111244 | hypothetical protein | 5.49 | 5.23 |
| | 419461 | AI452601 | Hs.288869 | nuclear receptor subfamily 2, group F, m | 5.49 | 4.40 |

| | | | | | | |
|----|--------|-----------|-----------|---|------|-------|
| | 430714 | AA484757 | Hs.287601 | Homo sapiens cDNA FLJ13830 fis, clone TH | 5.48 | 5.38 |
| | 407744 | AB020629 | Hs.38095 | ATP-binding cassette, sub-family A (ABC1 | 5.46 | 5.11 |
| | 400494 | | | ENSP00000238970":ClG30 (Fragment), | 5.45 | 3.63 |
| 5 | 415062 | H45100 | Hs.49753 | uveal autoantigen with coiled coil domain | 5.43 | 4.25 |
| | 449291 | BE176893 | Hs.23440 | KIAA1105 protein | 5.41 | 3.82 |
| | 435538 | AB011540 | Hs.4930 | low density lipoprotein receptor-related | 5.41 | 2.62 |
| | 417035 | AA192455 | Hs.22968 | Homo sapiens clone IMAGE:451939, mRNA se | 5.40 | 5.40 |
| | 434535 | AI611729 | Hs.167619 | ESTs, Moderately similar to ALUC_HUMAN I | 5.40 | 5.20 |
| | 408085 | N25929 | Hs.342849 | ADP-ribosylation factor-like 5 | 5.39 | 4.59 |
| 10 | 413778 | AA090235 | Hs.75535 | myosin, light polypeptide 2, regulatory, | 5.37 | 14.96 |
| | 436090 | AI640635 | Hs.332879 | EST | 5.37 | 5.33 |
| | 406805 | AI686003 | Hs.296031 | ESTs | 5.35 | 5.49 |
| | 426510 | AW861225 | Hs.251928 | BANP homolog, SMAR1 homolog | 5.35 | 6.83 |
| | 406706 | X03740 | Hs.231581 | myosin, heavy polypeptide 1, skeletal mu | 5.34 | 7.50 |
| 15 | 456332 | AA228357 | | gb:nc39d05.r1 NCI_CGAP_Pr2 Homo sapiens | 5.34 | 4.88 |
| | 421999 | U50535 | Hs.110630 | Human BRCA2 region, mRNA sequence CG006 | 5.34 | 4.75 |
| | 418479 | AA829976 | | mannosidase, alpha, class 1A, member 2 | 5.34 | 3.59 |
| | 417059 | AL037672 | Hs.81071 | extracellular matrix protein 1 | 5.34 | 4.71 |
| | 424008 | R02740 | Hs.137555 | putative chemokine receptor; GTP-binding | 5.34 | 4.75 |
| 20 | 415694 | AW194301 | Hs.339283 | Human DNA sequence from clone RP1-187J11 | 5.34 | 8.69 |
| | 452747 | BE153855 | Hs.61460 | Ig superfamily receptor LNIR | 5.31 | 5.81 |
| | 449271 | AW338067 | Hs.7869 | Homo sapiens cDNA FLJ11946 fis, clone HE | 5.30 | 4.35 |
| | 437135 | AL038624 | Hs.208752 | ESTs, Weakly similar to ALU8_HUMAN ALU S | 5.29 | 4.92 |
| | 419925 | AA159850 | Hs.93765 | lipoma HMGIC fusion partner | 5.29 | 5.02 |
| 25 | 415192 | D17793 | Hs.78183 | aldo-keto reductase family 1, member C3 | 5.28 | 5.33 |
| | 453999 | BE328153 | Hs.240087 | ESTs | 5.28 | 3.40 |
| | 408958 | T99607 | Hs.49346 | signal recognition particle 54kD | 5.28 | 2.84 |
| | 452496 | AA114926 | Hs.169531 | ESTs | 5.28 | 5.48 |
| | 424058 | AL121516 | Hs.138617 | thyroid hormone receptor interactor 12 | 5.27 | 3.72 |
| 30 | 443265 | AI916207 | Hs.9167 | SH3 domain binding glutamic acid-rich pr | 5.26 | 4.62 |
| | 407013 | U35637 | Hs.83870 | gb:Human nebulin mRNA, partial cds | 5.26 | 6.21 |
| | 414602 | AW630088 | Hs.76550 | Homo sapiens mRNA; cDNA DKFZp564B1264 (f | 5.26 | 4.21 |
| | 410284 | U50939 | Hs.61828 | amyloid beta precursor protein-binding p | 5.26 | 4.43 |
| | 445107 | AI208121 | Hs.147313 | ESTs, Weakly similar to I38022 hypothei | 5.25 | 5.61 |
| 35 | 446267 | AW450103 | Hs.151124 | ESTs | 5.24 | 4.44 |
| | 422278 | AF072873 | Hs.114218 | frizzled (Drosophila) homolog 6 | 5.23 | 3.14 |
| | 448585 | AB020676 | Hs.21543 | KIAA0869 protein | 5.23 | 6.21 |
| | 421993 | R22497 | Hs.110571 | growth arrest and DNA-damage-inducible, | 5.22 | 6.84 |
| | 414407 | AA147026 | Hs.76704 | ESTs | 5.22 | 5.29 |
| 40 | 423720 | AL044191 | Hs.23388 | hypothetical protein DKFZp434F0318 | 5.22 | 5.85 |
| | 415997 | NM_003590 | Hs.78946 | culin 3 | 5.21 | 3.66 |
| | 411531 | AB014511 | Hs.70504 | ATPase, Class II, type 9A | 5.21 | 3.95 |
| | 441619 | NM_014056 | Hs.7917 | DKFZP564K247 protein | 5.20 | 4.38 |
| | 435232 | NM_001262 | Hs.4854 | cyclin-dependent kinase inhibitor 2C (p1 | 5.19 | 4.52 |
| 45 | 415167 | AA160784 | Hs.26410 | ESTs | 5.19 | 3.13 |
| | 431416 | AA532718 | Hs.178604 | ESTs | 5.18 | 5.38 |
| | 439995 | AL137480 | Hs.6834 | KIAA1014 protein | 5.17 | 3.14 |
| | 416784 | AA334592 | Hs.79914 | lumican | 5.17 | 6.18 |
| | 446082 | AI274139 | Hs.156452 | ESTs | 5.16 | 5.14 |
| 50 | 400196 | | | Eos Control | 5.16 | 5.05 |
| | 414525 | C14904 | Hs.45184 | Homo sapiens cDNA FLJ12284 fis, clone MA | 5.16 | 4.31 |
| | 414242 | AA749230 | Hs.26433 | dolichyl-phosphate (UDP-N-acetylglucosam | 5.15 | 4.89 |
| | 430699 | AW969847 | Hs.292718 | ESTs, Weakly similar to RET2_HUMAN RETIN | 5.14 | 5.22 |
| | 440383 | AA884208 | Hs.30484 | ESTs | 5.13 | 5.09 |
| 55 | 431628 | AF146277 | | CD2-associated protein | 5.13 | 5.03 |
| | 407047 | X65965 | | gb:Hsapiens SOD-2 gene for manganese su | 5.13 | 4.31 |
| | 433688 | AA628467 | Hs.112572 | Homo sapiens cDNA FLJ14130 fis, clone MA | 5.12 | 3.57 |
| | 437704 | AA766142 | Hs.131810 | ESTs, Moderately similar to ALU1_HUMAN A | 5.12 | 3.30 |
| | 426101 | AL049987 | | Homo sapiens mRNA; cDNA DKFZp564F112 (tr | 5.11 | 6.08 |
| 60 | 428297 | AA236291 | Hs.183583 | serine (or cysteine) proteinase inhibito | 5.10 | 4.31 |
| | 416382 | D86985 | Hs.79276 | KIAA0232 gene product | 5.10 | 3.79 |
| | 437150 | R51407 | Hs.77910 | 3-hydroxy-3-methylglutaryl-Coenzyme A sy | 5.10 | 6.58 |
| | 454947 | AW846590 | | gb:QV0-CT0180-011099-025-d07 CT0180 Homo | 5.09 | 4.82 |
| | 434647 | W74158 | Hs.103189 | lipopolysaccharide specific response-68 | 5.09 | 4.90 |
| 65 | 418730 | AA091027 | Hs.325625 | Homo sapiens clone 23938 mRNA sequence | 5.09 | 3.46 |
| | 449338 | H73444 | Hs.394 | adrenomedullin | 5.09 | 6.26 |
| | 438962 | BE046594 | | gb:hn41c11.x1 NCI_CGAP_RDF2 Homo sapiens | 5.08 | 5.60 |
| | 431693 | AI459519 | | serine (or cysteine) proteinase inhibito | 5.07 | 2.83 |
| | 420583 | H77859 | Hs.65450 | reticulon 4 | 5.06 | 6.71 |
| 70 | 431048 | R50253 | Hs.249129 | cell death-inducing DFFA-like effector a | 5.06 | 6.06 |
| | 432125 | AW972657 | Hs.183006 | Homo sapiens cDNA FLJ12300 fis, clone MA | 5.05 | 6.32 |
| | 447945 | AI922838 | Hs.9670 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 5.05 | 3.72 |
| | 442547 | AA306997 | Hs.217484 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 5.05 | 2.86 |
| | 414176 | BE140638 | Hs.75794 | EDG-2 (endothelial differentiation, lys | 5.03 | 4.43 |
| 75 | 445263 | H57646 | Hs.42586 | KIAA1560 protein | 5.03 | 6.67 |
| | 448490 | AI523897 | Hs.271692 | ESTs, Weakly similar to I38022 hypothei | 5.03 | 4.88 |
| | 450515 | AW304226 | | biphenyl hydrolase-like (serine hydrolas | 5.03 | 4.36 |
| | 440624 | AF017987 | Hs.7306 | secreted frizzled-related protein 1 | 5.01 | 5.48 |
| | 417165 | R80137 | Hs.302738 | Homo sapiens cDNA: FLJ21425 fis, clone C | 5.01 | 5.61 |
| 80 | 417640 | D30857 | Hs.82353 | protein C receptor, endothelial (EPCR) | 5.01 | 5.32 |
| | 413475 | AW021488 | Hs.26981 | ESTs | 5.01 | 3.90 |
| | 414792 | BE314949 | Hs.87128 | hypothetical protein FLJ23309 | 5.00 | 4.54 |
| | 424074 | AI902456 | Hs.210761 | ESTs, Weakly similar to I38022 hypothei | 5.00 | 3.19 |

| | | | | | | |
|----|--------|-----------|-----------|---|------|-------|
| 5 | 424620 | AA101043 | Hs.151254 | kallikrein 7 (chymotryptic, stratum com | 4.99 | 6.25 |
| | 439039 | AI656707 | Hs.48713 | ESTs | 4.99 | 6.60 |
| | 422305 | AI928242 | Hs.293438 | ESTs, Highly similar to AF198488 1 trans | 4.98 | 9.59 |
| | 410579 | AK001628 | Hs.64691 | KIAA0483 protein | 4.98 | 4.52 |
| | 449710 | AA002207 | Hs.17385 | Homo sapiens clone IMAGE:119716, mRNA se | 4.98 | 3.84 |
| 10 | 434230 | AA551569 | | hypothetical protein PRO2822 | 4.98 | 3.63 |
| | 426468 | AA379306 | Hs.117558 | ESTs | 4.98 | 3.56 |
| | 421690 | AW162667 | Hs.106857 | calbindin 2, (29kD, calretinin) | 4.96 | 6.41 |
| | 448144 | AW169230 | | ESTs, Moderately similar to PC4259 ferri | 4.96 | 3.28 |
| | 412129 | M21984 | Hs.73454 | troponin T3, skeletal, fast | 4.96 | 5.75 |
| 15 | 450071 | AA018283 | Hs.24359 | Homo sapiens cDNA FLJ111174 fis, clone PL | 4.96 | 3.21 |
| | 433934 | AW273261 | Hs.216292 | ESTs | 4.95 | 4.39 |
| | 446320 | AF126245 | Hs.14791 | acyl-Coenzyme A dehydrogenase family, me | 4.95 | 4.01 |
| | 446161 | AA628206 | Hs.14125 | p53 regulated PA26 nuclear protein | 4.94 | 4.54 |
| | 453225 | BE258769 | | acetyl-Coenzyme A acyltransferase 2 (mit | 4.94 | 4.49 |
| 20 | 444476 | AF020038 | Hs.11223 | isocitrate dehydrogenase 1 (NADP), solub | 4.94 | 4.19 |
| | 445493 | AI915771 | | metallothionein 1E (functional) | 4.93 | 5.68 |
| | 422292 | AI815733 | Hs.114360 | transforming growth factor beta-stimulat | 4.93 | 5.47 |
| | 417054 | AF017060 | | aldehyde oxidase 1 | 4.93 | 4.51 |
| | 425917 | W28517 | Hs.117167 | Homo sapiens cDNA: FLJ23067 fis, clone L | 4.93 | 3.34 |
| 25 | 408681 | AW953853 | Hs.281462 | ESTs, Weakly similar to I38022 hypothe | 4.93 | 5.61 |
| | 451267 | AI033894 | Hs.117865 | solute carrier family 17 (anion/sugar tr | 4.92 | 3.27 |
| | 447137 | AW970192 | Hs.171942 | ras responsive element binding protein 1 | 4.91 | 4.26 |
| | 427451 | AI690916 | Hs.178137 | transducer of ERBB2, 1 | 4.90 | 6.00 |
| | 432314 | AA533447 | Hs.312989 | ESTs | 4.90 | 3.79 |
| 30 | 440692 | AL031591 | Hs.73770 | phosphatidylinositol transfer protein, b | 4.89 | 3.71 |
| | 428594 | BE387236 | Hs.75415 | beta-2-microglobulin | 4.89 | 3.27 |
| | 437802 | AI475995 | Hs.122910 | ESTs | 4.87 | 4.06 |
| | 437974 | T74445 | Hs.5957 | Homo sapiens clone 24416 mRNA sequence | 4.86 | 6.54 |
| | 427156 | BE621719 | Hs.173802 | KIAA0603 gene product | 4.86 | 5.15 |
| 35 | 433179 | AW362945 | Hs.162459 | ESTs | 4.86 | 5.50 |
| | 428957 | NM_003881 | Hs.194679 | WNT1 inducible signaling pathway protein | 4.85 | 5.29 |
| | 453855 | AA039576 | Hs.37858 | ESTs, Weakly similar to ALUB_HUMAN !!! | 4.85 | 3.59 |
| | 433143 | BE552155 | Hs.294035 | ESTs, Weakly similar to ALU5_HUMAN ALU S | 4.85 | 3.45 |
| | 429279 | AB018271 | Hs.198689 | KIAA0728 protein | 4.83 | 3.80 |
| 40 | 445773 | H73456 | Hs.13299 | Homo sapiens mRNA: cDNA DKF2p761M0111 (f | 4.82 | 4.20 |
| | 416349 | X69089 | Hs.79227 | myomesin (M-protein) 2 (165kD) | 4.82 | 4.01 |
| | 408138 | AA535740 | | tumor protein p53-binding protein, 1 | 4.81 | 4.19 |
| | 432566 | AW439330 | Hs.256889 | ESTs, Weakly similar to 2109260A B cell | 4.80 | 3.99 |
| | 444677 | AL110212 | Hs.301005 | purine-rich element binding protein B | 4.80 | 3.50 |
| 45 | 422658 | AF231981 | Hs.250175 | homolog of yeast long chain polyunsatura | 4.80 | 10.20 |
| | 431926 | AW972724 | | gb:EST384816 MAGE resequences, MAGL Homo | 4.79 | 4.39 |
| | 407839 | AA045144 | Hs.161566 | ESTs | 4.79 | 2.98 |
| | 421998 | R74441 | | poly(A)-binding protein, nuclear 1 | 4.77 | 4.78 |
| | 416987 | D86957 | Hs.80712 | KIAA0202 protein | 4.76 | 3.99 |
| 50 | 448988 | Y09763 | Hs.22785 | gamma-aminobutyric acid (GABA) A recepto | 4.76 | 7.59 |
| | 440494 | BE618768 | Hs.7232 | acetyl-Coenzyme A carboxylase alpha | 4.75 | 4.38 |
| | 453180 | N46243 | Hs.110373 | ESTs, Highly similar to T42626 secreted | 4.75 | 3.92 |
| | 413276 | Z24725 | Hs.75260 | mitogen inducible 2 | 4.75 | 5.68 |
| | 437239 | AW503395 | Hs.5541 | ATPase, Ca transporting, ubiquitous | 4.74 | 5.57 |
| 55 | 414622 | AI752666 | Hs.76669 | nicotinamide N-methyltransferase | 4.74 | 11.58 |
| | 429587 | AA283969 | Hs.334706 | Homo sapiens cDNA FLJ11801 fis, clone HE | 4.74 | 3.79 |
| | 407242 | M18728 | | gb:Human nonspecific crossreacting antig | 4.73 | 4.88 |
| | 445229 | BE276013 | Hs.172364 | Homo sapiens mRNA for FLJ00086 protein, | 4.73 | 4.79 |
| | 447429 | AB007920 | Hs.18586 | KIAA0451 gene product | 4.72 | 2.38 |
| 60 | 444930 | BE185536 | Hs.301183 | molecule possessing ankyrin repeats indu | 4.71 | 5.10 |
| | 414848 | AI803447 | Hs.77496 | small nuclear ribonucleoprotein polypept | 4.71 | 2.51 |
| | 439652 | W67826 | Hs.55412 | ESTs, Weakly similar to K1CJ_HUMAN KERAT | 4.70 | 6.13 |
| | 453145 | R63438 | Hs.183454 | Homo sapiens cDNA FLJ14883 fis, clone PL | 4.70 | 3.06 |
| | 421302 | T34462 | Hs.103291 | neurtin | 4.69 | 4.96 |
| 65 | 425118 | AU076611 | Hs.154672 | methylene tetrahydrofolate dehydrogenase | 4.68 | 5.01 |
| | 448079 | R76981 | | thyroid hormone receptor-associated prot | 4.68 | 3.97 |
| | 434558 | AW264102 | Hs.39168 | ESTs | 4.67 | 3.42 |
| | 408239 | AA053401 | | ESTs, Moderately similar to ALU7_HUMAN A | 4.67 | 6.17 |
| | 454416 | AI912097 | Hs.163208 | ESTs | 4.66 | 3.97 |
| 70 | 427215 | AW246148 | Hs.268371 | hypothetical protein FLJ20274 | 4.66 | 3.37 |
| | 451583 | AI653797 | Hs.24133 | ESTs | 4.65 | 3.81 |
| | 446525 | AW967069 | Hs.211556 | hypothetical protein MGC5487 | 4.65 | 6.14 |
| | 436176 | AL121422 | Hs.54900 | serologically defined colon cancer antig | 4.65 | 3.65 |
| | 450528 | NM_014072 | Hs.25063 | PRO0461 protein | 4.64 | 2.99 |
| 75 | 417259 | AW903838 | Hs.81800 | chondroitin sulfate proteoglycan 2 (vers | 4.64 | 4.72 |
| | 408741 | M73720 | Hs.646 | carboxypeptidase A3 (mast cell) | 4.63 | 5.55 |
| | 417733 | AL048678 | Hs.82503 | H.sapiens mRNA for 3'UTR of unknown prot | 4.63 | 5.04 |
| | 436280 | AI690734 | | Homo sapiens cDNA: FLJ22562 fis, clone H | 4.63 | 3.55 |
| | 428744 | BE267033 | Hs.192853 | ubiquitin-conjugating enzyme E2G 2 (homo | 4.63 | 2.85 |
| 80 | 427007 | NM_006283 | Hs.173159 | transforming, acidic coiled-coil contain | 4.63 | 3.00 |
| | 453767 | AB011792 | Hs.35094 | extracellular matrix protein 2, female o | 4.62 | 5.14 |
| | 449971 | AA807346 | Hs.288581 | Homo sapiens cDNA FLJ14296 fis, clone PL | 4.62 | 4.49 |
| | 409598 | NM_014018 | Hs.55097 | mitochondrial ribosomal protein S28 | 4.62 | 3.56 |
| | 413305 | NM_000426 | Hs.323511 | Homo sapiens cDNA: FLJ23176 fis, clone L | 4.62 | 4.24 |
| | 412577 | Z22968 | Hs.74076 | CD163 antigen | 4.61 | 8.03 |
| | 424046 | AF027866 | Hs.138202 | serine (or cysteine) proteinase inhibito | 4.61 | 6.86 |
| | 452289 | BE568205 | Hs.28827 | mitogen-activated protein kinase kinase | 4.61 | 4.33 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|-------|
| 5 | 458971 | AL119206 | Hs.101874 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 4.61 | 4.16 |
| | 433256 | AW604447 | Hs.339408 | ESTs, Weakly similar to S26689 hypothe | 4.61 | 3.58 |
| | 440596 | H13032 | Hs.103378 | hypothetical protein MGC11034 | 4.61 | 3.22 |
| | 427919 | AA173942 | Hs.326416 | Homo sapiens mRNA; cDNA DKFZp564H1916 (I | 4.60 | 4.74 |
| | 424651 | AI93206 | Hs.32425 | ESTs | 4.60 | 4.11 |
| 10 | 436701 | AW959032 | | ESTs, Moderately similar to I78885 serin | 4.60 | 2.34 |
| | 413691 | AB023173 | Hs.75478 | ATPase, Class VI, type 11B | 4.59 | 4.36 |
| | 448625 | AW970786 | Hs.178470 | hypothetical protein FLJ22662 | 4.59 | 4.00 |
| | 436283 | AI480319 | Hs.120058 | ESTs | 4.59 | 3.76 |
| | 451710 | AW867467 | Hs.278712 | eukaryotic translation initiation factor | 4.59 | 3.51 |
| 15 | 436086 | Z43133 | Hs.9961 | Homo sapiens cDNA: FLJ21954 fis, clone H | 4.59 | 3.64 |
| | 434697 | AL133033 | Hs.4084 | KIAA1025 protein | 4.58 | 5.10 |
| | 402294 | | | Target Exon | 4.57 | 5.47 |
| | 424098 | AF077374 | Hs.139322 | small proline-rich protein 3 | 4.57 | 5.12 |
| | 406648 | AA563730 | Hs.277477 | major histocompatibility complex, class | 4.57 | 4.66 |
| 20 | 428423 | AU076517 | Hs.184276 | solute carrier family 9 (sodium/hydrogen | 4.57 | 4.15 |
| | 441566 | AA604110 | Hs.151725 | ESTs | 4.57 | 3.21 |
| | 400109 | | | Eos Control | 4.56 | 4.76 |
| | 419740 | AB037835 | Hs.92991 | KIAA1414 protein | 4.56 | 3.63 |
| | 421481 | AW391972 | Hs.104696 | KIAA1324 protein | 4.55 | 7.16 |
| 25 | 440266 | AA088809 | Hs.19525 | hypothetical protein FLJ22794 | 4.55 | 4.44 |
| | 421979 | AW062518 | Hs.233150 | hypothetical protein MGC5560 | 4.55 | 4.36 |
| | 408702 | AW959893 | Hs.27099 | hypothetical protein FLJ23293 similar to | 4.54 | 5.78 |
| | 418021 | M15881 | Hs.1137 | uromodulin (uromucoid, Tamm-Horsfall gly | 4.54 | 4.61 |
| | 422068 | AI807519 | Hs.104520 | Homo sapiens cDNA FLJ13694 fis, clone PL | 4.54 | 4.32 |
| 30 | 421986 | AL137438 | Hs.110454 | SEC15 (S. cerevisiae)-like | 4.54 | 2.59 |
| | 414798 | AI286323 | Hs.97411 | hypothetical protein MGC12335 | 4.53 | 6.18 |
| | 410132 | NM_003480 | Hs.300946 | Microfibril-associated glycoprotein-2 | 4.53 | 5.87 |
| | 449843 | R85337 | Hs.24030 | solute carrier family 31 (copper transpo | 4.53 | 4.87 |
| | 424399 | AI905687 | | AI905687:IL-BT095-190199-019 BT095 Homo | 4.53 | 10.61 |
| 35 | 452924 | AW580939 | Hs.97199 | complement component C1q receptor | 4.51 | 6.07 |
| | 454000 | AA040620 | Hs.5672 | hypothetical protein AF140225 | 4.51 | 4.59 |
| | 404730 | | | Target Exon | 4.51 | 4.30 |
| | 449943 | AF104266 | Hs.24212 | latrophilin | 4.51 | 3.40 |
| | 414217 | AI309258 | Hs.275898 | Homo sapiens cDNA: FLJ23165 fis, clone L | 4.50 | 2.97 |
| 40 | 435992 | AI033259 | Hs.118317 | Homo sapiens cDNA FLJ12088 fis, clone HE | 4.50 | 4.77 |
| | 421311 | N71848 | Hs.283609 | hypothetical protein PRO2032 | 4.50 | 3.30 |
| | 449785 | AI225235 | Hs.288300 | hypothetical protein FLJ23231 | 4.49 | 5.06 |
| | 437611 | AA897108 | | gb:am08a06.s1 Soares_NFL_T_GBC_S1 Homo s | 4.49 | 4.24 |
| | 419612 | AI498267 | Hs.110613 | KIAA0421 protein | 4.49 | 4.16 |
| 45 | 414496 | W73853 | | ESTs | 4.49 | 3.15 |
| | 450306 | AL080080 | Hs.24766 | thioredoxin domain-containing | 4.48 | 3.38 |
| | 444895 | AI674383 | Hs.22891 | solute carrier family 7 (cationic amino | 4.47 | 4.45 |
| | 432559 | AW452948 | Hs.257631 | ESTs | 4.47 | 5.39 |
| | 442554 | AW467376 | Hs.129640 | ESTs | 4.47 | 4.00 |
| 50 | 421429 | NM_014922 | Hs.104305 | death effector filament-forming Ced-4-li | 4.46 | 4.47 |
| | 422313 | AF045941 | Hs.115166 | scellin | 4.45 | 5.07 |
| | 435748 | AA699756 | Hs.117335 | ESTs | 4.45 | 3.35 |
| | 453283 | AA694386 | Hs.290914 | ESTs | 4.45 | 3.28 |
| | 441925 | R83113 | | protein kinase C substrate 80K-H | 4.45 | 3.28 |
| 55 | 440030 | AA932693 | | EST | 4.45 | 3.20 |
| | 446515 | AL048875 | | hypothetical protein DKFZp5661133 | 4.44 | 3.66 |
| | 406707 | S73840 | Hs.931 | myosin, heavy polypeptide 2, skeletal mu | 4.44 | 5.90 |
| | 432341 | AL137662 | Hs.274401 | Homo sapiens mRNA; cDNA DKFZp434P086 (fr | 4.44 | 3.99 |
| | 410453 | AW749036 | | gb:RC2-BT0318-241199-011-f10 BT0318 Homo | 4.44 | 3.49 |
| 60 | 450196 | AW956868 | Hs.24608 | DKFZP564D177 protein | 4.43 | 4.13 |
| | 444147 | AB002306 | Hs.10351 | KIAA0308 protein | 4.43 | 3.95 |
| | 427809 | M26380 | Hs.180878 | lipoprotein lipase | 4.42 | 3.88 |
| | 428157 | AI738719 | Hs.198427 | hexokinase 2 | 4.42 | 5.46 |
| | 413299 | AA857487 | Hs.75275 | ubiquitination factor E4A (homologous to | 4.42 | 3.77 |
| 65 | 440245 | AK001913 | Hs.7100 | hypothetical protein | 4.42 | 3.51 |
| | 442379 | NM_004613 | Hs.8265 | transglutaminase 2 (C polypeptide, prote | 4.42 | 1.79 |
| | 408569 | BE066047 | Hs.86412 | chromosome 9 open reading frame 5 | 4.42 | 3.35 |
| | 430361 | AI033965 | Hs.239926 | sterol-C4-methyl oxidase-like | 4.41 | 5.78 |
| | 414489 | AI620677 | Hs.73105 | ESTs | 4.41 | 5.43 |
| 70 | 447731 | AA373527 | Hs.19385 | CGI-58 protein | 4.41 | 5.28 |
| | 443195 | BE148235 | Hs.193063 | Homo sapiens cDNA FLJ14201 fis, clone NT | 4.41 | 4.41 |
| | 448503 | BE243146 | Hs.21332 | BTB (POZ) domain containing 1 | 4.41 | 3.68 |
| | 432546 | BE618778 | Hs.180638 | hypothetical protein FLJ13081 | 4.41 | 3.55 |
| | 445620 | AI245225 | Hs.17441 | ESTs | 4.41 | 3.44 |
| 75 | 454065 | BE394588 | | gb:601311808F1 NIH_MGC_44 Homo sapiens c | 4.41 | 3.43 |
| | 418802 | AB028989 | Hs.88500 | mitogen-activated protein kinase 8 inter | 4.40 | 2.04 |
| | 431816 | T87431 | Hs.190738 | ESTs | 4.39 | 4.26 |
| | 429138 | AB020657 | Hs.197298 | NS1-binding protein | 4.39 | 4.47 |
| | 426643 | AA857131 | Hs.171595 | HIV TAT specific factor 1 | 4.39 | 3.09 |
| 80 | 448943 | AI608810 | Hs.193288 | ESTs | 4.39 | 2.63 |
| | 414002 | NM_006732 | Hs.75678 | FBJ murine osteosarcoma viral oncogene h | 4.37 | 19.16 |
| | 403593 | | | Target Exon | 4.37 | 6.35 |
| | 408104 | AW972927 | Hs.293968 | ESTs | 4.31 | 5.82 |
| | 429624 | AA458648 | Hs.99476 | ESTs, Weakly similar to 13131848 alpha1 | 4.31 | 4.14 |
| | 429538 | BE182592 | Hs.139322 | small proline-rich protein 2A | 4.25 | 6.61 |
| | 414505 | R45389 | Hs.23558 | ESTs, Weakly similar to A48042 lysosomal | 4.18 | 5.28 |
| | 438533 | AI440266 | Hs.170673 | ESTs, Weakly similar to T24832 hypothe | 4.18 | 5.81 |

| | | | | | | |
|----|--------|-----------|-----------|---|------|-------|
| 5 | 426143 | BE379836 | | proteasome (prosome, macropain) subunit, | | |
| | 414527 | BE241739 | Hs.76359 | catalase | 4.15 | 5.12 |
| | 422287 | F16365 | Hs.114346 | | 4.14 | 5.13 |
| | 408199 | AA132637 | Hs.15396 | cytochrome c oxidase subunit VIIa polype | 4.13 | 8.60 |
| | 412477 | AA150864 | | Homo sapiens, clone IMAGE:3948909, mRNA, | 4.12 | 5.94 |
| | 411558 | AA102670 | Hs.70725 | microsomal glutathione S-transferase 1 | 4.10 | 10.00 |
| | 444252 | R21135 | Hs.54985 | gamma-aminobutyric acid (GABA) A recepto | 4.09 | 5.39 |
| | 400295 | W72838 | | ESTs | 4.07 | 6.01 |
| 10 | 438746 | A1885815 | Hs.184727 | A1905687:IL-BT095-190199-019 BT095 Homo | 4.06 | 13.32 |
| | 429856 | AA971576 | Hs.225951 | Human melanoma-associated antigen p97 (m | 4.06 | 7.57 |
| | 422168 | AA586894 | Hs.112408 | topoisomerase-related function protein 4 | 4.05 | 6.24 |
| | 403710 | | | S100 calcium-binding protein A7 (psorias | 4.01 | 4.61 |
| | 406643 | N77976 | Hs.347939 | C4000160:gij12735793[refXP_011928.1] pr | 4.00 | 4.06 |
| 15 | 436372 | AW972301 | Hs.310286 | hemoglobin, alpha 2 | 3.97 | 7.22 |
| | 428340 | AF261088 | Hs.154721 | ESTs | 3.96 | 5.41 |
| | 424604 | AW865388 | Hs.151076 | aconitase 1, soluble | 3.94 | 5.33 |
| | 426653 | AA530892 | Hs.171695 | KIAA1243 protein | 3.91 | 7.59 |
| | 410204 | AJ243425 | Hs.326035 | dual specificity phosphatase 1 | 3.91 | 14.81 |
| 20 | 448520 | AB002367 | Hs.21355 | early growth response 1 | 3.87 | 9.96 |
| | 443021 | AA368546 | Hs.8904 | doublecortin and CaM kinase-like 1 | 3.87 | 5.09 |
| | 430418 | R98852 | Hs.36029 | Ig superfamily protein | 3.86 | 7.65 |
| | 447796 | AW953622 | Hs.223025 | heart and neural crest derivatives expre | 3.81 | 6.19 |
| | 419407 | AW410377 | Hs.41502 | RAB31, member RAS oncogene family | 3.76 | 5.10 |
| 25 | 443725 | AW245680 | Hs.9701 | hypothetical protein FLJ21276 | 3.76 | 5.12 |
| | 426281 | AK000987 | Hs.169111 | growth arrest and DNA-damage-inducible, | 3.75 | 5.46 |
| | 423973 | AF038461 | Hs.136574 | oxidation resistance 1 | 3.74 | 5.14 |
| | 445234 | AW137636 | Hs.146059 | arachidonate 12-lipoxygenase, 12R type | 3.74 | 6.30 |
| | 457411 | AW085961 | Hs.130093 | ESTs | 3.72 | 5.59 |
| 30 | 456063 | NM_006744 | Hs.76461 | iroquois-class homeobox protein IRX2 | 3.71 | 4.85 |
| | 413880 | A1660842 | Hs.110915 | retinol-binding protein 4, interstitial | 3.71 | 6.72 |
| | 422640 | M37984 | Hs.118845 | interleukin 22 receptor | 3.71 | 4.01 |
| | 452241 | AL050204 | Hs.28540 | troponin C, slow, | 3.71 | 9.10 |
| | 453560 | AA348626 | Hs.5890 | Homo sapiens mRNA: cDNA DKFZp586F1223 (f | 3.70 | 3.21 |
| 35 | 410197 | NM_005518 | Hs.59889 | hypothetical protein FLJ23306 | 3.69 | 5.13 |
| | 413922 | A1535895 | Hs.221024 | 3-hydroxy-3-methylglutaryl-Coenzyme A sy | 3.69 | 7.69 |
| | 426698 | AA852773 | Hs.334838 | ESTs | 3.68 | 4.80 |
| | 451951 | AW082870 | Hs.210954 | KIAA1866 protein | 3.64 | 5.22 |
| | 452308 | A167560 | Hs.61297 | ESTs | 3.64 | 3.69 |
| 40 | 441128 | AA570256 | | ESTs | 3.64 | 4.35 |
| | 421978 | AJ243652 | Hs.110196 | ESTs, Weakly similar to T23273 hypotheti | 3.63 | 2.91 |
| | 418533 | NM_004533 | Hs.85937 | NICE-1 protein | 3.61 | 6.05 |
| | 452413 | AW082633 | Hs.215030 | myosin-binding protein C, fast-type | 3.61 | 6.22 |
| | 453003 | AA808466 | Hs.103395 | ESTs | 3.58 | 3.03 |
| 45 | 408522 | A1541214 | Hs.46320 | hypothetical protein FLJ14146 | 3.55 | 6.39 |
| | 423503 | M92843 | Hs.343586 | Small proline-rich protein SPRK (human, | 3.54 | 10.68 |
| | 419879 | Z17805 | Hs.93564 | zinc finger protein homologous to Zfp-36 | 3.53 | 15.11 |
| | 428382 | AF007132 | Hs.184019 | Homer, neuronal immediate early gene, 2 | 3.53 | 5.29 |
| | 447165 | AL042400 | Hs.75668 | Homo sapiens clone Z3551 mRNA sequence | 3.51 | 4.46 |
| 50 | 418067 | A127958 | Hs.83393 | Homo sapiens, Similar to RIKEN cDNA 1700 | 3.51 | 3.67 |
| | 420202 | AL036557 | Hs.95910 | cystatin E/M | 3.51 | 3.74 |
| | 432543 | AA552690 | Hs.152423 | putative lymphocyte G0/G1 switch gene | 3.50 | 14.64 |
| | 442321 | AF207664 | Hs.8230 | Homo sapiens cDNA: FLJ21274 fis, clone C | 3.50 | 2.79 |
| | 450860 | AA021007 | | a disintegrin-like and metalloprotease (| 3.48 | 7.91 |
| 55 | 414665 | AA160873 | | integrin, beta 8 | 3.47 | 5.89 |
| | 413663 | BE247585 | Hs.75462 | serum amyloid A1 | 3.46 | 9.22 |
| | 427408 | AA583206 | Hs.2156 | BTG family, member 2 | 3.46 | 5.63 |
| | 430171 | AF086289 | Hs.234766 | RAR-related orphan receptor A | 3.45 | 3.08 |
| | 453655 | AW960427 | Hs.342874 | skin-specific protein | 3.45 | 4.77 |
| 60 | 450607 | AL050373 | Hs.25213 | transforming growth factor, beta recepto | 3.42 | 8.09 |
| | 412596 | AA161219 | Hs.799 | hypothetical protein | 3.41 | 6.43 |
| | 427681 | AB018263 | Hs.180338 | diphtheria toxin receptor (heparin-bindi | 3.41 | 6.10 |
| | 440590 | A1863446 | Hs.266308 | tumor necrosis factor receptor superfam | 3.39 | 6.59 |
| | 452669 | AA216363 | Hs.262958 | mosaic serine protease | 3.34 | 3.09 |
| 65 | 422101 | AW404176 | Hs.111611 | hypothetical protein DKFZp434B044 | 3.31 | 10.06 |
| | 431986 | AA536130 | Hs.149018 | ribosomal protein L27 | 3.30 | 3.93 |
| | 412649 | NM_002206 | Hs.74369 | Novel human gene mapping to chromosome 20 | 3.30 | 3.54 |
| | 423017 | AW178761 | Hs.227948 | integrin, alpha 7 | 3.28 | 6.89 |
| | 425163 | D10040 | Hs.154890 | serine (or cysteine) proteinase inhibito | 3.28 | 5.44 |
| 70 | 412061 | AA833763 | Hs.330211 | fatty-acid-Coenzyme A ligase, long-chain | 3.28 | 5.93 |
| | 437592 | NM_003851 | Hs.5710 | ESTs | 3.27 | 5.75 |
| | 452849 | AF044924 | Hs.30792 | cellular repressor of E1A-stimulated gen | 3.27 | 5.83 |
| | 421462 | AF016495 | Hs.104624 | hook2 protein | 3.26 | 5.66 |
| | 422083 | NM_001141 | Hs.111256 | aquaporin 9 | 3.25 | 4.98 |
| 75 | 444935 | AA262449 | Hs.223569 | arachidonate 15-lipoxygenase, second typ | 3.24 | 6.56 |
| | 422057 | A1205785 | Hs.30348 | ESTs | 3.24 | 5.96 |
| | 410017 | AW952426 | Hs.109438 | ESTs | 3.22 | 5.72 |
| | 407948 | AW085161 | Hs.56279 | Homo sapiens clone 24775 mRNA sequence | 3.21 | 5.26 |
| | 452089 | T97294 | Hs.271492 | ICEBERG caspase-1 inhibitor | 3.21 | 4.61 |
| 80 | 448249 | AW855331 | Hs.337124 | ESTs, Weakly similar to PC4211 hepatocel | 3.19 | 4.42 |
| | 430869 | D10511 | Hs.37 | ESTs | 3.18 | 2.97 |
| | 443623 | AA345519 | Hs.9641 | acetyl-Coenzyme A acetyltransferase 1 (a | 3.17 | 5.66 |
| | 452865 | A1924046 | Hs.119567 | complement component 1, q subcomponent, | 3.16 | 12.00 |
| | 452392 | L20815 | Hs.507 | ESTs, Weakly similar to A47582 B-cell gr | 3.16 | 6.03 |
| | | | | comedodermosin | 3.15 | 5.70 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|-------|
| 5 | 410231 | AA314163 | Hs.61153 | proteasome (prosome, macropain) 26S subu | 3.15 | 5.87 |
| | 420309 | AW043637 | Hs.21766 | ESTs, Weakly similar to ALU5_HUMAN ALU S | 3.15 | 4.98 |
| | 406791 | AI220684 | Hs.347939 | hemoglobin, alpha 2 | 3.13 | 17.37 |
| | 419648 | T73661 | Hs.91877 | thyroid hormone responsive SPOT14 (rat) | 3.12 | 4.63 |
| | 421485 | AA243499 | Hs.104800 | hypothetical protein FLJ10134 | 3.12 | 3.02 |
| 10 | 432375 | BE536069 | Hs.2962 | S100 calcium-binding protein P | 3.12 | 8.51 |
| | 417713 | D42047 | Hs.87432 | KIAA0089 protein | 3.12 | 5.82 |
| | 446948 | BE409053 | Hs.299629 | peroxisomal long-chain acyl-coA thioeste | 3.11 | 6.51 |
| | 444195 | AB002351 | Hs.10587 | KIAA0353 protein | 3.11 | 5.44 |
| | 415704 | NM_001677 | Hs.78629 | ATPase, Na ⁺ transporting, beta 1 polypep | 3.11 | 6.61 |
| 15 | 401905 | | | ENSP0000025232: Slerol regulatory eleme | 3.10 | 3.52 |
| | 443071 | AL080021 | Hs.8986 | complement component 1, q subcomponent, | 3.10 | 5.10 |
| | 427095 | AA316080 | Hs.173554 | ubiquinol-cytochrome c reductase core pr | 3.10 | 5.39 |
| | 413835 | AI272727 | Hs.249163 | fatty acid hydroxylase | 3.08 | 5.56 |
| | 448106 | AI800470 | Hs.171941 | ESTs | 3.07 | 5.19 |
| 20 | 432908 | AI861896 | | ESTs | 3.07 | 3.47 |
| | 422158 | L10343 | Hs.112341 | protease inhibitor 3, skin-derived (SKAL | 3.07 | 7.48 |
| | 429506 | D49835 | Hs.171942 | ras responsive element binding protein 1 | 3.05 | 3.97 |
| | 449498 | U58515 | Hs.154138 | chitinase 3-like 2 | 3.02 | 6.75 |
| | 419358 | T78763 | Hs.90063 | neurocalcin delta | 3.00 | 7.68 |
| 25 | 414541 | BE293116 | Hs.76392 | aldehyde dehydrogenase 1 family, member | 2.99 | 5.44 |
| | 426402 | BE387327 | Hs.80475 | polymerase (RNA) II (DNA directed) polyp | 2.99 | 6.84 |
| | 450472 | AI190071 | Hs.55278 | ESTs | 2.98 | 5.06 |
| | 421335 | X99977 | Hs.103505 | ARS component B | 2.97 | 9.31 |
| | 431316 | AA502663 | Hs.145037 | ESTs | 2.96 | 4.30 |
| 30 | 420996 | AK001927 | Hs.100895 | hypothetical protein FLJ10462 | 2.96 | 2.97 |
| | 451176 | AA046457 | Hs.60677 | ESTs | 2.95 | 6.59 |
| | 444204 | AI129194 | Hs.143040 | ESTs | 2.93 | 3.92 |
| | 435723 | AW975895 | Hs.307486 | ESTs | 2.93 | 6.64 |
| | 436664 | AW197887 | Hs.253353 | ESTs | 2.93 | 3.82 |
| 35 | 406962 | M13485 | | gb:Human metallothionein I-B gene, exon | 2.93 | 3.10 |
| | 453092 | X64838 | Hs.31638 | reslin (Reed-Steinberg cell-expressed in | 2.93 | 5.35 |
| | 444734 | NM_001360 | Hs.11806 | 7-dehydrocholesterol reductase | 2.91 | 9.84 |
| | 430310 | U60115 | Hs.239069 | four and a half LIM domains 1 | 2.91 | 7.02 |
| | 420876 | AA918425 | Hs.177744 | ESTs | 2.91 | 5.41 |
| 40 | 426050 | AF017307 | Hs.166096 | E74-like factor 3 (ets domain transcript | 2.91 | 5.64 |
| | 428232 | BE272452 | Hs.183109 | monoamine oxidase A | 2.90 | 9.54 |
| | 413796 | AW408094 | Hs.75545 | interleukin 4 receptor | 2.89 | 5.37 |
| | 413884 | AI668892 | Hs.239758 | hypothetical protein FLJ12389 similar to | 2.88 | 5.34 |
| | 411372 | AI147861 | Hs.213289 | low density lipoprotein receptor (famili | 2.85 | 6.31 |
| 45 | 428500 | AI815395 | Hs.184541 | fatty acid desaturase 2 | 2.86 | 3.93 |
| | 444135 | AK000374 | Hs.10346 | hypothetical protein FLJ20154 | 2.86 | 6.05 |
| | 452689 | F33868 | Hs.284176 | transferrin | 2.85 | 6.11 |
| | 403108 | | | ENSP00000241415: Hypothetical 67.7 kDa p | 2.85 | 3.17 |
| | 434433 | AW629759 | | gb:hh70e05.y1 NCI_CGAP_GU1 Homo sapiens | 2.84 | 3.35 |
| 50 | 434952 | T10269 | Hs.4285 | Homo sapiens cDNA: FLJ22505 fis, clone H | 2.83 | 4.05 |
| | 420544 | AA677577 | Hs.98732 | Homo sapiens Chromosome 16 BAC clone CIT | 2.83 | 3.57 |
| | 406922 | S70284 | Hs.119597 | gb:stearoyl-CoA desaturase [human, adipo | 2.82 | 3.80 |
| | 437470 | AL390147 | Hs.134742 | hypothetical protein DKFZp547D065 | 2.82 | 6.40 |
| | 429807 | AK002138 | Hs.306227 | Homo sapiens cDNA FLJ11276 fis, clone PL | 2.82 | 2.97 |
| 55 | 425180 | U00115 | Hs.155024 | B-cell CLL/lymphoma 6 (zinc finger prote | 2.81 | 5.15 |
| | 415409 | AW993701 | | NS1-associated protein 1 | 2.80 | 6.16 |
| | 433848 | AF095719 | Hs.93764 | carboxypeptidase A4 | 2.80 | 2.88 |
| | 425750 | AL050276 | Hs.42400 | zinc finger protein 288 | 2.79 | 5.99 |
| | 433638 | AW872507 | Hs.3462 | cytochrome c oxidase subunit VIc | 2.78 | 5.25 |
| 60 | 429128 | AA446869 | Hs.119316 | ESTs | 2.78 | 4.17 |
| | 446292 | AF081497 | Hs.279682 | Rh type C glycoprotein | 2.77 | 7.37 |
| | 430420 | AW140027 | Hs.26373 | Homo sapiens cDNA: FLJ23449 fis, clone H | 2.76 | 6.09 |
| | 419923 | AW081455 | Hs.120219 | ESTs | 2.76 | 4.31 |
| | 407555 | Z48511 | | gb:H.sapiens XG mRNA (clone PEP11). | 2.76 | 4.12 |
| 65 | 425240 | AA306495 | Hs.1869 | phosphoglucomutase 1 | 2.74 | 5.92 |
| | 459317 | BRCA1b | | Eos Control | 2.74 | 19.85 |
| | 425819 | N92165 | Hs.93231 | ESTs | 2.74 | 5.72 |
| | 408839 | AW277084 | | gb:xp61h09.x1 NCI_CGAP_Ov39 Homo sapiens | 2.73 | 3.93 |
| | 418253 | AA215539 | Hs.283643 | Homo sapiens cDNA FLJ11606 fis, clone HE | 2.72 | 5.94 |
| 70 | 409453 | AI885516 | Hs.95612 | ESTs | 2.72 | 6.51 |
| | 406625 | Y13647 | Hs.119597 | stearoyl-CoA desaturase (delta-9-desatur | 2.72 | 3.80 |
| | 420074 | AA253425 | Hs.190074 | ESTs | 2.71 | 4.04 |
| | 429547 | AW009166 | Hs.99376 | FGENESH predicted novel secreted protein | 2.71 | 2.84 |
| | 444026 | AA205759 | Hs.10119 | hypothetical protein FLJ14957 | 2.71 | 6.17 |
| 75 | 407112 | AA070801 | Hs.51615 | ESTs, Weakly similar to ALU7_HUMAN ALU S | 2.70 | 5.23 |
| | 429615 | AF258627 | Hs.211562 | ATP-binding cassette, sub-family A (ABC1 | 2.69 | 5.33 |
| | 419098 | AA234041 | Hs.87271 | ESTs | 2.69 | 3.22 |
| | 424206 | NM_003734 | Hs.198241 | amine oxidase, copper containing 3 (vasc | 2.69 | 6.64 |
| | 443102 | AI247472 | Hs.132965 | ESTs | 2.68 | 5.85 |
| 80 | 411939 | AI365585 | Hs.146246 | ESTs | 2.68 | 5.38 |
| | 453201 | AI432195 | Hs.135098 | ESTs | 2.68 | 3.69 |
| | 420231 | R06866 | Hs.19813 | ESTs | 2.67 | 4.70 |
| | 404996 | | | Target Exon | 2.67 | 4.97 |
| | 452955 | AW390282 | Hs.31130 | transmembrane 7 superfamily member 2 | 2.66 | 6.36 |
| | 447205 | BE617015 | Hs.11006 | ESTs, Moderately similar to T17372 plasrn | 2.65 | 15.65 |
| | 417365 | D50683 | Hs.82028 | transforming growth factor, beta recepto | 2.65 | 7.74 |
| | 444169 | AV648170 | Hs.58756 | ESTs | 2.64 | 3.40 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|-------|
| | 431247 | AL021578 | Hs.278489 | matrilin 4 | | |
| | 423960 | AA164516 | Hs.136309 | SH3-containing protein SH3GLB1 | 2.64 | 3.35 |
| | 432093 | H26383 | | gb:yl52c03.r1 Soares breast 3NbH8st Homo | 2.63 | 5.12 |
| 5 | 408669 | AI493591 | Hs.78146 | platelet/endothelial cell adhesion molec | 2.63 | 4.08 |
| | 440924 | AF151872 | Hs.7527 | small fragment nuclease | 2.61 | 6.44 |
| | 416232 | AW502678 | Hs.79090 | exportin 1 (CRM1, yeast, homolog) | 2.59 | 6.37 |
| | 425320 | U29344 | Hs.83190 | fatty acid synthase | 2.59 | 6.46 |
| | 402315 | | | NM_003430:Homo sapiens zinc finger prote | 2.59 | 3.93 |
| 10 | 449539 | W80363 | Hs.58446 | ESTs | 2.58 | 6.09 |
| | 418271 | NM_000919 | Hs.83920 | peptidylglycine alpha-amidating monooxyg | 2.58 | 4.05 |
| | 449967 | R40978 | Hs.271438 | ESTs, Moderately similar to ALU1_HUMAN A | 2.58 | 5.61 |
| | 438752 | AW238673 | Hs.146038 | ESTs | 2.58 | 3.54 |
| | 424675 | NM_005512 | Hs.151641 | glycoprotein A repetitions predominant | 2.57 | 5.24 |
| 15 | 438763 | AI583207 | Hs.99029 | CCAA1/enhancer binding protein (C/EBP) | 2.57 | 5.16 |
| | 413630 | AL036883 | Hs.75450 | delta sleep inducing peptide, immunoreac | 2.57 | 6.45 |
| | 424834 | AK001432 | Hs.153408 | Homo sapiens cDNA FLJ10570 fs, clone NT | 2.56 | 6.38 |
| | 427666 | AI791495 | Hs.180142 | calmodulin-like skin protein (CLSP) | 2.56 | 2.90 |
| | 426403 | NM_000361 | Hs.2030 | thrombomodulin | 2.56 | 2.67 |
| 20 | 432906 | BE265489 | Hs.3123 | lethal giant larvae (Drosophila) homolog | 2.56 | 5.19 |
| | 420924 | R01026 | Hs.245321 | ESTs | 2.55 | 5.62 |
| | 427527 | AI809057 | Hs.153261 | immunoglobulin heavy constant mu | 2.55 | 3.22 |
| | 407083 | Z48511 | | H.sapiens XG mRNA (clone PEP11) | 2.55 | 5.45 |
| | 445437 | AI224165 | Hs.148725 | ESTs | 2.55 | 4.50 |
| 25 | 425097 | NM_014247 | | PDZ domain containing guanine nucleotide | 2.54 | 4.72 |
| | 420105 | AW015571 | Hs.32244 | ESTs, Weakly similar to FMOO_HUMAN FIBRO | 2.54 | 5.28 |
| | 429554 | NM_012275 | Hs.207224 | interleukin 1, delta | 2.53 | 6.55 |
| | 408896 | AI610447 | Hs.48778 | niban protein | 2.53 | 2.84 |
| | 409169 | F00991 | Hs.50889 | (clone PWHLC2-24) myosin light chain 2 | 2.53 | 7.08 |
| 30 | 420235 | AA256756 | Hs.31178 | ESTs | 2.52 | 8.68 |
| | 436314 | AI983409 | | ESTs | 2.51 | 4.21 |
| | 440602 | AI743491 | Hs.292692 | ESTs | 2.51 | 3.11 |
| | 444946 | AW139205 | Hs.156457 | hypothetical protein FLJ22408 | 2.50 | 2.71 |
| 35 | 430235 | BE268048 | Hs.236494 | RAB10, member RAS oncogene family | 2.48 | 2.86 |
| | 423929 | M69136 | Hs.135626 | chymase 1, mast cell | 2.48 | 5.37 |
| | 426689 | BE245550 | Hs.171825 | basic helix-loop-helix domain containing | 2.48 | 3.21 |
| | 421811 | AA022550 | Hs.108548 | PABP-interacting protein 2 | 2.48 | 7.88 |
| | 414420 | AA043424 | Hs.76095 | immediate early response 3 | 2.48 | 5.28 |
| 40 | 420693 | NM_001972 | Hs.99863 | elastase 2, neutrophil | 2.47 | 8.33 |
| | 420139 | NM_005357 | Hs.95351 | lipase, hormone-sensitive | 2.47 | 2.78 |
| | 447179 | AW015633 | Hs.157299 | ESTs | 2.46 | 10.12 |
| | 451687 | AL041260 | Hs.26837 | Homo sapiens mRNA: cDNA DKF2p586K1123 (f | 2.46 | 3.45 |
| | 420322 | AB014555 | Hs.96731 | huntingtin interacting protein-1-related | 2.46 | 5.47 |
| | 421064 | AI245432 | Hs.101382 | tumor necrosis factor, alpha-induced pro | 2.45 | 6.18 |
| 45 | 421818 | AW992976 | Hs.50088 | NM_002489:Homo sapiens NADH dehydrogenas | 2.45 | 5.75 |
| | 412524 | AA417813 | Hs.44208 | hypothetical protein FLJ23153 | 2.45 | 6.73 |
| | 439639 | AA370045 | Hs.6607 | AXIN1 up-regulated | 2.44 | 10.55 |
| | 436009 | H57130 | Hs.120925 | ESTs | 2.44 | 5.22 |
| | 414814 | D14697 | Hs.77393 | farnesyl diphosphate synthase (farnesyl | 2.44 | 2.94 |
| 50 | 434060 | AA744902 | Hs.197922 | hypothetical protein PRO1489 | 2.43 | 5.17 |
| | 425335 | BE394327 | Hs.296267 | folistatin-like 1 | 2.43 | 5.56 |
| | 406997 | U07807 | | metallothionein IV | 2.43 | 10.52 |
| | 431545 | AF095703 | Hs.8110 | L-3-hydroxyacyl-Coenzyme A dehydrogenase | 2.42 | 4.35 |
| | 417029 | AW952192 | Hs.273385 | guanine nucleotide binding protein (G pr | 2.42 | 6.72 |
| 55 | 412825 | AW167439 | Hs.190651 | Homo sapiens cDNA FLJ13625 fs, clone PL | 2.41 | 5.22 |
| | 445462 | AA378776 | Hs.288649 | hypothetical protein MGC3077 | 2.41 | 5.56 |
| | 448954 | AB014564 | Hs.22616 | KIAA0664 protein | 2.41 | 5.24 |
| | 447218 | BE617762 | Hs.10748 | hypothetical protein DKF2p434B195 | 2.40 | 5.31 |
| 60 | 423810 | AL132665 | Hs.132955 | BCL2/adenovirus E1B 19kD-interacting pro | 2.40 | 5.24 |
| | 450440 | AB024334 | Hs.25001 | tyrosine 3-monooxygenase/tryptophan 5-mo | 2.39 | 5.55 |
| | 430356 | N87990 | Hs.239870 | Homo sapiens mRNA: cDNA DKF2p564H0764 (f | 2.39 | 7.63 |
| | 418355 | L42563 | Hs.1165 | ATPase, H7 transporting, nongastric, alp | 2.38 | 5.99 |
| | 416273 | AW575691 | Hs.79123 | KIAA0084 protein | 2.38 | 3.84 |
| | 427272 | NM_001096 | Hs.174140 | ATP citrate lyase | 2.38 | 5.22 |
| 65 | 437186 | AA338305 | Hs.5472 | hypothetical protein FLJ20173 | 2.38 | 5.41 |
| | 443679 | AK001810 | Hs.9670 | hypothetical protein FLJ10948 | 2.35 | 5.13 |
| | 431179 | AI338644 | Hs.195432 | aldehyde dehydrogenase 2 family (mitocho | 2.33 | 5.81 |
| | 418400 | BE243026 | Hs.301989 | KIAA0246 protein | 2.33 | 7.89 |
| | 456876 | AL044870 | Hs.208780 | ESTs, Weakly similar to T29647 hypothe | 2.33 | 5.36 |
| 70 | 407082 | Z47055 | | gb:Human partial cDNA sequence, farnesyl | 2.32 | 3.27 |
| | 426508 | W23184 | Hs.170171 | glutamate-ammonia ligase (glutamine synt | 2.31 | 4.65 |
| | 408536 | AW381532 | Hs.135188 | ESTs | 2.31 | 9.37 |
| | 410552 | XG6945 | Hs.748 | fibroblast growth factor receptor 1 (fms | 2.31 | 2.60 |
| | 437201 | F29279 | Hs.171625 | hypothetical protein MGC14697 | 2.30 | 5.94 |
| 75 | 417314 | N68168 | | gb:za11c01.s1 Soares fetal liver spleen | 2.30 | 5.75 |
| | 433738 | AI684802 | | ESTs | 2.30 | 3.12 |
| | 410531 | AW752953 | | gb:QV0-CT0224-261099-035-g02 CT0224 Homo | 2.30 | 3.91 |
| | 422491 | AA338548 | Hs.117546 | neurotatin | 2.29 | 3.61 |
| | 434411 | AA632649 | Hs.201372 | ESTs | 2.29 | 5.66 |
| 80 | 451926 | AW134519 | Hs.96125 | Homo sapiens, Similar to clone FLB3816, | 2.28 | 4.40 |
| | 401131 | | | NM_001651":Homo sapiens aquaporin 5 (AQP | 2.28 | 5.14 |
| | 401205 | | | Target Exon | 2.27 | 5.62 |
| | 422109 | S73265 | Hs.1473 | gastrin-releasing peptide | 2.27 | 2.98 |
| | 456646 | AJ243662 | Hs.110196 | NICE-1 protein | 2.26 | 3.94 |
| | | | | | 2.26 | 2.52 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|-------|
| | 443049 | AI028613 | Hs.132343 | ESTs | 2.25 | 3.13 |
| | 440160 | BE560269 | Hs.7010 | NPD002 protein | 2.25 | 4.93 |
| | 438367 | N79688 | Hs.204354 | ras homolog gene family, member B | 2.25 | 9.58 |
| 5 | 442987 | AA075975 | | Homo sapiens clone TCCIA00427 mRNA sequ | 2.24 | 6.19 |
| | 421545 | AA292810 | Hs.90034 | hypothetical protein FLJ21916 | 2.24 | 2.58 |
| | 447150 | AI439011 | Hs.86386 | myeloid cell leukemia sequence 1 (BCL2-r | 2.23 | 9.03 |
| | 450014 | N41322 | Hs.18441 | ESTs | 2.23 | 4.50 |
| | 426611 | BE178050 | Hs.171271 | catenin (cadherin-associated protein), b | 2.22 | 5.64 |
| 10 | 434039 | L32977 | Hs.3712 | ubiquinol-cytochrome c reductase, Rieske | 2.22 | 5.57 |
| | 427569 | BE299197 | Hs.179665 | cyclin-dependent kinase inhibitor 1A (p2 | 2.22 | 5.10 |
| | 444637 | T19101 | Hs.11494 | fibulin 5 | 2.22 | 6.43 |
| | 406710 | AI708347 | Hs.184014 | ribosomal protein L31 | 2.21 | 9.10 |
| | 424909 | S78187 | Hs.153752 | cell division cycle 25B | 2.20 | 6.13 |
| 15 | 407228 | M25079 | Hs.155376 | hemoglobin, beta | 2.20 | 11.34 |
| | 450612 | AL359946 | Hs.14779 | acetyl-CoA synthetase | 2.20 | 7.03 |
| | 458568 | AI769067 | Hs.127824 | ESTs, Weakly similar to T28770 hypothe | 2.20 | 5.68 |
| | 407370 | AA682384 | Hs.182084 | ESTs | 2.20 | 7.00 |
| | 438942 | AW875398 | Hs.6451 | PRO0659 protein | 2.19 | 6.09 |
| 20 | 400228 | | | NM_021724: Homo sapiens nuclear receptor | 2.19 | 6.95 |
| | 410185 | BE294068 | Hs.737 | immediate early protein | 2.18 | 11.72 |
| | 428150 | AW950547 | Hs.70312 | cytochrome c oxidase subunit VIIa polype | 2.17 | 7.05 |
| | 400307 | AF005081 | | Homo sapiens skin-specific protein (xp32 | 2.17 | 6.41 |
| | 424425 | AB031480 | Hs.146824 | SPR1 protein | 2.17 | 3.68 |
| 25 | 414459 | Y11525 | Hs.76171 | CCAA1/enhancer binding protein (C/EBP), | 2.17 | 3.11 |
| | 400082 | | | Eos Control | 2.16 | 8.40 |
| | 434702 | AL039734 | Hs.4099 | nardilysin (N-arginine dibasic convertas | 2.16 | 6.83 |
| | 439651 | AF086480 | Hs.56255 | ESTs | 2.16 | 3.72 |
| | 431838 | AI097229 | Hs.217484 | ESTs, Weakly similar to ALU1_HUMAN ALU S | 2.15 | 3.34 |
| 30 | 420225 | AW243046 | Hs.282076 | Homo sapiens mRNA for KIAA1650 protein, | 2.14 | 6.20 |
| | 428848 | NM_000230 | Hs.194236 | leptin (murine obesity homolog) | 2.14 | 3.42 |
| | 415213 | NM_002933 | Hs.78224 | ribonuclease, RNase A family, 1 (pancrea | 2.14 | 9.81 |
| | 434454 | AF217798 | Hs.3850 | US1-interacting protein NUDEL; endoolig | 2.14 | 6.75 |
| | 452467 | AW500815 | | ESTs | 2.13 | 4.66 |
| 35 | 418226 | AA424202 | Hs.83834 | cytochrome b-5 | 2.13 | 5.41 |
| | 414815 | AW292140 | Hs.130286 | ESTs | 2.12 | 4.14 |
| | 430967 | H16791 | Hs.100895 | ESTs | 2.12 | 4.14 |
| | 426102 | AF200496 | Hs.166371 | interleukin 1, zeta | 2.12 | 3.77 |
| | 410223 | S73775 | Hs.60708 | cathepsin 1 (fast-twitch, skeletal m | 2.11 | 5.30 |
| 40 | 439518 | W76326 | | gb:zd60d04.r1 Soares_fetal_heart_NbHH19W | 2.11 | 4.01 |
| | 427228 | AA115770 | Hs.174051 | small nuclear ribonucleoprotein 70kD pol | 2.10 | 5.13 |
| | 436961 | AW375974 | Hs.156704 | ESTs | 2.10 | 3.33 |
| | 417139 | M69043 | Hs.81328 | nuclear factor of kappa light polypeptid | 2.10 | 8.13 |
| | 445831 | NM_006055 | Hs.13351 | LanC (bacterial lanthiotic synthetase c | 2.08 | 5.42 |
| 45 | 431593 | NM_002108 | Hs.276590 | ESTs | 2.08 | 4.43 |
| | 423887 | AL080207 | Hs.134585 | DKFZP434G232 protein | 2.08 | 3.92 |
| | 424389 | AA339786 | | lymphocyte-specific protein 1 | 2.07 | 5.52 |
| | 407394 | AF005081 | | gb:Homo sapiens skin-specific protein (x | 2.06 | 5.93 |
| | 400198 | | | Eos Control | 2.05 | 10.48 |
| 50 | 426335 | AI054347 | Hs.2017 | ribosomal protein L38 | 2.04 | 5.57 |
| | 443652 | AI080692 | Hs.134229 | ESTs, Weakly similar to I54401 hypertens | 2.04 | 3.36 |
| | 448804 | AW512213 | Hs.342849 | ADP-ribosylation factor-like 5 | 2.02 | 3.32 |
| | 443932 | AW888222 | Hs.9973 | tensin | 2.02 | 9.28 |
| | 421324 | BE257515 | Hs.103503 | deoxyribonuclease I-like 2 | 2.02 | 5.71 |
| 55 | 426406 | AI742501 | Hs.169756 | complement component 1, s subcomponent | 2.01 | 5.49 |
| | 410669 | AW805749 | | superoxide dismutase 2, mitochondrial | 2.01 | 3.05 |
| | 446193 | AI279390 | Hs.144658 | ESTs, Weakly similar to T17257 hypothe | 2.01 | 2.77 |
| | 400078 | | | Eos Control | 2.00 | 11.41 |
| | 456267 | AI127958 | Hs.83393 | cystatin EM | 1.99 | 3.59 |
| 60 | 413125 | BE244589 | Hs.75207 | glyoxalase I | 1.98 | 6.70 |
| | 415433 | W70067 | Hs.58066 | ESTs | 1.98 | 5.59 |
| | 434699 | AA643687 | Hs.149425 | Homo sapiens cDNA FLJ11980 fis, clone HE | 1.98 | 3.52 |
| | 417553 | L09190 | | trichohyalin | 1.98 | 3.39 |
| | 403105 | | | Target Exon | 1.98 | 5.05 |
| 65 | 414081 | AW969976 | | matrix Gla protein | 1.97 | 8.74 |
| | 422639 | AI929377 | Hs.173724 | creatine kinase, brain | 1.97 | 5.51 |
| | 452208 | AA024792 | Hs.31895 | hypothetical protein MGC4093 | 1.97 | 5.67 |
| | 436106 | AI050715 | Hs.2331 | E2F transcription factor 5, p130-binding | 1.97 | 5.75 |
| | 439265 | AL134430 | Hs.6906 | Homo sapiens cDNA: FLJ23197 fis, clone R | 1.96 | 5.09 |
| 70 | 430037 | BE409649 | Hs.227789 | mitogen-activated protein kinase-activat | 1.96 | 5.49 |
| | 440054 | AW661947 | Hs.6891 | splicing factor, arginine/serine-rich 6 | 1.95 | 5.95 |
| | 417088 | M54915 | Hs.81170 | pim-1 oncogene | 1.95 | 8.19 |
| | 429451 | BE409861 | Hs.202833 | heme oxygenase (decycling) 1 | 1.95 | 5.19 |
| | 415274 | AF001548 | Hs.78344 | myosin, heavy polypeptide 11, smooth mus | 1.95 | 6.78 |
| 75 | 452472 | AW957300 | Hs.294142 | ESTs, Weakly similar to C55663 oligodend | 1.94 | 5.98 |
| | 414860 | BE255593 | Hs.77502 | methionine adenosyltransferase II, alpha | 1.94 | 5.13 |
| | 437220 | AL117542 | Hs.334305 | GS1999tutl | 1.94 | 3.42 |
| | 450461 | BE408081 | Hs.46736 | hypothetical protein FLJ23476 | 1.94 | 5.66 |
| | 424924 | AL039103 | Hs.153834 | pumilio (Drosophila) homolog 1 | 1.93 | 5.28 |
| 80 | 413945 | NM_000591 | Hs.75627 | CD14 antigen | 1.93 | 5.38 |
| | 428193 | NM_004235 | | Kruppel-like factor 4 (gut) | 1.93 | 5.75 |
| | 415988 | BE407713 | Hs.78943 | bleomycin hydrolase | 1.92 | 4.65 |
| | 425783 | AI026740 | Hs.1948 | ribosomal protein S21 | 1.92 | 9.79 |
| | 431476 | BE612705 | Hs.256697 | histidine triad nucleotide-binding prote | 1.91 | 7.00 |

| | | | | | | |
|----|--------|-----------|-----------|--|------|-------|
| | 456653 | AJ807519 | Hs.104520 | Homo sapiens cDNA FLJ13694 fis, clone PL | 1.91 | 3.41 |
| | 401846 | | | NM_000988*:Homo sapiens ribosomal protein | 1.91 | 5.62 |
| | 428368 | BE440042 | Hs.83326 | matrix metalloproteinase 3 (stromelysin | 1.90 | 4.00 |
| 5 | 400199 | | | Eos Control | 1.89 | 15.74 |
| | 429367 | AB007867 | Hs.278311 | plexin B1 | 1.88 | 5.58 |
| | 400083 | | | Eos Control | 1.88 | 9.07 |
| | 433465 | AV657778 | Hs.3314 | selenoprotein P, plasma, 1 | 1.88 | 5.16 |
| | 400079 | | | Eos Control | 1.87 | 8.57 |
| 10 | 411807 | AK000290 | Hs.44033 | dipeptidyl peptidase 8 | 1.86 | 5.19 |
| | 409178 | BE393948 | Hs.50915 | kallikrein 5 | 1.85 | 2.75 |
| | 422624 | BE616678 | Hs.76152 | KDEL (Lys-Asp-Glu-Leu) endoplasmic retic | 1.85 | 5.33 |
| | 443121 | Z19267 | Hs.9006 | VAMP (vesicle-associated membrane protei | 1.85 | 6.01 |
| | 451092 | AI207256 | Hs.13766 | Homo sapiens mRNA for FLJ00074 protein, | 1.84 | 2.82 |
| | 430572 | U33114 | Hs.245188 | tissue inhibitor of metalloproteinase 3 | 1.83 | 5.10 |
| 15 | 426812 | AF105365 | Hs.172613 | solute carrier family 12 (potassium/chlo | 1.83 | 6.48 |
| | 439927 | AA854650 | Hs.124597 | ESTs | 1.82 | 3.63 |
| | 415089 | N25117 | Hs.299465 | ribosomal protein S26 | 1.82 | 6.69 |
| | 406400 | | | kallikrein 8 (neuropsin/ovasin) (KLKB) | 1.82 | 2.95 |
| 20 | 406467 | | | Target Exon | 1.79 | 2.65 |
| | 426672 | AW270555 | Hs.171774 | hypothetical protein | 1.79 | 5.24 |
| | 414088 | AW797956 | Hs.75748 | proteasome (prosome, macropain) subunit, | 1.78 | 6.02 |
| | 433271 | BE621697 | Hs.14317 | nucleolar protein family A, member 3 (H/ | 1.78 | 5.92 |
| | 429307 | AU076592 | Hs.198951 | jun B proto-oncogene | 1.77 | 5.44 |
| 25 | 433640 | AW390125 | Hs.240443 | Homo sapiens cDNA: FLJ23538 fis, clone L | 1.77 | 5.79 |
| | 425503 | W92517 | Hs.158203 | actin binding LIM protein 1 | 1.77 | 9.27 |
| | 429191 | AF065215 | Hs.198161 | phospholipase A2, group IVB (cytosolic) | 1.77 | 5.44 |
| | 425875 | AU077333 | Hs.160483 | erythrocyte membrane protein band 7.2 (s | 1.77 | 6.97 |
| | 431021 | AI869664 | | thiosulfate sulfurtransferase (rhodanese | 1.77 | 5.23 |
| 30 | 432891 | AF161483 | Hs.279761 | HSPC134 protein | 1.75 | 5.73 |
| | 432872 | AI908984 | Hs.279623 | selenoprotein X, 1 | 1.75 | 5.72 |
| | 451335 | AB023192 | Hs.26285 | imidazole receptor candidate | 1.75 | 6.87 |
| | 428975 | NM_004672 | Hs.194694 | mitogen-activated protein kinase kinase | 1.74 | 3.01 |
| | 417824 | AA084798 | Hs.82646 | DnaJ (Hsp40) homolog, subfamily B, membe | 1.74 | 5.75 |
| 35 | 439908 | AI168031 | Hs.155507 | ESTs | 1.74 | 2.63 |
| | 427349 | AA360154 | Hs.177415 | Finkel-Biskis-Reilly murine sarcoma viru | 1.74 | 6.80 |
| | 445919 | T53519 | Hs.334692 | hypothetical protein MGC14141 | 1.74 | 5.65 |
| | 427391 | W60675 | | hypothetical protein FLJ10350 | 1.73 | 6.13 |
| | 425299 | AW505214 | Hs.155560 | cathexin | 1.73 | 5.88 |
| 40 | 430449 | AA352723 | Hs.241471 | RNB6 | 1.72 | 5.14 |
| | 456766 | R87310 | Hs.7740 | oxysterol binding protein-like 1 | 1.71 | 4.35 |
| | 407694 | U77594 | Hs.37682 | retinoic acid receptor responder (lazar | 1.71 | 6.16 |
| | 412374 | X01388 | Hs.73849 | apolipoprotein C-III | 1.70 | 5.18 |
| | 417483 | BE549343 | Hs.82208 | acyl-Coenzyme A dehydrogenase, very long | 1.70 | 7.46 |
| 45 | 410584 | AB011112 | Hs.64742 | KIAA0540 protein | 1.69 | 6.19 |
| | 431882 | NM_001426 | Hs.271977 | engrailed homolog 1 | 1.68 | 2.63 |
| | 441379 | AW175787 | Hs.334841 | selenium binding protein 1 | 1.67 | 7.42 |
| | 422115 | AI878953 | Hs.111811 | microsomal glutathione S-transferase 3 | 1.67 | 6.93 |
| | 406742 | AI468091 | Hs.279860 | tumor protein, translationally-controlle | 1.66 | 6.26 |
| 50 | 432191 | AA043193 | Hs.273186 | hypothetical protein, clone Telethon/Ita | 1.65 | 5.83 |
| | 452363 | AI582743 | Hs.94953 | Homo sapiens, Similar to complement comp | 1.65 | 7.54 |
| | 446623 | AF279865 | Hs.15711 | kinesin family member 13B | 1.65 | 5.36 |
| | 406712 | M31212 | Hs.77385 | myosin, light polypeptide 6, alkali, smo | 1.65 | 12.30 |
| | 400202 | | | NM_002795*:Homo sapiens proteasome (pros | 1.64 | 5.70 |
| 55 | 401429 | | | C14001067:gi4126465[dbj]BAA36581.1[AB | 1.64 | 3.82 |
| | 415166 | NM_003652 | Hs.78068 | carboxypeptidase Z | 1.62 | 5.95 |
| | 410169 | AJ373741 | Hs.59384 | hypothetical protein MGC3047 | 1.61 | 6.60 |
| | 406713 | U02629 | Hs.77385 | myosin, light polypeptide 6, alkali, smo | 1.60 | 11.13 |
| | 453027 | AJ879341 | Hs.539 | ribosomal protein S29 | 1.60 | 10.97 |
| 60 | 416955 | AW889150 | Hs.80595 | NM_004552*:Homo sapiens NADH dehydrogena | 1.60 | 5.90 |
| | 439053 | BE244588 | Hs.6456 | chaperonin containing TCP1, subunit 2 (b | 1.57 | 5.60 |
| | 400201 | | | NM_006156*:Homo sapiens neural precursor | 1.57 | 5.32 |
| | 407049 | X72632 | | NM_021724*:Homo sapiens nuclear receptor | 1.57 | 5.42 |
| 65 | 430775 | AJ879186 | Hs.250895 | ribosomal protein L34 | 1.57 | 7.09 |
| | 427380 | NM_005534 | Hs.177559 | interferon gamma receptor 2 (interferon | 1.56 | 5.37 |
| | 407143 | C14076 | Hs.332329 | EST | 1.56 | 6.54 |
| | 436127 | W94824 | Hs.11565 | RIKEN cDNA 2010100O12 gene | 1.56 | 6.35 |
| | 413659 | BE155647 | | gb:PM2-HT0353-130100-002-e09 HT0353 Homo | 1.55 | 5.96 |
| 70 | 445624 | AW140103 | Hs.78880 | livB (bacterial acetolactate synthase)-I | 1.55 | 4.09 |
| | 435044 | NM_002802 | Hs.4745 | proteasome (prosome, macropain) 26S subu | 1.55 | 5.71 |
| | 410397 | AF217517 | Hs.63042 | DKFZp564J157 protein | 1.54 | 5.14 |
| | 429071 | AW794126 | Hs.195453 | ribosomal protein S27 (metalloproteinstimuli | 1.54 | 8.70 |
| | 412915 | AW087727 | Hs.74823 | NM_004541:Homo sapiens NADH dehydrogenas | 1.54 | 6.57 |
| | 446429 | AI681807 | Hs.201391 | ESTs | 1.53 | 2.87 |
| 75 | 414551 | AI815639 | Hs.76394 | enoyl Coenzyme A hydratase, short chain, | 1.53 | 6.07 |
| | 406801 | AW242054 | Hs.190813 | ribosomal protein L9 | 1.52 | 5.63 |
| | 437895 | AB014568 | Hs.5898 | KIAA0668 protein | 1.51 | 5.74 |
| | 413929 | BE501689 | Hs.75617 | collagen, type IV, alpha 2 | 1.51 | 6.40 |
| | 425456 | T70445 | Hs.157850 | ribosomal protein L9 | 1.51 | 7.08 |
| 80 | 409635 | Z37166 | Hs.55296 | HLA-B associated transcript-1 | 1.50 | 5.26 |
| | 404467 | | | Target Exon | 1.50 | 5.82 |
| | 406743 | AA911568 | Hs.279860 | tumor protein, translationally-controlle | 1.50 | 5.25 |
| | 454098 | W27953 | Hs.292911 | Plakophilin | 1.48 | 3.14 |
| | 429205 | AI492393 | Hs.198248 | UDP-Gal:betaGalNAc beta 1,4- galactosylt | 1.48 | 6.24 |

| | | | | | | |
|----|--|---------------------------------------|--|--|------|-------|
| | 413825 | BE299181 | Hs.75564 | CD151 antigen | 1.47 | 5.64 |
| | 421143 | AB024536 | Hs.102171 | immunoglobulin superfamily containing le | 1.45 | 6.19 |
| | 440254 | AI879332 | Hs.7101 | anaphase-promoting complex subunit 5 | 1.45 | 5.50 |
| 5 | 406711 | N25514 | Hs.77385 | myosin, light polypeptide 6, alkali, smo | 1.42 | 11.24 |
| | 423513 | AF035960 | Hs.129719 | transglutaminase 5 | 1.42 | 3.18 |
| | 406896 | D00159 | | gb:Homo sapiens gene for pancreatic elas | 1.41 | 6.92 |
| | 433453 | BE548307 | Hs.3297 | ribosomal protein S27a | 1.40 | 5.38 |
| | 406800 | AA505535 | | gb:nh84h10.s1 NC1_CGAP_Br1.1 Homo sapien | 1.37 | 5.51 |
| 10 | 421748 | NM_014718 | Hs.107809 | KIAA0726 gene product | 1.37 | 5.46 |
| | 424372 | AW952803 | Hs.21732 | Homo sapiens cDNA FLJ11780 fis, clone HE | 1.36 | 4.06 |
| | 408250 | R92918 | Hs.19597 | KIAA1694 protein | 1.27 | 2.74 |
| | 431931 | AB035302 | Hs.272212 | cadherin 9, type 2 (T1-cadherin) | 1.15 | 2.65 |
| | 406587 | | | C15000544:gi5454148[ref]NP_006368.1 U | 1.06 | 3.11 |
| 15 | 409574 | AW419080 | Hs.250645 | ESTs | 1.00 | 3.60 |
| | 404175 | | | Target Exon | 1.00 | 3.08 |
| | 452640 | AA027115 | Hs.100206 | ESTs, Weakly similar to A53856 aryl-acyl | 1.00 | 2.82 |
| | 443564 | AI921685 | Hs.199713 | ESTs | 1.00 | 2.51 |
| 20 | TABLE 65B: | | | | | |
| | Pkey: | Unique Eos probeset identifier number | | | | |
| | CAT number: | Gene cluster number | | | | |
| | Accession: | Genbank accession numbers | | | | |
| 25 | Pkey | CAT Number | Accession | | | |
| | 407328 | 534268_1 | AI673735 AA978066 | | | |
| | 427890 | 1373988_1 | AA417099 AA435761 AA972917 AI660387 | | | |
| | 444207 | 9172_3 | BE739425 AA514221 AA865491 AI828293 AA470456 AI276739 AA169357 BE932464 AA514889 AW819039 AW819083 BE843048 AI432496 AI470335 | | | |
| 30 | AI247243 BG533994 AA513783 AI887309 AA528036 AW972006 AW873028 AI924914 AI818810 AW152378 AW084946 AI521413 AI669583 BE932521 | | | | | |
| | AI581370 BE180238 AW089750 AW771461 AW089714 AI590949 AI819148 AA731056 BF815234 BF911506 AA235803 AA485373 AI735658 | | | | | |
| | AW393133 AW073080 AI707637 BF353320 BE843111 AW819036 AW393135 BG697291 AV648670 AV654332 AV687530 BG566964 AI807430 | | | | | |
| | AI676072 AA837010 AI452482 AI625817 AW241750 BE048616 AI290928 AI680714 AA485530 BE175687 AV648513 AW130312 AI000556 AA632893 | | | | | |
| | BE674169 BF001208 AA948166 BE175650 AA524664 AA490345 AI244948 AA602956 AA483492 AA918178 AW802049 BG675859 AV658871 | | | | | |
| | BG678060 AI565004 AW819026 BE843092 AV686437 AV723049 BG616948 AI911647 AI743490 AI091096 BE857251 AI962074 AA040027 AW769317 | | | | | |
| 35 | AA343477 AA640112 BF876213 R82948 H26425 H82876 BE843095 BE843140 BG536641 BG617830 AA235802 BE774985 BE006682 BF342375 | | | | | |
| | AA903144 BF338083 BF984258 AV657996 AI749532 BE768614 BE857252 BE932516 BE768573 AV657993 AV657777 AV752631 BE774974 T55847 | | | | | |
| | 407102 | 7177_2 | BF095761 BF911511 BE710793 BE180119 BG617338 H45942 T55897 AV657718 BG563497 | | | |
| | AW945170 BF930905 F33652 BG057818 AI368018 AI421485 AI300352 AI378525 AI264177 AI276281 AI245302 AI281050 AI190036 AW451438 | | | | | |
| | AW242903 AA910870 F22289 F19647 F22375 AW473816 BF445785 AA774528 F33447 C01077 AW772227 F17759 H42812 R09701 AA349096 | | | | | |
| 40 | R48772 H42892 H42537 R47898 N28263 H25721 F32386 H43971 R48205 F21390 H45809 AA007629 R47897 R83734 H45844 AW983653 H43970 | | | | | |
| | H42536 H24495 R48875 H42961 H22079 R86018 | | | | | |
| | 437596 | 2875_1 | BC022398 AV743635 AW976922 AW152652 AA910013 AA834629 BG536317 AW849807 AV713062 AI684337 BE044081 AA761490 | | | |
| | 440116 | 454673_1 | R69942 BG655457 BF111453 AI149320 N23160 AI446431 AI758316 AV741781 BI791950 BM055014 AI798851 AA865357 AI417230 N67277 T55592 | | | |
| | T52179 | | | | | |
| 45 | 443072 | 449629_1 | AV734838 AI937532 AI032318 AW749500 AA091720 | | | |
| | 442679 | 31783_3 | BG621493 BI056706 BG496376 R53718 W65356 R79357 BG434247 AA357769 AW978686 BG573200 BF132113 BF086709 AA366938 D79234 | | | |
| | BG494628 AA156754 BG434311 AW978683 AW273417 BM054662 AI799886 AI433351 AI160798 AI433742 BF056186 AI281606 AW015046 AI439585 | | | | | |
| | AI245530 AI078267 AA807170 AA837395 W61252 AA831085 AA287371 AW768354 AA890606 AI302539 AI078575 AI673031 AI242260 AW514069 | | | | | |
| | AA283958 AA825452 AI371234 AA425696 AA453422 AA827697 R23653 D20240 AA772517 H13802 R66972 R79360 R27351 F03379 AA031952 | | | | | |
| 50 | N69504 R33143 R79358 R39136 R38800 R15089 R52937 R37502 H01021 R33634 R46551 Z40404 BG291052 BG570357 AW391046 BG496872 | | | | | |
| | H23558 | | | | | |
| | 424571 | 9758_1 | BE379766 AW152643 AI803450 AI564343 AI092711 AI140525 AW152156 AI620740 AI554689 AI161209 AI290242 AI339745 AI374611 AI347388 | | | |
| | AI858298 AI140529 AI366124 AA493912 AA406235 AA493889 AI057160 AW022264 AI097277 AI144126 AI080051 AA983529 AA860507 N53469 | | | | | |
| | AA843767 N81163 N70628 AA424577 AA983357 BF003004 AA626688 AA235977 AI057152 AI095366 AI095356 AA458646 AW194479 AA150439 | | | | | |
| 55 | AI375272 AW571777 AI359198 AA993793 BE614394 BE738239 AA127883 AI034344 T59504 D81608 AA908704 AW051665 AA382785 AA307208 | | | | | |
| | N24639 AI370715 BE244980 AA548596 AW449675 AI191008 BF223749 N70752 N22266 AI191012 AA028001 AI419106 BF215661 BF591548 | | | | | |
| | BG942356 AI474968 BE858217 BF793358 AV756758 BG483603 AI093724 BF693395 BG545345 AI744294 T59549 AA811773 BG499757 | | | | | |
| | 420787 | 55832_7 | BE674920 AA564248 AA280309 | | | |
| | 456332 | 21353_10 | BG740624 AV720262 BG198346 BG215119 AW841716 AA228357 AW841786 | | | |
| 60 | 418479 | 175360_1 | BF966791 BG564455 BE672212 AI151416 AI566231 AI417585 AI378391 AA236264 AI337574 AI346166 AA406590 AA748618 AW771957 AA478626 | | | |
| | AW338072 AI889444 AI810315 BE503662 BG231886 AI888230 AI289102 BF594638 AW074094 AW512456 AA832229 AI056108 AI025868 AI245806 | | | | | |
| | D61957 AI093841 AI721013 AI597594 AA993022 AI128620 AI285106 W37459 W35410 N90037 AA890323 R39943 AI468741 AA829976 AA479201 | | | | | |
| | AI539018 AA875875 AA448827 AW779493 Z39056 H84925 AA232923 AW517592 AI804400 AA911882 BM353143 D62885 AI457883 AI880626 | | | | | |
| 65 | 431628 | 30288_1 | R31694 R42772 R68804 R44147 R71463 AV742540 BF966987 | | | |
| | AF146277 NM_012120 AF164377 AW976054 AW662923 AW770101 AL597184 AA713959 AA088021 AW444640 AI018159 AL050105 AW958324 | | | | | |
| | BI858773 BM312584 BF594436 AI629024 AA311487 BG617872 AW629675 AA384810 AW953668 BF171208 BE768429 BF326254 AW181992 | | | | | |
| | AW118462 AW572001 BG533184 AA768779 AA825697 AA808149 BF036424 AJ420469 AW175925 AA173981 AA557142 AW302163 AW088608 | | | | | |
| | AA847195 AI418480 BM353163 AI015673 AI357621 AI374592 AI245029 AI580659 AI370154 AA767503 AA643885 BM091307 BG496655 AW364502 | | | | | |
| | AW377222 AW371202 BE138896 R80586 BM090998 D25882 M85322 AI541363 BF675114 BG926529 AA627866 BE879221 BF594796 BF675714 | | | | | |
| | BI086785 BG190411 BG217933 BG219447 BF886143 BG403278 | | | | | |
| 70 | 426101 | 3211_1 | AL049987 BG620667 BG571984 AW362842 BE150456 BE326485 AW872412 AA868553 AI024689 AA442638 AA813604 AA442648 AA663108 | | | |
| | AA442379 AA229448 N56349 AA460220 AW971193 AA453725 AI742087 AI850142 AW769479 AI917507 AI850141 BE045272 AW277065 AI921333 | | | | | |
| | AI354470 BE466760 AI827987 AI005467 AA833517 AA563934 AA522837 AA812876 AW020895 AA600372 AA663178 AI187977 AA229164 AW270324 | | | | | |
| | AA703066 T78981 AA632986 BE708493 R31132 AI253986 AI916737 T84796 T84294 AW961515 AI459289 BF109829 BI491853 AI084517 AW103830 | | | | | |
| | BE835233 AI472712 AV741009 AA551512 N28268 AA436880 AA447794 BE835410 BE835385 BE818352 BE818350 R64648 BE646467 AA493776 | | | | | |
| 75 | AA437299 BE818343 R95914 R31089 BF576826 AU186065 BF802058 AI217018 AA247541 AI191725 BE766918 | | | | | |
| | 454947 | 1083824_1 | AW846590 AW846615 AW846584 AW846592 AW846621 AW846610 | | | |
| | 438962 | 195763_1 | AI207343 BF813684 BF928775 AA828585 | | | |
| | 431693 | 1414_4 | AB075855 AI799883 AI952039 BM313847 AW167132 AW264027 AI394192 BM272158 BM272359 BG057287 BE464852 AI620722 BE046016 | | | |
| 80 | AI758979 AW474705 AW474624 AW440580 AI289435 AW002172 AI458169 AI634183 AI125609 AI951377 AI631154 AI453490 AI857358 AI469756 | | | | | |
| | BG683503 AI434048 F09546 AW518770 BF855622 AI659151 AA985193 AI814412 AW298184 H09775 AI869379 AW207026 AI659678 AI826075 | | | | | |
| | BF940660 AA744971 C00469 AI672560 AL045697 BF847489 BF842860 T65400 AI863491 H24845 T54772 BE090906 BE090917 BE090877 AA152265 | | | | | |
| | BE244301 BI038346 BI038045 W94876 AA093121 BI523346 AW470130 N92723 AA258877 R62397 BI523168 | | | | | |

| | | |
|--------|-----------|---|
| 450515 | 13638_2 | BE299605 AI589870 AA847598 AI470122 BF939896 AI304356 BE223045 BF435800 AI394207 AI708171 AW025415 AI079409 AW008420 AW304226 N34543 AW603578 AA526961 AA983631 N99134 AA626645 R45023 AA902417 AW672925 AAA49985 AA953982 AW675471 AA010062 N80194 H14620 H28475 H26247 BF333581 AW642359 H06848 H05608 H81745 H15016 R51905 AA860423 AI860904 AA876023 AF119900 NM.018539 AA702388 N53043 BF351064 N70103 AI207469 AA551569 AW383189 W00906 W00935 N54252 BC015871 AI521618 AI471709 AW169230 BG539605 BI058963 BI058949 BG548398 BG952412 AW842037 AW842040 AW890573 AK054673 D16294 NM.006111 BC001918 BI758758 AU125294 AU121192 AU118572 AL517117 BE793962 BI826721 AW149620 BG721751 BI916889 BE795064 AI934471 BF435179 BE797475 BG744432 BF733017 BI261710 BF435252 BE267474 BE219495 AV653212 AW248975 BI832737 BE264857 BG36198 AA773811 AI826904 BF732388 AI281977 BF732958 BF434612 AA480672 BF724595 AA058529 BG500189 AV687020 AA934427 AV696822 BG674590 BI262247 BE748762 BG568992 BG180336 BE748454 BG876983 BE222517 W61060 BG993321 BG742061 BG696266 BG740805 BG698598 AA031863 AF006747 AA129619 BG745080 H29767 AA011078 T88743 BG216950 AI608941 AW166202 AA522692 AI927649 AW237367 AI935538 AI689743 AW966083 BE326704 AU147054 AW129250 BE463425 AU148980 AI242161 AW615658 AU145096 BE465120 AU159062 AI679419 AW473145 BG236394 AI292110 AI985496 AA958557 BE551066 AI632625 AW511387 AI080003 AW243240 AI640340 AI075293 AW205957 AI579929 AI681080 AI753324 BF593137 AW337148 BE326667 AI637787 AI659936 F22148 AI332985 AI650925 AW248532 BE048931 F30242 AI524808 BE939886 AI340251 AI962198 BE463831 AI347479 BE221712 AW193412 BF434502 BE939895 AI373314 AW270842 AW024782 AI272109 AW772225 AW052130 F36818 AW269249 AW838580 AL565549 AI927017 AI821667 AI796037 AW772479 AA995455 AA470517 R00503 AI765977 BF196432 AW341091 AL517116 BG683620 F26241 AI160675 AU160539 BG876391 BF083008 AI795938 BF739968 AI001107 AI985556 BE792113 BI700879 BG545253 BE313692 AI339338 BF195296 AA352395 BE258769 AA160087 AA781222 AA100912 BE886334 AL534518 H02114 BG740469 AA330736 H93334 BE622370 BG426627 AA352143 BG743030 BG695884 W42513 BG674719 AW802577 BF313256 BF211944 BG489143 T68371 AA773564 AA470563 W42415 T61648 AA171398 AI695223 AI640567 AI915875 AI640318 AA669837 AA743161 AA834774 AA186698 AI766899 AA031697 AA129593 D25761 AA100913 AW134585 AA129330 BF434518 BE622820 AA587251 AW149318 H07926 RA0908 AA011079 BE967287 BE253428 AI681438 |
| 445493 | 423456_1 | AV711317 AI809938 AI808768 AI240593 AI915771 |
| 417054 | 12405_2 | BG533564 BG618564 AW296119 AI269233 BF508326 AW364777 AW292258 AA371049 AI452471 AI092522 BG618376 AL049080 AA631068 BG564643 T53833 AV702544 BG533452 AV705004 AA588281 T28665 BG569026 AV646874 AV647253 AV647455 AV647749 BI759444 AV652457 AV695354 AV696010 AV697248 BG617586 AV722549 AI435836 AI590676 AI245019 AW338243 AA530898 D52191 AI435352 D57473 BG566952 AI240505 AA035245 AV704972 BG564113 AI439237 AI287456 AV695686 AA349017 AW374043 BG568336 AW374058 AW961372 AA328028 BF438186 AI268678 AV724415 BG029720 AW725816 AI926580 BM310209 AA968470 BF430989 AI85775 AW002091 AI969941 AI718705 AI360440 AW008856 AA862294 AA625752 AI610753 AA471020 AA723203 AL044614 D80637 BF17377 AA745928 AA743114 W25004 AI127139 AA953939 AA908426 AI800072 AI417080 AW874111 AI439293 AI370639 AI277179 AA883338 AA469058 AI002097 W94913 AA047544 W91966 W69102 W84439 W52870 W67288 W69103 H98077 AA111874 AI913850 AA535740 N92824 AA973639 W68358 BE170126 T81345 N50135 AI567418 W67220 BF437728 |
| 431926 | 1237041_1 | AW972724 AA877998 AA522631 AU185388 |
| 421998 | 133592_1 | BI757233 BG911321 BF351759 AW244016 AW026834 AW024260 AI420138 AA779354 AI093360 AI934858 AW151292 AI373133 AI335587 AI969728 AI401632 BE218525 AI802114 AI783721 AA845265 AW088826 AI832852 F03967 AI611148 AI720358 AW293764 N91161 R79192 W85852 AW771263 BG820263 BG012864 R74441 R86080 W04256 BE707244 BF899452 BE327552 BE669500 AI923388 AI241532 BF448184 AI209012 AA885528 N70309 AW582776 BF110563 BF448329 BE326537 AW770471 BF444926 BE674147 AI793266 AI991774 AI807726 AI218667 AA301750 R44328 |
| 448079 | 74377_1 | AK054894 AW978550 AI984051 AW205843 AW205839 AI379941 AI383948 AW129532 BF197455 AI954133 AI668869 AI360826 AW614392 AI619505 AA927599 R64287 AI803003 AI675123 AW023079 AI638324 AW134959 AA831069 BE772132 F29901 BF210719 AI376624 AW960171 AI275045 BE856533 AW243724 AI051487 R68631 C17731 Z44230 AA309094 BI837972 AA122297 BE929614 BE006483 AA098802 BG252168 BG928816 BI091300 AW963375 AA213871 BE925757 T90131 BG426009 BG611801 BE090425 BF672863 BF132610 BF184312 |
| 408239 | 103120_1 | AW469418 AA053401 AA053416 |
| 436280 | 36296_1 | AK026215 AI201248 BE671206 AA860436 AA730787 AA834507 D79304 D79806 AW961628 AI017068 BE044373 AA322458 AA987927 AA385869 BI492783 AW021853 R79299 N73200 AI016622 N24609 AW192569 AA707819 AI690734 R79189 AI535900 AW589301 AI128434 BE838011 BE837891 BFB94555 H95408 |
| 436701 | 28142_1 | Z69892 AA210833 BM353155 AI473754 AI147901 AI803109 AA843296 AA418925 AI478552 AI400067 AI360304 AA418828 AW301673 BE218952 AI632804 BF433234 AA394157 BF378047 BE467036 AA319724 AW290940 AI222671 AI347724 AW001711 AI028652 AA398130 AA70582 AI915936 AA908929 C75102 N36920 H50440 AI919034 AI004399 AI383862 AI123606 AA648518 AA516258 AI655321 N22865 AA848101 AI588992 AA758196 AA214630 AI373911 AW194733 AA213447 AI290291 BF437165 AA757592 BF086904 AW959032 AW992466 BF446888 AI936337 BE938849 AW149064 AI701629 N90021 |
| 424399 | 2196_1 | NM.058173 AF414087 W72837 BF742809 AW070916 BE092421 AI905687 AA340069 BE074512 AI905623 AI905633 BG202312 W72838 AI139456 BG218084 BE926938 BE186013 AW176044 AW291950 BG185269 BG197186 BG192597 BG183176 BG207535 AI127172 BE815819 AI905624 R75793 BG202313 AI905837 BE815853 |
| 437611 | 240436_1 | H93046 AA897108 AI652046 AA761626 BF882276 N68615 T88896 H93912 T84424 |
| 414496 | 1526_1 | AK058006 BF724822 W65303 AW887764 AW023806 Z25353 AW022095 AA730973 W00417 W73819 BF982096 AI927669 AW188021 AW770478 AI913512 AA604358 AI697341 AI691028 AI338392 AI079403 H97538 AI144448 AI253102 AI051402 AI335900 AI868132 N28900 H98465 AF268386 AI799915 AI819228 BE048413 AW304723 AI819923 BF223106 AA155907 AW298079 BF055272 BF446804 BF197697 W58588 BF197538 AA032180 AA992597 AW590254 AA027824 AI129369 AI131331 AI655843 AW332907 AW104493 AI150615 BF110226 AW172271 AI312659 AA057312 BE673669 AA722984 AW104985 AI129232 AI078648 AI653086 AI703481 AW515897 AI352206 N67076 AW297281 AI686162 AA029184 AI610743 AW772016 AI091778 W65401 AI687374 AI218085 AI765158 AI018002 AI653068 AI335704 AI520850 AW275228 AW275204 AI420247 AA975336 AI697042 AW182235 AA736386 AI281682 AW169698 AW263325 BE645834 AI377438 AI146706 AA613808 AA716538 BI496247 AA032248 AI698930 AI193399 N70026 H86792 AA404489 W61267 BF447230 AA910805 AA150774 AA621907 AA902526 AI827634 AW022037 BF059000 BI496246 BG577007 BG571077 AA460779 AW816890 AW816893 AW816891 AA029183 AA010295 H86850 T83320 BE160823 H12925 N40087 AA096372 BE160847 AW816892 AW816889 AW816882 AW816868 AW816941 AW816578 AW816940 AW816577 AI431628 AI828113 AA033677 AA033654 AA452704 AA317582 AA346971 BF836584 H48669 BI861605 BG925200 AA463277 H89048 AA155952 W03252 W01510 W00915 W58589 AA164519 N24017 N24622 N27149 N70109 RA3771 AA010296 W84611 H98889 H88965 AW594424 AA034139 AA065223 N99696 BG981481 N94371 AA767970 W47146 N70977 H05510 W61268 T90796 AA164518 W47244 AA150883 AA034138 BF338483 F13671 H51317 W72716 N21488 AI188071 AI370541 AI754442 AA148524 AI749182 W95221 W92522 R20385 |
| 441925 | 59915_1 | AK057669 AK054977 AL519747 BE893744 BM313248 BG913430 H07993 BF813504 N36311 N39276 H95973 BF791919 BE739392 BE144239 AA074615 AI291059 AI681053 AA702355 BF439899 AW055166 AI096957 BF223853 AL119659 AI692209 BM312961 AI869297 BE466252 AI292024 AA002764 AI214620 AA765312 BF380770 AA442682 AL519746 AW295039 AI037878 AW473433 AI499437 AI401618 AI130831 AA427406 AI042138 BG272488 AI828769 AI828764 AI189390 W84635 AA398496 AA761672 AA699520 AI200406 N68093 AI143913 AI493133 AA613306 AI050971 AA661905 AA722687 AI749977 AA829345 BG057324 BF001339 AA910169 AA765133 AI360722 AI071849 AI365083 H95974 AI830377 AI312866 AI370491 BE858907 N62185 AA705746 BE379632 W93803 AI440333 AW367670 AW367640 N77131 BF993216 AI858263 W52329 N68106 R83113 R85153 BE380058 AA082537 AA729731 W234595 W31190 BF995236 BF968827 BF355168 N24508 AA215711 BF170735 AA280395 BE738851 AW367707 AA630879 AA428420 R76236 BG567847 N25931 AA173568 AI073567 AA004957 AI359585 N95093 H99798 H95072 H96853 AA215712 AA034214 R85096 H82051 H80794 RA4954 AA278972 H68352 H68346 R94750 R89010 R67951 H65817 N24891 AA173731 AI693577 BE181027 AW709461 BE181002 W60239 BF987598 BF995279 H17483 R76237 AL119133 BF964815 AW663315 H65903 H17591 R20167 AA310039 R58734 R58506 |
| 440030 | 843417_1 | AW467127 AA932693 AA861505 |
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| | | | BF445607 AA699324 AA025643 AW573103 AI167444 AA580002 AW103144 AI640654 AA857115 AA923021 AI066439 AI358865 AA843287 AI824604 AA732370 AW002202 AI219540 AA621697 AI950639 AA904277 AI867527 BF437695 AA808593 AI784144 AI648539 AV752557 AV752603 AA025642 AW764744 AW149075 N30700 H92303 W79523 AI762795 AA282784 H78923 AA252879 H98107 R23754 AA005152 N99239 N74632 H80133 H24710 R38907 R66368 R42466 R52648 H11010 R9493 |
| 5 | 410453 454065 426143 | 1027545_1 517162_1 3806_1 | BE065904 AW749036 BE175748 BE175746 BE175747 BE175745 T64217 BE394588 AW024754 BE183167 BE183166 BE378353 BC005265 BG176720 AW06027 BM352064 AW026316 AI635822 AI880584 AI693769 AI092211 BI492387 AI400449 AW166297 BF939910 AA232282 AW021432 AI333893 AA494308 AA854899 AI436795 AW069256 AA682373 AI092748 AA993184 AI126077 AI081758 AI240686 AI261863 AI378423 AA465237 AI376096 AA035579 AI087306 AA448162 AA129977 AI090903 AI080686 AI288939 N33004 AI801240 AW021546 AI370773 AI086064 AA669528 AI250053 AI870113 AA853181 AA858014 BG055562 BG939559 AW080765 AA032283 AW467587 H40506 D00762 NM_002788 AA641134 AI582295 AI417525 AI563975 AI093566 AI077743 AI290741 AW073417 BE875418 BM264076 BG876884 AI680535 AW854219 BE774635 AW854212 BG952443 AW854221 AW854208 BE156348 BE843056 AW858991 BE937569 BG878291 BG876450 AW819099 AI908570 AA449871 AU135228 BM478404 BF126296 AA375499 AA248473 |
| 10 | | | AIZ20117 AI857837 AI218371 BM091400 AI304964 AI198508 AI400738 AW571549 AW950042 AI089943 AA437280 AI150878 BF197070 AI267984 BF594181 BF196688 AI433152 AI338921 AI620364 AI280197 AA652531 AI674938 AI342447 AI620350 AI281295 AI148621 N54787 AI338121 AI281153 N51899 AI087072 AA954788 AW069054 AI346309 BG529629 AI340135 BF083036 AI167365 AW819657 AA935468 AI467858 AW148701 AI383720 BE047685 AW015498 AA937149 AW708346 AW771478 AW802508 H53334 AW389204 AW798230 AI533922 AI560688 AW950043 AI961682 AV706506 R01853 AA126514 N62757 AI536893 AI926052 AI418720 N99964 AI568933 AI915737 AI080691 AI185358 AA8996 N68575 H82824 H60037 AI247247 T95664 BF593863 AI749637 AW088541 AA991294 AA887452 AI073726 AA633132 AA629674 AA629649 AA629656 AA578595 AI168758 AA804572 AI085786 AA994396 AA991209 AA948663 AA929054 AA927952 T87001 AA928210 AA629296 AW802267 AW384129 BF744400 AA194110 AI382839 AI194837 AA406284 AI250750 R37035 AI525586 W01244 |
| 15 | 412477 | 8669_2 | NM_058173 AF414087 W72837 BF742809 AW070916 BE092421 AI905687 AA340069 BE074512 AI905623 AI905633 BG202312 W72838 AI139456 BG218084 BE926938 BE186013 AW176044 AW291950 BG185269 BG197186 BG192597 BG183176 BG207535 AI127172 BE15819 AI905624 R75793 BG202313 AI905837 BE158553 |
| 20 | 400295 | 2196_1 | BC014072 BE328850 AI356567 AI148171 AI022165 BG149661 BF000671 AA233101 AA573721 AA447991 AW016855 AI005068 AA554071 BF478215 AA906902 AW014761 BE905651 BE152923 BM047129 AA243852 AA232991 AA127550 AA127551 AA570256 AI473237 BF033706 N90525 AW973623 AI359627 BG674574 BE903322 |
| 25 | 441128 | 20932_1 | AK026697 BE938558 BE843975 BE843962 AW304313 AI735759 AA021055 AI769145 AI188319 BF064105 AI677654 AA723627 AA781580 AI611167 BE162152 R77997 BG059091 AV722360 AA370451 AA033786 AV729790 AW953851 AW953855 BE504303 AI765853 BF059302 AA410685 AI978745 AA399236 BG149495 BE670366 AI694777 BE503109 AA633474 AI700568 AI432181 AI637714 AW302164 AA196790 AI928519 BE673464 BF437523 AI281974 AI306156 AW418884 AA523952 AA683187 AW075563 AA877270 AW204404 AW771341 AI913892 AW770312 AW242851 AU154858 AA021007 AI521932 AA034044 AI760631 R34679 AI915923 AI911609 AW242360 AA059025 AA370450 BF432186 AW862279 AW859976 BE159936 BF514075 B1057841 R34781 R77900 AA011413 |
| 30 | 414665 | 23751_3 | BG567713 AW665841 AI814924 AW978339 AW264036 AI373950 AW183157 AW082249 AI201658 AI364196 AA150743 AA160873 AA453757 BF871646 BF871640 AA565311 AA589511 R10152 AA807154 T77900 AV751591 |
| 35 | 432908 434433 415409 | 452541_1 111338_1 34886_1 | AF150424 AI861896 AA570057 AV738855 AA633408 AW749955 AW629759 AI651005 AK056188 BM455117 BG527027 AA480032 AW993701 AA164703 AL537682 AA836491 AA515961 AL537681 BF437856 AA683484 AW152367 AI769509 AA907521 AW105404 AI521557 AA570165 AI564471 N22106 AA479060 AI472006 AA164704 N30335 AI224391 AA969890 BE856571 AI284716 AA918763 AA773661 BG942266 AA507486 AI934383 AA502847 AA516351 AA653124 AI360432 R75834 AA636111 AI972795 BI870444 BE891404 AI631952 AI346655 AI285030 AA928471 AL520908 AA385324 D80465 D80464 AI554371 AI907655 BF221524 AI091545 AA411631 AI028196 AA406581 AA228115 AA227977 BG929224 BF593158 |
| 40 | 408839 432093 425097 | 234669_1 1237011_1 23175_2 | AJ355222 BF378422 AA366587 BF874552 AW277084 R26970 D79194 R27662 AW972670 AA525808 H28359 H28383 AF070570 BF439282 BF109960 AI480268 AI038060 AW082339 BF516290 BE218214 AI469956 AA039955 BE644674 AI861871 AA766231 AA845840 W85716 AA676253 AI087188 AA022908 AW953178 T33195 BF594711 AA488969 R55652 D81245 D80778 D81560 AW960933 BF930897 BE698103 AA404024 BF515960 BE168475 AA453247 AI267601 R60894 R44223 T33194 AA114936 W31640 W38829 W39109 AA004849 H41952 W88634 BF031932 BM423354 AL041825 H29654 AI908178 W85754 AI905762 AA309860 C04540 AA340246 H84669 |
| 45 | | | AA708982 AI095911 AI983409 |
| 50 | 436314 406997 417314 433738 410531 442987 | 142774_1 29867_1 2097082_1 593682_1 1030559_1 66995_1 | NA N68168 N69188 N90450 AL037666 AW607643 AI280025 AL037665 AW291619 AI280142 AA765506 AI684802 AW085941 AI688062 H88044 BE156092 AW752953 |
| 55 | | | BC016329 BG530458 AW811919 AW811918 BG777252 N28284 AA280517 N26361 BC612488 BI491654 BE042557 AI921004 AW665869 AA845400 BF057417 AI735558 BM146017 AI538936 AI439915 AI745155 AA993066 AA935277 AI161350 AA884866 AI692463 AA938040 AV717682 AI439961 AA399556 AI885932 AI538058 H60829 AA513966 AI249944 Z39473 H832915 AA565386 AA074079 BM145279 BF791544 AW811909 BF964902 BG113250 N99606 AA312166 BF696463 D61610 AV757976 AA092342 BE972583 BG776159 |
| 60 | 400228 | 462_3 | NM_021724 M24898 X72631 BE550221 BF436030 F18898 AL567477 BG033127 BG747927 BF823716 AA371902 AL137978 AL577786 BI490529 AA021622 AA151679 AA745053 AA454168 R85506 AA016015 |
| 65 | 400307 452467 439518 424389 | 27110_2 90115_1 23842_1 1059_4 | AF005081 BG193848 AA026381 AW500815 AI806691 AW502933 AW303573 BE328059 AI201422 BE673566 AW182125 H13705 AF086341 W76326 W72300 BG190758 AW961118 W77994 AA339877 AW845121 AW845129 BG181820 BE716719 AI125483 AI161017 W73951 AI250771 AA912611 AA339786 BE838286 BE838282 BE716636 AA777158 W94063 BE716628 BE716625 BE838371 BF371044 BE716631 BE716402 |
| 70 | 407394 410669 417553 | 27110_2 4273_16 258857_1 | AF005081 BG193848 AW796921 AW798102 AW805749 AW805872 BF985060 AW794380 BF380449 AW794466 AW794538 AL545411 AI096369 BF431750 AI130946 W60065 W80663 AA258580 W73279 W76156 W80662 AW058658 AI204699 W60115 N56751 N30878 AI769345 R17120 AI363766 R22777 R17009 R27985 R28243 |
| 75 | 414081 | 19335_1 | BI754027 BF696071 AI351939 BG151298 AI919334 AI401620 BI770165 W72057 T96158 T29478 AA181252 BG927793 AA714431 AA600749 AA181247 AA614756 AA081092 H52207 BG926934 BF222579 BG899001 N64245 AA953040 AI832406 AA102441 BG928081 AA993445 AA916041 AA987847 AA983329 AA737219 AA916443 AW128994 AI92560 AI761847 BC005272 NM_000900 X53331 M58549 BI758966 AL598829 BI754530 BG699770 BE439699 BE440148 AV704365 AV733652 BG212015 BG184149 BG200180 BG212690 BI761222 BG182079 AW338822 AI925631 AI423041 AW071181 AI889836 AW129112 BG925339 AI017633 AA568964 BF725590 AI004210 AI080799 BE083097 BG896220 AW997681 BF668788 BE083134 AW631281 BG193052 BG183095 BE440088 BG185728 AI499579 AA188162 AA864282 BI493352 AI415584 AA836749 AA836844 AA985478 AW082299 AI816747 AA450221 AA971294 BE327509 AI719662 BG576669 AI479382 BF824747 AI741800 BG982962 AI088473 AA916151 AW473324 BG901177 BE439998 AW032669 BE813871 AW999947 BE839108 AV707983 AA369722 AW796627 AW890608 AI341771 AA320459 |
| 80 | | | BI493353 AA366332 AA371104 AA367277 AL547972 BG928011 AI678903 AI699886 AI56165 AA484893 AA643953 AW591063 BG203275 BG211093 AI334791 AA916589 AW058266 AI362370 AI143352 AA508721 AI28079 D57214 BE045265 AA541785 BG219510 BG201686 BG195572 AW019904 AW089242 AA953322 AI686698 F27562 AA614749 D56645 F20774 F30660 AW023542 AA827300 AA582214 AI701289 AA228293 AI906950 AA230156 AA384572 AW438988 AW442516 BI490938 AA731082 BF665869 BG190518 AV704158 BE439643 AA910666 AA155913 AA923097 AA975721 AA985555 BG927032 AA948389 AA451625 AA916141 AL572719 AV707258 AW083733 AA128053 AI953789 AI911993 AA421798 BG429150 AI915306 Z30130 AA126929 BG926630 AA081013 AA553696 AA916094 BG924321 AI039722 AI954968 AI372839 AI401406 AI538215 |

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| 428193 | 430_1 | AF105036 U70663 NM_004235 AF022184 AU141767 AU141110 AL040569 D44830 BI011351 AL575805 AJ290876 AI014784 AI393429 AI266211 AW074303 AA620711 BF197792 AW008766 D25944 AI687397 AE621680 AV714408 BF446905 BM314505 BF514079 BM314197 AA845201 AW874084 BE720622 AI127241 AA236239 AI679709 AI679135 AI572470 AA573434 AI568487 BE049325 AA687950 BG925989 AI338031 AI365073 AI024576 AA298805 H04001 HA5668 BG682146 AL552388 BI462361 BG547513 BG896863 BI256651 NM_003312 BC010148 AK000862 D87292 BG709214 BF972766 BG740474 BI771592 BI159859 BI820468 BI523933 AI869664 AA314620 BF724353 BG194276 BG195282 BI524679 BF435589 AI300546 AA481682 AW780207 AI800832 AI380540 BE222877 AW300707 AA481445 AW015893 AI381541 AA768558 AI138798 AA432063 AA948713 AI869485 AI307419 AI336589 AI301672 BF055581 AI312785 AI521208 AI927918 AI989759 M78015 BF718621 AI927654 AI795909 AI335381 BF334524 AW007444 AA706797 AA975178 AA884739 AA443837 AA933897 AI826464 AI271737 AA053419 H79704 AI984483 BG952614 BF345358 AW083336 AA643660 AI478232 AA603071 BE714413 AW078660 AW070418 R02364 BG925951 AL568823 AA053459 AA446748 BG954446 BF760569 | |
| 427391 | 9048_3 | AY007099 AU150467 AI127583 BE735800 AI125772 AI373009 AI215670 AJ769136 AA586848 AW451158 N50799 AA936337 AI355427 BE677905 AW338020 BG151557 AA657954 AI754947 AW467279 AI128755 BF448136 AI369247 BF439175 BE207948 AI089272 B911455 AA420720 F36980 AI494204 AA953319 AA155753 AJ052675 AA044804 AI282678 BG741226 F25798 AA180204 AI682613 AI152630 AA420766 AI373393 AI885767 T03896 BF939430 AA974325 AW072996 AW005963 BG252471 AI192002 AI918908 AA776144 BI834864 AI753954 BE908511 AW628731 AA034958 BF447074 AW194549 AI915192 AL567164 BF691569 AL565970 AW471137 AW276992 AL536717 BF591783 AI571746 BF939172 BG745029 BG575588 BI054960 H51485 AW799491 AI370437 H26413 AA585334 AU151276 AA074274 AA936883 AW131643 AI221650 AW105476 AW952294 H23835 BI035010 F22360 BF849322 | |
| 400202 | 11771_2 | BE873890 BF745945 AA156007 AA573157 AW874610 AA916387 N75963 BM083306 AW044671 BC013008 NM_002795 D26598 BG118716 BI910891 BF972860 BG119842 BI094093 AL538757 BE271653 BI856538 BE909573 BG109826 BE784430 BE899255 BI833973 BM010809 BE621321 BG684956 BE904726 BI871370 AV708990 BF971483 BE298241 BI197007 BE272092 BG120374 AW963509 BE540572 AV744947 BG943041 AW327463 BG472870 BE393697 N28533 AA315042 N42043 AW404246 AW892094 AA379896 AW801110 AW406977 AA379791 BG941889 BE076254 AA360459 AA379385 AA320056 BG942618 D31230 AA308300 AA360371 AA371733 AA732937 AA494241 W32225 BF745937 AI383690 BG202360 NM_006156 D23662 BF038671 BI670321 BI603145 BI666956 BG176628 BG707476 BG768814 BE312007 BF125930 BF037916 BG942671 AI752472 AW009362 BE379126 BI198555 BF126026 N28289 BE388301 BG327102 AJ571450 BF038400 AI884649 AJ178962 AJ742314 AA977058 AJ150699 BG944784 AA187402 BG283893 AV712007 W01301 BG774109 W77840 C15672 BI670016 AI752473 AA484409 C14921 N41745 C15220 F30164 AA133181 BF768974 H30334 AA034968 AA384232 AA353297 AW407023 AA337516 F36177 AA374444 AA402758 AI141545 BI021470 AA973914 BE155647 BE155627 | |
| 413659 | 1526081_1 | | |
| 406800 | 0_0 | AA505535 | |
| TABLE 65C: | | | |
| Pkey: | Unique number corresponding to an Eos probeset | | |
| Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. | | |
| Strand: | Indicates DNA strand from which exons were predicted. | | |
| Nt_position: | Indicates nucleotide positions of predicted exons. | | |
| Pkey | Ref | Strand | Nt_position |
| 405121 | 8102330 | Minus | 35816-36004,36587-36684 |
| 401203 | 9743387 | Minus | 172961-173056,173868-173928 |
| 400494 | 9714719 | Plus | 169845-170272 |
| 402294 | 2282012 | Minus | 2575-3000 |
| 404730 | 8389582 | Plus | 119832-120016,124110-124275 |
| 403593 | 6862650 | Minus | 62554-62712,69449-69602 |
| 403710 | 6437516 | Plus | 27413-28978 |
| 401905 | 8671966 | Plus | 153965-154441,156599-156819 |
| 403108 | 8980955 | Plus | 93253-93667 |
| 404996 | 6007890 | Plus | 37999-38145,38652-38998,39727-39872,4055 |
| 402315 | 7381741 | Minus | 30728-32065 |
| 401131 | 8699812 | Minus | 94802-94987,95804-95887,96323-96487,9759 |
| 401205 | 9743388 | Plus | 167373-167433,167936-168031 |
| 403105 | 8980016 | Minus | 145287-145744 |
| 401846 | 7712190 | Minus | 82775-82823,82912-83022 |
| 406400 | 9256298 | Plus | 1553-1712,1878-2140,4252-4385,5922-6077 |
| 406467 | 9795551 | Plus | 182212-182958 |
| 401429 | 8217890 | Minus | 86946-87579 |
| 404467 | 8077630 | Minus | 24951-25853 |
| 406587 | 8189273 | Minus | 120577-120718 |
| 404175 | 9931117 | Minus | 107420-107547,109625-109796 |

TABLE 66A. DISEASE INDICATIONS AND PREFERRED UTILITIES FOR SELECTED GENES

Table 66A provides disease indications and preferred utilities for about 439 selected genes. These genes were identified using Eos/Affymetrix Genechip arrays.

Primekey: Unique Eos probeset identifier number

ExAcn: Exemplar Accession number

UgID: Unigene ID number

UgTitle: Unigene title

Disease: diseases indicated for selected gene as described in table 1 and abbreviated as follows: AWP (androgen independent prostate diseases), arth (arthritic diseases), bph (benign prostatic hyperplasia), blad (bladder diseases), angio (blood vessel diseases), EWS (bone diseases), glio (brain diseases), breast (breast diseases), cerv (cervical diseases), colon (colorectal diseases), esoph (esophageal diseases), fibro (fibrotic diseases), headnk (head & neck diseases), leio (leiomyoma diseases), leuk (leukocyte diseases), hepC (liver diseases), lung (lung diseases), ovar (ovarian diseases), endo (ovarian endometrioid diseases), omuc (ovarian mucinous diseases), panc (pancreatic diseases), pros (prostate diseases), renal (renal diseases), meta (skin diseases), stom (stomach diseases), test (testicular diseases), uter (uterine diseases)

Utility: preferred utilities for selected gene as described in the text and abbreviated as follows: CTL (DNA vaccine target), diag (diagnostic or prognostic target), mAb (monoclonal antibody target), s.m. (small molecule target)

| Primekey | Ex Acn | UgID | Ug Title | Disease | Utility |
|----------|----------|-----------|---|--|---------------|
| 400289 | X07820 | Hs.2258 | matrix metalloproteinase 10 (stromelysin) | angio, blad, lung, cerv, ovar, headnk, esoph | mAb+diag+s.m. |
| 400297 | AI127076 | Hs.306201 | hypothetical protein DKFZp56401278 | breast, blad, colon, pros | mAb |
| 400303 | AA242758 | Hs.79136 | LIV-1 protein, estrogen regulated | breast, ovar, pros, stom, uter, blad, lung, headnk | mAb |
| 400843 | | | NM_003105:Homo sapiens sortilin-related | blad | s.m. |
| 402075 | | | ENSP00000251056:Plasma membrane calcium | blad, lung, headnk, cerv, meta, esoph | mAb+diag |
| 402901 | | | NM_025206:Homo sapiens hypothetical pro | blad | CTL |
| 404287 | | | FGENESH predicted novel CUB-domain conta | panc, lung, colon, uter, esoph | mAb+s.m. |

| | | | | | |
|----|--------|-----------|--|---|---------------|
| 5 | 404682 | | ortholog of mouse polydomain protein | panc | diag |
| | 404875 | | NM_022819: Homo sapiens phosphatase A2 | blad | CTL+s.m. |
| | 404977 | | Insulin-like growth factor 2 (somatomedi | blad, ovar | mAb+diag |
| | 405033 | | C1002652: gi544327 sp Q04799 FMO5_RABIT | blad | s.m. |
| | 405547 | | NM_018833: Homo sapiens transporter 2, A | cerv, mela | mAb+s.m. |
| | 406400 | | kallikrein 8 (neurosin/ovasin) (KLK8) | ovar, uter | diag |
| | 406964 | M21305 | FGENES predicted novel secreted protein | angio, blad, fibro | diag |
| 10 | 407603 | AW955705 | Homo sapiens, clone IMAGE:4299322, mRNA, | glio, blad | CTL |
| | 407792 | A1077715 | putative secreted ligand homologous to f | ovar, uter, cerv, panc | mAb+diag |
| | 407811 | AW190902 | cysteine knot superfamily 1, BMP antagon | blad, panc, stom, uter, lung, esoph | diag |
| | 407836 | T79340 | B-cell CLL/lymphoma 6, member B, zinc fi | angio | CTL |
| | 407975 | X89426 | endothelial cell-specific molecule 1 | angio, renal | diag |
| | 408243 | Y00787 | interleukin 8 | blad, stom, headnk, cerv, lung, angio, esoph, panc | diag |
| 15 | 408367 | AK001178 | Homo sapiens orphan neurotransmitter tra | mela | mAb+s.m. |
| | 408369 | R38438 | SLC15A2 Solute carrier family 15 (H+pep | pros, lung, fibro, uter, glio, cerv, ovar | mAb |
| | 408380 | AF123050 | diubiquitin | lung, blad, headnk, panc, stom, fibro, esoph, mela | CTL |
| | 408482 | NM_000676 | adenosine A2b receptor | lung, esoph, headnk | mAb+s.m. |
| | 408562 | AJ436323 | roundabout (axon guidance receptor, Dros | uter, fibro | mAb+s.m. |
| 20 | 408790 | AW580227 | neurotrophic tyrosine kinase, receptor, | lung | mAb+s.m. |
| | 408908 | BE296227 | serine/threonine kinase 15 | blad, lung, headnk, stom | s.m. |
| | 409041 | A8033025 | Hypothetical protein, XP_051860 (KIAA119 | uter, ovar, lung, colon, stom, headnk, breast, panc | CTL+diag |
| | 409079 | W87707 | interleukin 6 signal transducer (gp130, | breast, pros | mAb+s.m. |
| | 409103 | AF251237 | XAGE-1 protein | lung | CTL |
| 25 | 409178 | BE393948 | kallikrein 5 | ovar, breast, mela | diag |
| | 409220 | BE243323 | tumor necrosis factor receptor superfam | angio, renal, colon, stom | mAb+s.m. |
| | 409348 | AJ401535 | ESTs | renal, glio | mAb+s.m.+CTL |
| | 409389 | AB007979 | Homo sapiens mRNA, chromosome 1 specific | glio | mAb+diag |
| | 409420 | Z15008 | laminin, gamma 2 (nicein (100kD), kalini | lung, headnk, panc, stom, cerv, esoph, blad | diag |
| | 409632 | W74001 | serine (or cysteine) proteinase inhibito | lung, blad, headnk | diag |
| 30 | 409637 | AA323948 | Homo sapiens mRNA; cDNA DKFZp434K0621 (f | renal | mAb+s.m.+CTL |
| | 409663 | AJ743750 | KIAA1862 protein | renal | CTL |
| | 409745 | AA077391 | gb:7B14E12 Chromosome 7 Fetal Brain cDNA | ovar, renal | mAb+s.m.+CTL |
| | 409757 | NM_001898 | cystatin SN | panc, stom, lung, blad, | diag |
| 35 | 409893 | AW247090 | minichromosome maintenance deficient (S. | lung, cerv, blad, test, esoph | CTL+s.m. |
| | 409956 | AW103364 | inhibin, beta A (activin A, activin AB a | breast, panc, ovar, colon, headnk, lung, blad, esoph | diag |
| | 410001 | AB041036 | kallikrein 11 | ovar, pros, uter, cerv, lung | diag |
| | 410055 | AJ250839 | gene for serine/threonine protein kinase | renal | s.m. |
| | 410153 | BE311926 | hypothetical protein FLJ12691 | renal, blad | CTL |
| 40 | 410274 | AA381807 | hypoxia-inducible protein 2 | lung, renal | CTL |
| | 410309 | BE043077 | alpha-2,8-sialyltransferase III | panc | s.m. |
| | 410407 | X66839 | carbonic anhydrase IX | renal, lung, colon, stom, ovar, uter, blad | mAb+s.m. |
| | 410418 | D31382 | transmembrane protease, serine 4 | colon, blad, lung, ovar, panc, headnk | mAb+diag+s.m. |
| | 411274 | NM_002776 | kallikrein 10 | colon, ovar, uter, cerv, headk, panc | diag |
| 45 | 411411 | AA345241 | ESTs, Weakly similar to KIAA1330 protein | renal | mAb+s.m. |
| | 411773 | NM_006799 | protease, serine, 21 (testisin) | ovar | diag |
| | 412078 | X69699 | paired box gene 8 | ovar | CTL |
| | 412140 | AA219691 | RAB6 interacting, kinesin-like (rabkines | lung, blad, headnk, breast, ovar, panc, angio, test, mela | s.m. |
| | 412580 | AA113262 | similar to CABLES [Homo sapiens] | mela | mAb+s.m.+CTL |
| 50 | 412609 | Z48804 | ocular albinism 1 (Nettleship-Falls) | mela | s.m. |
| | 412628 | AJ972402 | hypothetical protein MGC2648 | pros | diag |
| | 412709 | AL022327 | KIAA0027 protein | glio | mAb+s.m. |
| | 412719 | AW016610 | ESTs | lung, headnk, blad, glio, cerv | s.m. |
| | 412959 | D87458 | KIAA0282 protein | glio | CTL+s.m. |
| 55 | 412986 | X81120 | cannabinoid receptor 1 (brain) | glio | mAb+s.m. |
| | 413048 | M93221 | mannose receptor, C type 1 | fibro, panc | mAb |
| | 413063 | AL035737 | chitinase 3-like 1 (cartilage glycoprote | glio, ovar, blad, lung | diag |
| | 413278 | BE563085 | interferon-stimulated protein, 15 kDa | panc, lung, blad, breast, cerv, ovar, headnk, esoph, mela, stom | CTL+s.m. |
| | 413324 | V00571 | corticotropin releasing hormone | blad | diag |
| 60 | 413385 | M34455 | indoleamine-pyrole 2,3 dioxygenase | blad, lung, mela, fibro, uter | s.m. |
| | 413554 | AA319146 | secretogranin II (chromogranin C) | panc, glio | diag |
| | 413719 | BE439580 | small inducible cytokine subfamily A (Cy | panc, lung, headnk, cerv, colon, uter, stom, esoph | diag |
| | 414577 | AJ056548 | hypothetical protein FLJ20992 similar to | angio | CTL+diag |
| | 414774 | X02419 | plasminogen activator, urokinase | lung, blad, headnk, panc, stom, ovar, esoph | diag |
| 65 | 414812 | X72755 | monokine induced by gamma interferon | breast, blad, lung, fibro, panc, colon, headnk, | |
| | | | | cerv, stom, renal, ovar, test, mela, esoph | diag |
| | 414825 | X06370 | epidermal growth factor receptor (avian | glio, lung, renal, esoph, panc, headnk, arth | mAb+s.m.+CTL |
| | 414883 | AA926960 | CDC28 protein kinase 1 | lung, ovar, stom, colon, cerv, headnk, test | s.m. |
| | 414907 | X90725 | polo (Drosophila)-like kinase | blad, lung, ovar, test | s.m. |
| 70 | 414945 | BE076358 | lymphocyte antigen 6 complex, locus E | mela | mAb+s.m. |
| | 415138 | C18356 | tissue factor pathway inhibitor 2 | angio, panc, stom, lung, uter | CTL+diag |
| | 415511 | AJ732617 | ESTs | blad, ovar, renal | mAb+s.m.+CTL |
| | 415539 | AJ733881 | BMP-R1B | breast, uter, pros | mAb+s.m. |
| | 415668 | AW957684 | Homo sapiens lysyl oxidase-like 4 (LOXL4 | mela | diag |
| 75 | 415669 | NM_005025 | serine (or cysteine) proteinase inhibito | lung | mAb+diag+s.m. |
| | 415817 | U88967 | protein tyrosine phosphatase, receptor-t | lung, glio, headnk, cerv, mela, esoph, fibro | mAb+s.m. |
| | 415910 | U20350 | chemokine (C-X3-C) receptor 1 | glio | mAb+s.m. |
| | 415929 | AA724373 | Homo sapiens mucopolip-3 (MCOLN3) | mela | mAb |
| | 415989 | AJ267700 | ESTs | pros, ovar, blad, lung, headnk, panc, colon, stom | mAb+s.m.+CTL |
| | 416091 | AF295370 | defensin, beta 3 | headnk, esoph, mela | CTL+diag |
| 80 | 416209 | AA236776 | MAD2 (mitotic arrest deficient, yeast, h | lung, headnk, colon, uter, stom | CTL+s.m. |
| | 416250 | AA581386 | Kremen 2 | esoph, lung, cerv, ovar | mAb+s.m. |
| | 416350 | AF188625 | phospholipase A2, group IID | test, mela, fibro | CTL |
| | 416530 | U62801 | kallikrein 6 (neurosin, zyme) | ovar, uter | diag |

| | | | | | | |
|----|--------|-----------|-----------|---|---|---------------|
| 5 | 416636 | N32536 | Hs.42645 | solute carrier family 16 (monocarboxylic | breast, panc, uter, mela | mAb+s.m. |
| | 416658 | U03272 | Hs.79432 | fibrillin 2 (congenital contractural ara | lung, ovar, uter, blad, angio, test | diag |
| | 416836 | D54745 | Hs.80247 | cholecystokinin | pros, EWS, glio | diag |
| | 416857 | AA188775 | Hs.292453 | FGENES predicted TM containing protein | glio | mAb+s.m. |
| | 417034 | NM_006183 | Hs.80962 | neurotensin | lung, headnk, cerv | diag |
| | 417079 | U65590 | Hs.81134 | interleukin 1 receptor antagonist | blad, lung, headnk, cerv, esoph | diag |
| | 417166 | AA431323 | Hs.42146 | Paired box protein Pax-3 | mela | CTL |
| | 417355 | D13168 | Hs.82002 | endothelin receptor type B | glio, mela | mAb+s.m. |
| 10 | 417389 | BE270964 | Hs.82045 | midkine (neurite growth-promoting factor | ovar, lung, blad, uter, cerv, panc, stom, mela, test, colon | mAb+diag |
| | 417433 | BE270266 | Hs.82128 | ST4 oncofetal trophoblast glycoprotein | panc, breast, blad, lung, headnk, cerv, uter, ovar, stom, renal | mAb |
| | 417542 | J04129 | Hs.82269 | progesterone-associated endometrial prote | lung, mela | mAb+diag |
| | 417771 | AA804698 | Hs.82547 | retinoic acid receptor responder (tazaro | blad, cerv, panc, ovar | mAb |
| | 417866 | AW067903 | Hs.82772 | collagen, type XI, alpha 1 | lung, panc, breast, ovar, headnk, stom | CTL |
| | 417931 | W95642 | Hs.82961 | retinoic acid receptor 3 (intestinal) | ovar, panc, stom, colon, uter, pros | diag |
| 15 | 417933 | X02308 | Hs.82962 | thymidylate synthetase | blad, lung, angio, colon, panc, esoph | s.m. |
| | 418007 | M13509 | Hs.83169 | matrix metalloproteinase 1 (interstitial | lung, blad, fibro, headnk, panc, stom, colon, ovar, esoph, mela | mAb+diag+s.m. |
| | 418030 | BE207573 | Hs.83321 | neuromedin B | glio, panc | diag |
| | 418064 | BE387287 | Hs.83384 | S100 calcium-binding protein, beta (neur | uter, ovar | diag |
| 20 | 418281 | U09550 | Hs.1154 | oviductal glycoprotein 1, 120kD (mucin 9 | mela | CTL+diag |
| | 418478 | U38945 | Hs.1174 | cyclin-dependent kinase inhibitor 2A (me | lung, blad, ovar, headnk, panc, cerv, mela | s.m. |
| | 418506 | AA084248 | Hs.372651 | Unknown protein for MGC:29643 (formerly | angio, ovar, glio, uter, lung, blad, panc, mela | mAb+diag |
| | 418526 | BE019020 | Hs.85838 | solute carrier family 16 (monocarboxylic | lung, blad, renal, panc, stom, colon, ovar | mAb+s.m. |
| | 418558 | AW082266 | Hs.86131 | Fas (TNFRSF6)-associated via death domain | esoph, headnk | s.m. |
| 25 | 418678 | NM_001327 | Hs.167379 | cancer/testis antigen (NY-ESO-1) | lung, blad, stom, ovar, panc, esoph, cerv, mela | CTL |
| | 418830 | BE513731 | Hs.88959 | hypothetical protein MGC4816 | lung | CTL |
| | 418867 | D31771 | Hs.89404 | rsh (Drosophila) homeo box homolog 2 | blad | s.m. |
| | 418870 | AF147204 | Hs.89414 | chemokine (C-X-C motif), receptor 4 (fus | leuk, ovar, breast, blad, renal | mAb+s.m. |
| | 419080 | AW150835 | Hs.18878 | hypothetical protein FLJ21620 | renal, uter, lung | CTL |
| 30 | 419121 | AA374372 | Hs.89626 | parathyroid hormone-like hormone | lung, esoph, headnk, blad | diag |
| | 419171 | NM_002846 | Hs.89655 | protein tyrosine phosphatase, receptor I | lung | mAb+s.m. |
| | 419172 | AW338625 | Hs.22026 | ESTs; similar to TRANSMEMBRANE 4 SUPERF | angio, renal | mAb+s.m. |
| | 419183 | U06069 | Hs.89663 | cytochrome P450, subfamily XXIV (vitamin | blad, lung, headnk, panc | CTL+s.m. |
| | 419216 | AU076718 | Hs.164021 | small inducible cytokine subfamily B (Cy | panc, lung, stom, cerv, pros, headnk, esoph | diag |
| 35 | 419235 | AW470411 | Hs.288433 | neurotrophin | panc, fibro, headnk, lung | mAb+diag |
| | 419452 | U33635 | Hs.90572 | PTK7 protein tyrosine kinase 7 | ovar, pros, lung, breast, uter, test, panc, stom | mAb+s.m. |
| | 419508 | AW997938 | Hs.90786 | ATP-binding cassette, sub-family C (CFTR | glio, omuc, stom, lung, panc, colon, renal, uter | mAb+diag |
| | 419556 | U29615 | Hs.91093 | chitinase 1 (chitinohydrolase) | lung, fibro, test | mAb+s.m. |
| | 419704 | AA429104 | Hs.45057 | ESTs | glio | CTL+s.m. |
| 40 | 419723 | AL120193 | Hs.339810 | longevity assurance (LAG1, S. cerevisiae | glio | mAb+diag |
| | 419741 | NM_007019 | Hs.93002 | ubiquitin carrier protein E2-C | blad, lung, colon, ovar, test, esoph, mela | CTL+s.m. |
| | 420159 | A1572490 | Hs.99785 | Homo sapiens cDNA: FLJ21245 fs, clone C | blad, stom | mAb |
| | 420162 | BE378432 | Hs.95577 | cyclin-dependent kinase 4 | lung, mela | s.m. |
| | 420208 | BE276055 | Hs.95972 | silver (mouse homolog) like | mela | CTL |
| 45 | 420370 | Y13645 | Hs.97234 | uroplakin 2 | blad | mAb |
| | 420440 | NM_002407 | Hs.97644 | mammaglobin 2 | ovar, uter, cerv | diag |
| | 420602 | AF060877 | Hs.99236 | regulator of G-protein signalling 20 | headnk, glio, cerv, mela | CTL+s.m. |
| | 420610 | A1683183 | Hs.99348 | distal-less homeo box 5 | uter, endo, lung | CTL |
| | 420737 | L08096 | Hs.99899 | CD70; tumor necrosis factor (ligand) s | renal | mAb+s.m. |
| 50 | 420789 | AJ670057 | Hs.199882 | ESTs | renal | mAb+s.m.+CTL |
| | 420876 | AA918425 | Hs.177744 | FGENES predicted novel protein containin | panc, blad | s.m. |
| | 421066 | AU076725 | Hs.101408 | branched chain aminotransferase 2, mito | blad, lung | CTL+s.m. |
| | 421110 | AJ250717 | Hs.1355 | cathepsin E | blad, panc, stom, lung, fibro, ovar, esoph | sm+diag |
| 55 | 421340 | F07783 | Hs.1369 | decay accelerating factor for complement | angio, panc, stom | diag |
| | 421379 | Y15221 | Hs.103982 | small inducible cytokine subfamily B (Cy | breast, panc, headnk, lung, stom, blad, cerv, colon, fibro, test, mela, esoph | diag |
| | 421471 | U90545 | Hs.327179 | solute carrier family 17 (sodium phospho | renal | mAb+s.m. |
| | 421474 | U76362 | Hs.104637 | solute carrier family 1 (glutamate trans | lung | mAb+s.m. |
| | 421508 | NM_004833 | Hs.105115 | absent in melanoma 2 | blad, esoph, lung, mela | mAb+s.m.+CTL |
| 60 | 421524 | AA312082 | Hs.105445 | GDNF family receptor alpha 1 | breast | mAb+s.m. |
| | 421552 | AF026692 | Hs.105700 | secreted frizzled-related protein 4 | breast, ovar, panc, cerv, uter, pros, lung, stom, headnk | diag |
| | 421574 | AJ000152 | Hs.105924 | defensin, beta 2 | headnk, lung | CTL+diag |
| | 421582 | A1910275 | Hs.350470 | trefoil factor 1 (breast cancer, estroge | breast, panc, lung, omuc | diag |
| | 421666 | AL035250 | Hs.1408 | endothelin 3 | mela | mAb+diag |
| 65 | 421753 | BE314828 | Hs.107911 | ATP-binding cassette, sub-family B (MDR/ | lung | mAb+s.m. |
| | 421817 | AF146074 | Hs.108660 | ATP-binding cassette, sub-family C (CFTR | lung, cerv, headnk, blad | mAb+s.m. |
| | 422033 | AW245805 | Hs.110903 | claudin 5 (transmembrane protein deleted | glio | mAb+s.m. |
| | 422048 | NM_012445 | Hs.288126 | spondin 2, extracellular matrix protein | panc, pros | diag |
| | 422109 | S73265 | Hs.1473 | gastrin-releasing peptide | panc, lung, colon, fibro | diag |
| 70 | 422158 | L10343 | Hs.112341 | protease inhibitor 3, skin-derived (SKAL | headnk, blad, lung, cerv, stom, esoph | diag |
| | 422163 | AF027208 | Hs.112360 | prominin (mouse)-like 1 | colon, breast, fibro | mAb+s.m. |
| | 422192 | AA305159 | Hs.113019 | fts485 | mela | s.m. |
| | 422260 | AA315993 | Hs.105484 | regenerating gene type IV | colon, omuc, stom, panc | mAb+diag |
| 75 | 422282 | AF019225 | Hs.114309 | apolipoprotein L | blad, lung, headnk, renal | diag |
| | 422283 | AW411307 | Hs.114311 | CDC45 (cell division cycle 45, S.cerevis | lung, blad, test, cerv, headnk, esoph | s.m. |
| | 422309 | U79745 | Hs.114924 | solute carrier family 16 (monocarboxylic | mela | mAb+s.m.+CTL |
| | 422330 | D30783 | Hs.115263 | epiregulin | panc, colon, blad | mAb+diag |
| | 422397 | AJ223366 | Hs.116051 | MYEOV Myeloma overexpressed gene (in a | panc, stom, colon, esoph, renal, blad | CTL+s.m. |
| | 422424 | A1186431 | Hs.296638 | prostate differentiation factor | blad, panc, pros, angio, colon, stom, lung, mela | diag |
| 80 | 422627 | BE336857 | Hs.118787 | transforming growth factor, beta-induced | colon, renal | mAb+diag |
| | 422765 | AW409701 | Hs.1578 | baculoviral IAP repeat-containing 5 (sur | lung, blad | s.m. |
| | 422809 | AK001379 | Hs.121028 | hypothetical protein FLJ10549 | blad, cer, lung, uter, angio, stom, test | s.m. |
| | 422867 | L32137 | Hs.1584 | cartilage oligomeric matrix protein (pse | breast, ovar, pros, panc, lung, colon, uter | diag |
| | 422956 | BE545072 | Hs.122579 | ECT2 protein (Epithelial cell transformi | ovar, blad, panc, lung, headnk, colon, stom | CTL+s.m. |
| | 423161 | AL049227 | Hs.124776 | downstream of cadherin 6 (by 3.3kb) | renal, ovar, blad | mAb+s.m. |

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| 5 | 423184 | NM_004428 | Hs.1624 | ephrin-A1 | pros, panc, renal | mAb+s.m. |
| | 423242 | AL039402 | Hs.125783 | DEME-6 protein | breast, renal, ovar, pros, colon | CTL |
| | 423422 | AC005175 | Hs.128425 | NY-REN-24 antigen | glio | mAb |
| | 423508 | AW604297 | Hs.129711 | hepatitis A virus cellular receptor 1 | renal, colon | mAb |
| | 423583 | AL122055 | Hs.129836 | KIAA1028 protein | pros | s.m. |
| | 423634 | AW595908 | Hs.1690 | heparin-binding growth factor binding pr | lung, blad, headnk, panc | diag |
| | 423673 | BE003054 | Hs.1695 | matrix metalloproteinase 12 (macrophage | blad, lung, headnk, ovar, panc, colon, stom, uter, cerv, esoph, test | mAb+diag+s.m. |
| | 423936 | U77629 | Hs.135639 | achaete-scute complex (Drosophila) homol | colon, stom, ovar | CTL |
| 10 | 423951 | D13666 | Hs.136348 | periostrin (OSF-2os) | breast, colon, blad, lung, fibro, panc, headnk, ovar, mela | mAb+diag |
| | 424008 | R02740 | Hs.137555 | putative chemokine receptor; GTP-binding | blad, headnk, stom, cerv, esoph | mAb+s.m. |
| | 424046 | AF027866 | Hs.138202 | serine (or cysteine) proteinase inhibitor | headnk, lung, cerv | diag |
| | 424252 | AK000520 | Hs.143811 | hypothetical protein FLJ20513 | colon, stom | mAb+s.m.+CTL |
| | 424321 | W74048 | Hs.1765 | lymphocyte-specific protein tyrosine kin | mela, fibro | s.m. |
| | 424381 | AA285249 | Hs.146329 | protein kinase Chk2 (CHEK2) | lung, colon, test | s.m. |
| 15 | 424411 | NM_005209 | Hs.146549 | crystallin, beta A2 | panc | s.m. |
| | 424502 | AF242388 | Hs.149585 | lensin | lung | s.m. |
| | 424503 | NM_002205 | Hs.149609 | integrin, alpha 5 (fibronectin receptor, | panc, pros, angio, blad, lung | mAb+s.m. |
| | 424620 | AA101043 | Hs.151254 | kallikrein 7 (chymotryptic, stratum com | ovar | diag |
| 20 | 424687 | J05070 | Hs.151738 | matrix metalloproteinase 9 (gelatinase B | headnk, panc, lung, blad, uter, cerv, colon, stom, test, mela | diag |
| | 424735 | U01875 | Hs.152749 | short-chain alcohol dehydrogenase family | blad, breast | CTL+s.m. |
| | 424825 | AF207069 | Hs.153357 | procollagen-lysine, 2-oxoglutarate 5-dio | mela | CTL+s.m. |
| | 424905 | NM_002497 | Hs.153704 | NIMA (never in mitosis gene a)-related k | ovar, blad, lung, headnk, panc, stom | s.m. |
| | 425009 | X58288 | Hs.154151 | protein tyrosine phosphatase, receptor t | renal, fibro | mAb+s.m. |
| 25 | 425071 | NM_013989 | Hs.154424 | deiodinase, iodothyronine, type II | pros, colon, stom, uter, cerv, headnk, esoph, panc | diag |
| | 425088 | AA663372 | Hs.169395 | hypothetical protein FLJ12015 | glio, mela | mAb+s.m.+CTL |
| | 425115 | R44664 | Hs.123956 | downstream of: G protein-coupled recept | glio | mAb+s.m. |
| | 425247 | NM_005940 | Hs.155324 | matrix metalloproteinase 11 (stromelysin | breast, ovar, lung, colon, panc, headnk, stom, uter, cerv, blad, esoph | mAb+diag+s.m. |
| | 425322 | U63630 | Hs.155637 | protein kinase, DNA-activated, catalytic | lung, headnk | s.m. |
| 30 | 425535 | AB007937 | Hs.158287 | syndecan 3 | mela, glio | mAb+s.m. |
| | 425650 | NM_001944 | Hs.1925 | desmoglein 3 (pemphigus vulgaris antigen | lung, headnk, cerv, esoph, blad | mAb |
| | 425721 | AC002115 | Hs.159309 | uroplakin 1A | blad | mAb |
| | 425723 | NM_014420 | Hs.159311 | diccdop1 (Xenopus laevis) homolog 4 | endo, uter, colon | CTL+diag |
| | 425734 | AF056209 | Hs.159396 | peptidylglycine alpha-amidating monooxyg | lung | s.m. |
| 35 | 425776 | U25128 | Hs.159499 | parathyroid hormone receptor 2 | ovar, uter, lung | mAb+diag |
| | 425842 | AI587490 | Hs.159623 | NK-2 (Drosophila) homolog B | panc, glio | s.m. |
| | 425852 | AK001504 | Hs.159651 | death receptor 6, TNF superfamily member | blad, lung, headnk | mAb+s.m. |
| | 425883 | AL137708 | Hs.161031 | Homo sapiens mRNA: cDNA DKFZp434K0322 (I | blad, panc | mAb |
| | 425921 | NM_007231 | Hs.162211 | solute carrier family 6 (neurotransmitte | stom, panc | mAb+s.m. |
| 40 | 425998 | AU076629 | Hs.165950 | fibroblast growth factor receptor 4 | renal | mAb+s.m. |
| | 426028 | NM_001110 | Hs.172028 | a disintegrin and metalloproteinase doma | blad | mAb+diag |
| | 426215 | AW963419 | Hs.155223 | stanniocalcin 2 | breast, lung, renal, colon, ovar, uter | mAb+diag |
| | 426227 | U67058 | Hs.154299 | Human proteinase activated receptor-2 mR | panc, lung, colon, esoph, stom | mAb+s.m. |
| | 426322 | J05068 | Hs.2012 | transcobalamin I (vitamin B12 binding pr | panc, blad, stom | diag |
| 45 | 426344 | H41821 | Hs.322469 | transcriptional activator of the c-fos p | glio | CTL+s.m. |
| | 426427 | M86699 | Hs.169840 | TTK protein kinase | ovar, lung, headnk, cerv, colon, uter, stom, test | CTL+s.m. |
| | 426451 | AJ908165 | Hs.169946 | GATA-binding protein 3 (T-cell receptor | blad, breast | s.m. |
| | 426514 | BE616633 | Hs.170195 | bone morphogenetic protein 7 (osteogenic | ovar, colon, blad, lung, cerv | mAb+diag |
| | 426600 | NM_003378 | Hs.171014 | VEGF nerve growth factor inducible | mela | diag |
| 50 | 426761 | AI015709 | Hs.172089 | PORIMIN Pro-oncosis receptor inducing me | lung, esoph, pros, uter, panc, colon, ovar, headnk | mAb+s.m. |
| | 426812 | AF105365 | Hs.172613 | solute carrier family 12 (potassium/chlo | renal | mAb+s.m. |
| | 426890 | AA393167 | Hs.41294 | ESTs | renal, colon, ovar, uter, stom | CTL |
| | 427239 | BE270447 | Hs.356512 | ubiquitin carrier protein | lung, blad, test, mela | CTL+s.m. |
| | 427335 | AA448542 | Hs.251677 | G antigen 7B | lung, headnk, blad, mela, esoph | CTL |
| 55 | 427343 | AJ880044 | Hs.176977 | protein kinase C binding protein 2 | glio | CTL+s.m. |
| | 427722 | AK000123 | Hs.180479 | hypothetical protein FLJ20116 | colon, stom, panc | CTL |
| | 427747 | AW411425 | Hs.180655 | serine/threonine kinase 12 | blad, lung, ovar, stom, test, esoph | s.m. |
| | 427923 | AW274357 | Hs.301406 | FGENESH predicted 11 TM protein | mela | mAb |
| | 427969 | NM_001963 | Hs.2230 | epidermal growth factor (beta-urogastron | panc | mAb+diag |
| 60 | 428093 | AW594506 | Hs.104830 | ESTs | ovar, panc | CTL |
| | 428141 | D50402 | Hs.182611 | solute carrier family 11 (proton-coupled | glio | mAb+s.m. |
| | 428179 | AI127772 | Hs.279696 | serum/glucocorticoid regulated kinase-II | breast | s.m. |
| | 428187 | AI687303 | Hs.285529 | G protein-coupled receptor 49 | ovar, uter, colon, stom | mAb+s.m. |
| | 428242 | H55709 | Hs.2250 | leukemia inhibitory factor (cholinergic | ovar, panc, lung | diag |
| 65 | 428296 | NM_003058 | Hs.183572 | solute carrier family 22 (organic cation | renal | mAb+s.m. |
| | 428330 | L22524 | Hs.2256 | matrix metalloproteinase 7 (matrilysin, | uter, ovar, fibro, pros, panc, lung, blad, headnk, esoph, mela, stom | mAb+diag+s.m. |
| | 428368 | BE440042 | Hs.83326 | matrix metalloproteinase 3 (stromelysin | headnk, stom, esoph, colon | diag |
| | 428392 | H10233 | Hs.2265 | secretory granule, neuroendocrine protei | panc | diag |
| 70 | 428450 | NM_014791 | Hs.184339 | KJAA0175 gene product | ovar, cerv, panc, lung, blad, mela | s.m. |
| | 428479 | Y00272 | Hs.334562 | cell division cycle 2, G1 to S and G2 to | lung, blad, colon, uter, ovar | s.m. |
| | 428484 | AF104032 | Hs.184601 | solute carrier family 7 (cationic amino | lung, blad, headnk, cerv, esoph, glio, uter, stom, colon, mela | mAb+s.m. |
| | 428486 | AW583497 | Hs.184604 | pancreatic polypeptide | panc | diag |
| | 428505 | AL035461 | Hs.2281 | chromogranin B (secretogranin I) | panc, lung | diag |
| | 428513 | BE220806 | Hs.184697 | plexin C1 | mela, panc, stom, headnk | mAb |
| 75 | 428579 | NM_005756 | Hs.184942 | G protein-coupled receptor 64 | ovar, EWS, uter | mAb+s.m. |
| | 428664 | AK001666 | Hs.189095 | similar to SALL1 (sal (Drosophila)-like | blad, ovar, pros, lung, stom, test | CTL+s.m. |
| | 428698 | AA852773 | Hs.334838 | KJAA1866 protein | breast, colon, lung, panc, stom, headnk, ovar, EWS | mAb |
| | 428748 | AW593206 | Hs.98785 | Ksp37 protein | lung | diag |
| | 428758 | AA433988 | Hs.98502 | CA125 antigen; mucin 16 | ovar, cerv, lung, panc, stom, renal | diag |
| 80 | 428778 | AK000530 | Hs.193326 | fibroblast growth factor receptor-like 1 | ovar | mAb+s.m. |
| | 428784 | Y12851 | Hs.193470 | purinergic receptor P2X, ligand-gated io | glio, mela | mAb+s.m. |
| | 428841 | AM18430 | Hs.104935 | ESTs | renal | mAb+s.m.+CTL |
| | 428953 | AA306610 | Hs.348183 | tumor necrosis factor receptor superfam | cerv, panc, colon, stom, headnk, renal | mAb+diag |
| | 428969 | AF120274 | Hs.194689 | artemin | lung, cerv | diag |

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|--------|-----------|-----------|---|--|---------------|
| 428970 | BE276891 | Hs.194691 | retinoic acid induced 3 (RAIG1); metabo | stom, panc, colon, ovar | |
| 429149 | AW193360 | Hs.197962 | Homolog of mouse ADP-ribosylation factor | glio | mAb+s.m. |
| 429211 | AF052693 | Hs.198249 | gap junction protein, beta 5 (connexin 3) | lung, blad, headnk, cerv, esoph, stom, mela | mAb+s.m. |
| 429263 | AA019004 | Hs.198396 | ATP-binding cassette, sub-family A (ABC1 | lung | mAb+s.m. |
| 429276 | AF056085 | Hs.198612 | G protein-coupled receptor 51 | angio, blad, glio | mAb+s.m. |
| 429353 | AL117406 | Hs.335891 | ATP-binding cassette transporter MRP8 | breast, pros | mAb+s.m. |
| 429547 | AW009166 | Hs.99376 | FGENESH predicted novel secreted protein | panc, headnk, lung, ovar | mAb+s.m. |
| 429610 | AB024937 | Hs.211092 | LUNX protein; PLUNC (palate lung and nas | lung, fibro | diag |
| 429903 | AL134197 | Hs.93597 | cyclin-dependent kinase 5, regulatory su | lung, mela | mAb+diag |
| 429910 | NM_000867 | Hs.2507 | 5-hydroxytryptamine (serotonin) receptor | leio | s.m. |
| 430147 | R60704 | Hs.234434 | hairly/enhancer-of-split related with YRP | glio | mAb+s.m. |
| 430280 | AA361258 | Hs.237868 | interleukin 7 receptor | mela, lung, panc, stom, esoph, headnk | s.m. |
| 430377 | NM_001922 | Hs.301865 | dopachrome tautomerase (dopachrome delta | mela | mAb+s.m.+CTL |
| 430486 | BE062109 | Hs.241551 | chloride channel, calcium activated, tam | lung, blad, headnk, cerv, esoph | CTL |
| 430822 | AJ005371 | Hs.248017 | glyceraldehyde-3-phosphate dehydrogenase | mela | mAb+s.m. |
| 430890 | XS4232 | Hs.2699 | glypican 1 | glio, lung, cerv, blad, esoph | s.m. |
| 431053 | S40369 | Hs.249141 | Glutamate receptor subunit | glio | mAb+s.m. |
| 431130 | NM_006103 | Hs.2719 | HE4; epididymis-specific, whey-acidic pr | ovar, uter | mAb |
| 431462 | AW583672 | Hs.256311 | granin-like neuroendocrine peptide precu | panc, lung, glio, test | diag |
| 431515 | NM_012152 | Hs.258583 | EDG-7 (endothelial differentiation, lys | ovar, pros, lung, blad | diag |
| 431620 | AA126109 | Hs.264981 | Z'-S'-oligoadenylate synthetase 2 (69-71 | esoph, cerv | mAb+s.m. |
| 431629 | AJ077025 | Hs.265827 | interferon, alpha-inducible protein (clo | panc, uter, cerv, stom, esoph, mela | CTL+s.m. |
| 431630 | NM_002204 | Hs.265829 | integrin, alpha 3 (antigen CD49C, alpha | ovar, panc, blad, headnk, mela, renal | mAb+diag |
| 431840 | AA534908 | Hs.2860 | POU domain, class 5, transcription facto | test, renal, blad | mAb+s.m. |
| 431846 | BE019924 | Hs.271580 | uroplakin 1B | lung, blad, headnk, uter, cerv, stom, ovar | CTL |
| 431870 | AW449902 | Hs.105500 | ESTs | renal | mAb+diag |
| 431939 | AW008061 | Hs.231994 | ESTs | renal, colon | mAb+s.m.+CTL |
| 431958 | X63629 | Hs.2877 | cadherin 3, type 1, P-cadherin (placenta | lung, blad, cerv, headnk, ovar, colon, pros, panc, breast, esoph, test, mela | mAb+s.m.+CTL |
| 432196 | AW300888 | Hs.273230 | hypothetical protein FLJ10830 | renal | mAb+diag |
| 432201 | AIS38613 | Hs.298241 | Transmembrane protease, serine 3 | breast, colon, ovar, stom, panc, uter, cerv, lung | CTL |
| 432579 | AF043244 | Hs.278439 | nucleolar protein 3 (apoptosis repressor | renal | mAb+diag+s.m. |
| 432596 | AJ224741 | Hs.278461 | matrilin 3 | panc, breast | CTL |
| 432606 | NM_002104 | Hs.3066 | granzyme K (serine protease, granzyme 3; | renal, breast, lung, stom, hepC, fibro | diag |
| 432800 | BE391046 | Hs.278962 | AIM-1 protein | mela, pros | CTL |
| 432829 | W60377 | Hs.57772 | ESTs | blad | mAb+s.m. |
| 432867 | AW016936 | Hs.233364 | ESTs | stom, colon | CTL+s.m. |
| 432874 | W94322 | Hs.279651 | melanoma inhibitory activity | panc, stom, mela | mAb+s.m.+CTL |
| 432990 | AL036071 | Hs.279899 | tumor necrosis factor receptor superfami | pros, renal | diag |
| 433001 | AF217513 | Hs.279905 | clone HQ0310 PRO0310p1 | colon, breast, lung, blad, cerv, uter, test, mela | mAb+s.m. |
| 433447 | U29195 | Hs.3281 | neuronal pentraxin II | mela, esoph, colon, renal | s.m. |
| 433848 | AF095719 | Hs.93764 | carboxypeptidase A4 | headnk, esoph, lung | diag |
| 433867 | AK000596 | Hs.3618 | hippocalcin-like 1 | renal | s.m. |
| 434206 | AW136973 | Hs.362915 | ESTs, Weakly similar to S69890 mitogen i | stom, colon | CTL |
| 434276 | AF123659 | Hs.93605 | leucine zipper, putative tumor suppresso | mela | CTL+s.m. |
| 435013 | H91923 | Hs.110024 | NM_020142:Homo sapiens NADH:ubiquinone o | renal, lung | s.m. |
| 435472 | AW972330 | Hs.283022 | triggering receptor expressed on myeloid | glio | CTL |
| 435505 | AF200492 | Hs.211238 | interleukin-1 homolog 1 | lung, headnk | mAb |
| 435869 | AF255910 | Hs.54650 | junctional adhesion molecule 2 | angio, glio | diag |
| 436456 | AW292677 | Hs.248122 | melanin-concentrating hormone receptor (| mela, glio | mAb |
| 436480 | AJ271643 | Hs.87469 | putative acid-sensing ion channel | glio | mAb+s.m. |
| 436481 | AA379597 | Hs.5199 | HSPC150 protein similar to ubiquitin-con | lung, blad, colon, ovar, uter, headnk, test | mAb+s.m. |
| 436576 | AI458213 | Hs.77542 | ESTs | renal, panc, headnk, lung | s.m. |
| 436608 | AA628980 | Hs.192371 | down syndrome critical region protein DS | blad, lung | mAb+s.m. |
| 436895 | AF037335 | Hs.5338 | carbonic anhydrase XII | lung, headnk, cerv, esoph, blad, colon | CTL+s.m. |
| 436961 | AW375974 | Hs.156704 | ESTs | breast, renal, ovar, glio | mAb+s.m. |
| 436982 | AB018305 | Hs.5378 | spondin 1, (I-spondin) extracellular mat | lung, panc, renal, uter, colon | CTL |
| 437016 | AJ076916 | Hs.5398 | guanine monophosphate synthetase | ovar, fibro | diag |
| 437044 | AL035864 | Hs.69517 | differentially expressed in Fanconi's an | lung, blad, cerv, esoph, headnk | s.m. |
| 437100 | AI761073 | Hs.14535 | Homo sapiens cDNA: FLJ22314 fis, clone H | headnk, cerv, lung, blad, breast, pros, ovar, stom, esoph | CTL |
| 437212 | AI765021 | Hs.210775 | ESTs | panc, renal | mAb+s.m.+CTL |
| 437789 | AI581344 | Hs.127812 | ESTs, Weakly similar to T17330 hypotheti | renal, uter, ovar | mAb+s.m.+CTL |
| 437852 | BE001836 | Hs.256897 | putative GPCR | lung | CTL |
| 437938 | AI950087 | Hs.369628 | gb:wq05c02.x1 NCL CGAP_Kid12 Homo sapien | blad, lung | mAb+s.m. |
| 438380 | T06430 | Hs.6194 | chondroitin sulfate proteoglycan BEHAB/b | renal, ovar, uter, cerv, blad, renal | mAb+s.m.+CTL |
| 438549 | BE386801 | Hs.21858 | trinucleotide repeat containing 3 | glio, mela | diag |
| 438859 | AI559626 | Hs.93522 | Homo sapiens mRNA for KIAA1647 protein, | mela | mAb |
| 438929 | AW195515 | Hs.253177 | ESTs | renal | CTL+diag |
| 438966 | AW979074 | | gb:EST391184 MAGE resequences, MAGP Ho | renal | mAb+s.m.+CTL |
| 439018 | AW300887 | Hs.26638 | membrane-spanning 4-domains, subfamily A | renal | mAb+s.m.+CTL |
| 439223 | AW238299 | Hs.250618 | UL16 binding protein 2 | uter, stom, pros, fibro | mAb+s.m.+CTL |
| 439477 | W69813 | Hs.58042 | ESTs, Moderately similar to GFR3_HUMAN G | lung, headnk, cerv, esoph, blad, colon | mAb |
| 439569 | AW602166 | Hs.222399 | CEGP1 protein | lung | mAb |
| 439606 | W79123 | Hs.58561 | G protein-coupled receptor 87 | breast, AWPC, pros, blad | mAb+s.m. |
| 439738 | BE246502 | Hs.9598 | sema domain, immunoglobulin domain (Ig) | lung, blad, headnk, cerv, esoph | diag |
| 439759 | AL359055 | Hs.67709 | Homo sapiens mRNA full length insert cDN | blad, lung, cerv, renal | mAb+s.m. |
| 439799 | AW600291 | Hs.6823 | hypothetical protein FLJ10430 | colon, stom, panc, lung | mAb+s.m. |
| 440006 | AK000517 | Hs.6844 | NALP2 protein; PYRIN-Containing APAF1-i | renal, cerv, pros, headnk, colon, test | mAb+s.m.+CTL |
| 440065 | W03476 | Hs.266331 | Homo sapiens Fc receptor homolog express | blad, ovar, lung, headnk, test | mAb |
| 440225 | BE295782 | Hs.159 | tumor necrosis factor receptor superfami | mela | s.m. |
| 440304 | BE159984 | Hs.125395 | hepatitis A virus cellular receptor 1 | glio | diag |
| 440311 | AI733079 | Hs.125407 | ESTs, Moderately similar to ALUE_HUMAN ! | renal, colon, blad | mAb |
| 440516 | S42303 | Hs.161 | cadherin 2, type 1, N-cadherin (neuronal | renal | mAb+s.m. |
| 440672 | AF083811 | Hs.7345 | MAD1 (mitotic arrest deficient, yeast, h | glio, ovar, uter, renal, hepC | mAb+s.m.+CTL |
| | | | | mela | mAb+diag |
| | | | | | s.m. |

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| 5 | 441362 | BE614410 | Hs.23044 | RAD51 (S. cerevisiae) homolog (E coli Re | lung, blad, headnk, test, mela, esoph | s.m. |
| | 441392 | AW451831 | Hs.222119 | ESTs, Weakly similar to S30433 keratin 1 | renal | mAb+s.m.-CTL |
| | 442006 | AW975183 | Hs.372210 | ESTs, Weakly similar to S72482 hypothe | fibro, angio | mAb |
| | 442117 | AW664964 | Hs.128899 | ESTs: hypothetical protein for IMAGE:447 | breast, lung, blad, panc, headnk, stom, ovar, pros | mAb+s.m. |
| | 442133 | AW874138 | Hs.129017 | ESTs: type Ia transmembrane protein | ovar, uter | mAb |
| | 442438 | AA995998 | | gbrs26b03.s1 NCI_CGAP_Kid5 Homo sapiens | uter, ovar, renal | mAb+s.m.-CTL |
| | 443105 | X96753 | Hs.9004 | chondroitin sulfate proteoglycan 4 (mela | mela | mAb+diag |
| | 443211 | AI128388 | Hs.143655 | ESTs | blad, ovar, lung, headnk, stom | mAb+s.m.-CTL |
| | 443247 | BE614387 | Hs.333893 | c-Myc target JPO1 | colon, lung, blad, panc | CTL |
| 10 | 443426 | AF098158 | Hs.9329 | chromosome 20 open reading frame 1 | colon, lung, blad, stom, test, mela | CTL |
| | 443595 | AF169312 | Hs.9613 | PPAR(gamma) angiotensin related protein | renal | diag |
| | 443646 | AI085198 | Hs.164226 | Thrombospondin 1 | angio, panc, uter | diag |
| | 443785 | AW449952 | Hs.190125 | basic-helix-loop-helix-PAS protein | gio, uter, ovar | mAb+s.m.-CTL |
| | 443859 | NM_013409 | Hs.9914 | folistatin | lung, cerv, headnk, blad, esoph | diag |
| 15 | 443987 | AW163123 | Hs.10071 | seven transmembrane protein TM7SF3 | renal | mAb+s.m. |
| | 444006 | BE395085 | Hs.10086 | type I transmembrane protein Fn14 | panc, colon, lung, ovar, renal, esoph, mela, blad, stom, cerv | mAb |
| | 444371 | BE540274 | Hs.239 | forkhead box M1 | lung, headnk, blad, gio, test, mela | s.m. |
| | 444381 | BE387335 | Hs.283713 | hypothetical protein BC014245 | breast, colon, blad, lung, panc, headnk, ovar, stom, uter, | |
| | | | | | renal, angio, test, mela, esoph | diag |
| 20 | 444488 | AW192879 | Hs.355660 | ancient conserved domain protein 4 | renal | mAb+s.m. |
| | 444527 | NM_005408 | Hs.11383 | small inducible cytokine subfamily A (Cy | fibro, esoph | diag |
| | 444781 | NM_014400 | Hs.11950 | GPI-anchored metastasis-associated prote | lung, blad, headnk, cerv | mAb+diag |
| | 444783 | AK001468 | Hs.62180 | anillin (Drosophila Scraps homolog), act | ovar, lung, blad, headnk, panc, cerv, stom, uter, colon, esoph | CTL+s.m. |
| | 444809 | BE207568 | Hs.208219 | oculostriatin | mela | mAb+s.m. |
| 25 | 445070 | NM_000677 | Hs.258 | adenosine A3 receptor | gio, renal | mAb+s.m. |
| | 445417 | AK001058 | Hs.12680 | a disintegrin-like and metalloprotease w | panc, headnk, stom, lung, esoph | diag |
| | 445537 | AJ245671 | Hs.12844 | EGF-like-domain, multiple 6 | ovar, blad, uter, breast, lung, headnk, renal, fibro, panc, cerv | mAb+diag |
| | 445891 | AW391342 | Hs.199460 | DPCR1 protein | stom, panc, esoph, omuc, esoph | mAb |
| | 445895 | D29954 | Hs.13421 | KIAA0056 protein | pros | CTL |
| 30 | 446051 | BE048061 | Hs.37054 | ephrin-A3 | colon, breast | mAb+diag |
| | 446163 | AA026880 | Hs.25252 | prolactin receptor | breast, cerv, uter | mAb+s.m. |
| | 446232 | AI281848 | Hs.194691 | retinoic acid induced 3 | stom, panc, colon, ovar | mAb+s.m. |
| | 446341 | AI040763 | Hs.310735 | FGENESH prediction similar to multidrug | mela | mAb+s.m. |
| | 446619 | AU076543 | Hs.313 | secreted phosphoprotein 1 (osteopontin, | ovar, fibro, panc, headnk, lung, colon, blad, mela, esoph, uter | diag |
| 35 | 446650 | AB016625 | Hs.15813 | solute carrier family 22 (organic cation | renal | mAb+s.m. |
| | 446921 | AB012113 | Hs.16530 | small inducible cytokine subfamily A (Cy | breast, panc, headnk, lung, fibro, mela | diag |
| | 447004 | AW296968 | Hs.157539 | FGENESH predicted secreted protein | gio | mAb+diag |
| | 447033 | AI357412 | Hs.157601 | Predicted gene: Eos cloned; secreted w/V | colon, pros, fibro, breast, ovar, lung, panc | CTL+diag |
| | 447072 | D61594 | Hs.17279 | tyrosylprotein sulfotransferase 1 | gio, panc | CTL+s.m. |
| 40 | 447131 | NM_004585 | Hs.17466 | retinoic acid receptor responder (lazarus | renal, breast, stom, lung, mela, ovar | mAb+s.m. |
| | 447208 | BE315291 | Hs.237971 | hypothetical protein MGC5627 | esoph, stom, colon | CTL+diag |
| | 447269 | NM_004861 | Hs.17958 | cerebroside (3-phosphoadenylylsulfate) | renal | CTL |
| | 447342 | AI199268 | Hs.19322 | Homo sapiens, Similar to RIKEN cDNA 2010 | colon, blad, pros, lung, stom, AWPC, ovar | CTL |
| | 447400 | AK000322 | Hs.18457 | hypothetical protein FLJ20315 | colon, pros, stom, uter | CTL |
| 45 | 447674 | BE270640 | Hs.19192 | cyclin-dependent kinase 2 | mela | s.m. |
| | 447835 | AW591623 | Hs.164129 | ESTs, Weakly similar to I38022 hypothe | renal, ovar, uter | mAb+s.m.-CTL |
| | 447937 | AL109716 | Hs.20034 | Homo sapiens mRNA full length insert cDN | mela | mAb+s.m. |
| | 448105 | AW591433 | Hs.298241 | Transmembrane protease, serine 3 | breast, panc, colon, lung, ovar, stom | mAb+s.m.-CTL |
| | 448243 | AW369771 | Hs.367688 | integrin, beta 8 | ovar, uter, lung, stom, headnk, gio, panc | mAb+s.m. |
| 50 | 448321 | NM_005883 | Hs.20912 | adenomatous polyposis coli like | gio | mAb+s.m.-CTL |
| | 448499 | BE613280 | Hs.77550 | p53-regulated DDA3 | gio | CTL+s.m. |
| | 448595 | AB014544 | Hs.21572 | KIAA0644 gene product | breast, gio | mAb+s.m. |
| | 448610 | NM_006157 | Hs.21602 | nel (chicken)-like 1 | mela | diag |
| | 448733 | NM_005629 | Hs.187958 | solute carrier family 6 (neurotransmitte | lung, renal | mAb+s.m. |
| 55 | 448844 | AI581519 | Hs.177164 | FGENESH predicted novel cell surface pr | panc, lung, stom, omuc | mAb+s.m. |
| | 449048 | Z45051 | Hs.22920 | similar to S68401 (cattle) glucose induc | panc, ovar, uter, gio, headnk, lung | mAb |
| | 449444 | AW818436 | Hs.351306 | solute carrier family 16 (monocarboxylic | renal, panc | mAb+s.m. |
| | 449523 | NM_000579 | Hs.54443 | chemokine (C-C motif) receptor 5 | lung, panc, renal, stom, hepC, fibro, mela | mAb+s.m. |
| 60 | 449720 | AA311152 | Hs.288708 | hypothetical protein FLJ21562 | colon | CTL |
| | 449722 | BE280074 | Hs.23960 | cyclin B1 | headnk, blad, lung, panc, angio, test, mela, esoph | s.m. |
| | 450001 | NM_001044 | Hs.406 | solute carrier family 6 (neurotransmitte | renal | mAb+s.m. |
| | 450375 | AA009647 | Hs.352537 | a disintegrin and metalloproteinase doma | breast, ovar, headnk, panc, lung, esoph, colon | mAb+diag+s.m. |
| | 450531 | AW301032 | Hs.203800 | (BC017500) Similar to hypothetical prote | colon | CTL |
| 65 | 450701 | H39960 | Hs.288467 | hypothetical protein XP_098151 (leucine- | lung, headnk, panc, breast, stom, ovar, esoph, colon | mAb+diag |
| | 450726 | AW204600 | Hs.355462 | HUMPSPBA Human pulmonary surfactant-asso | fibro, lung | s.m. |
| | 450931 | N25156 | Hs.25648 | tumor necrosis factor receptor superfam | lung, renal | mAb+s.m. |
| | 450983 | AA305384 | Hs.25740 | ERO1 (S. cerevisiae)-like | blad, lung, ovar, panc | diag |
| | 451099 | RS2795 | Hs.25954 | interleukin 13 receptor, alpha 2 | gio, fibro, mela | mAb+s.m. |
| 70 | 451310 | AW250651 | Hs.26213 | Human DNA sequence from clone RP3-447F3 | colon, panc | CTL |
| | 451527 | AF022813 | Hs.26518 | transmembrane 4 superfamily member 7 | renal | mAb |
| | 451537 | RS6631 | Hs.26550 | retinoid X receptor, gamma | mela | CTL+s.m. |
| | 451668 | Z43948 | Hs.326444 | cartilage acidic protein 1 | blad, ovar, lung | mAb+diag |
| | 451939 | U80456 | Hs.27311 | single-minded (Drosophila) homolog 2 | pros | CTL |
| | 451979 | UB6972 | Hs.27372 | endothelial tyrosine kinase (Etk) (BMX), | angio | CTL+s.m. |
| 75 | 451988 | AF263928 | Hs.27410 | papillomavirus regulatory factor PRF-1 | renal | CTL |
| | 452097 | AB002364 | Hs.27916 | a disintegrin-like and metalloprotease (| ovar | mAb+s.m.+diag |
| | 452190 | H26735 | Hs.91668 | Homo sapiens clone PP1498 unknown mRNA | breast, stom, panc | mAb |
| | 452194 | AI694413 | Hs.373599 | olfactory receptor, family 2, subfamily | stom, panc, renal, colon, mela, fibro | mAb+s.m. |
| | 452203 | X57522 | Hs.352018 | transporter 1, ATP-binding cassette, sub | cerv, esoph, blad, stom, mela, renal | mAb+s.m. |
| 80 | 452281 | T93500 | Hs.28792 | Homo sapiens cDNA FLJ11041 fis, clone PL | breast, headnk, panc, stom, lung, esoph, fibro | diag |
| | 452355 | NS4926 | Hs.29202 | G protein-coupled receptor 34 | gio, fibro, panc | mAb+s.m. |
| | 452401 | NM_007115 | Hs.29352 | tumor necrosis factor, alpha-induced pro | blad, breast, panc, headnk, stom, lung, arth, renal, esoph | diag |
| | 452431 | U88879 | Hs.29499 | tol-like receptor 3 | renal, hepC | mAb |

| | | | | | | | |
|----|----------------|---|---|--|--|--------------|--|
| 5 | 452747 | BE153855 | Hs.61460 | Ig superfamily receptor LNIR | breast, blad, lung, headnk, ovar, stom, uter, panc | mAb | |
| | 452795 | AW392555 | Hs.18878 | hypothetical protein FLJ21620 | renal, headnk, colon, lung, panc | mAb+s.m.-CTL | |
| | 452838 | U65011 | Hs.30743 | preferentially expressed antigen in mela | lung, ovar, breast, mela, test, esoph, renal | CTL | |
| | 452862 | AW378065 | Hs.8687 | ADAMTS2 (a disintegrin-like and metallo | headnk, breast, colon, arth, lung, blad, esoph, stom | mAb+diag | |
| | 453195 | BE241876 | Hs.32352 | hypothetical protein DKFZp434K1210 | renal | CTL | |
| | 453496 | AA442103 | Hs.33084 | solute carrier family 2 (facilitated glu | renal, pros | mAb+s.m. | |
| | 453642 | AJ370936 | Hs.34074 | dipeptidylpeptidase VI | renal, mela | mAb+s.m. | |
| 10 | 453837 | AL138387 | Hs.256126 | baculoviral IAP repeat-containing 7 (liv | renal, mela | s.m. | |
| | 453857 | AL080235 | Hs.35861 | Ras-induced senescence 1 (RIS1) | glio, lung, uter, headnk, cerv, panc, pros | mAb+s.m. | |
| | 453968 | AA847843 | Hs.62711 | High mobility group (nonhistone chromoso | lung, uter, blad, test | CTL+s.m. | |
| | 456546 | AI690321 | Hs.203845 | KCNK15 potassium channel, subfamily K, m | ovar | mAb+s.m. | |
| | 456662 | NM_002448 | Hs.1494 | msh (Drosophila) homeo box homolog 1 (fo | uter, ovar | CTL | |
| 15 | 456759 | BE259150 | Hs.127792 | della (Drosophila)-like 3 | glio, lung | mAb+s.m. | |
| | 457133 | M54968 | Hs.351221 | v-Ki-ras2 Kirsten rat sarcoma 2 viral on | panc | s.m. | |
| | 457489 | AI693815 | Hs.127179 | cryptic gene | panc, pros, lung | diag | |
| | 457561 | AA331517 | Hs.286055 | chimerin (chimaerin) 2 | glio | mAb+s.m. | |
| | 458079 | AI796870 | Hs.54277 | Homo sapiens similar to RIKEN cDNA 28100 | mela, fibro | mAb | |
| | 458435 | AJ187118 | Hs.144121 | ESTs, Weakly similar to T46916 hypothesi | glio | mAb+s.m.-CTL | |
| 20 | 458627 | AW088642 | Hs.97984 | SRY (sex determining region Y)-box 17 (S | ovar, uter, test | CTL | |
| 25 | TABLE 66B: | | | | | | |
| | Pkey: | Unique Eos probeset identifier number | | | | | |
| | CAT number: | Gene cluster number | | | | | |
| | Accession: | Genbank accession numbers | | | | | |
| 30 | Pkey | CAT Number | Accession | | | | |
| | 409745 | MH1944_5 | BI030997 AA921874 AW188822 BI027862 AJ347618 AJ361453 AI088754 AW207491 AA077391 BG012775 BG997382 AA286833 AA150722 BI007625 | | | | |
| | | | BI027864 BI009100 BI006275 BI006270 BI031000 BI029864 BI006277 BI007627 BI006266 BI006991 BI006990 BI007763 BI007762 BG997377 | | | | |
| | | | AA150780 BI033518 BI027818 BG015789 BI033807 AA341445 | | | | |
| | 438966 | 1242593_1 | AW979074 AA834841 AA828650 | | | | |
| | 442438 | 24590_1 | AK022175 AU147222 AI124945 AU121400 F07756 AW979025 AA828595 AA828577 BE935573 AA829588 AI743616 BE315309 BE047365 AI761053 | | | | |
| | | | AW168960 AA833900 BG679419 BE171071 BF034368 BF754297 R61781 F08149 F07647 T77332 AA897461 AI829714 AJ376820 AI809991 | | | | |
| | | | AW661854 | | | | |
| 35 | TABLE 66C: | | | | | | |
| | Pkey: | Unique number corresponding to an Eos probeset | | | | | |
| | Ref: | Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA | | | | | |
| 40 | Strand: | sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495. | | | | | |
| | NI_position: | Indicates DNA strand from which exons were predicted. | | | | | |
| | | Indicates nucleotide positions of predicted exons. | | | | | |
| 45 | Pkey | Ref | Strand | NI_position | | | |
| | 400843 | 9188605 | Plus | 5863-5970,7653-7784,8892-9023,9673-9807, | | | |
| | 402075 | 8117407 | Plus | 121907-122035,122804-122921,124019-12416 | | | |
| | 402901 | 8894222 | Minus | 175426-175667 | | | |
| | 404287 | 2326514 | Plus | 53134-53281 | | | |
| | 404682 | 9797231 | Minus | 40977-41150 | | | |
| | 404875 | 9801324 | Plus | 96588-96732,97722-97831 | | | |
| 50 | 404977 | 3738341 | Minus | 43081-43229 | | | |
| | 405033 | 7107731 | Minus | 142358-142546 | | | |
| | 405547 | 1054740 | Plus | 124361-124520,124914-125050 | | | |
| | 406400 | 9256298 | Plus | 1553-1712,1878-2140,4252-4385,5922-6077 | | | |
| 55 | TABLE 67: | | | | | | |
| | Pkey: | Unique Eos probeset identifier number | | | | | |
| | ExAccn: | Exemplar Accession number, Genbank accession number | | | | | |
| | UnigeneID: | Unigene number | | | | | |
| 60 | Unigene Title: | Unigene gene title | | | | | |
| | Seq ID No: | Sequence Identification Number linking the information in Table 67 to the sequences in Table 68 | | | | | |
| 65 | Pkey | ExAccn | UnigeneID | Unigene Title | Seq ID No | | |
| | 418007 | M13509 | Hs.83169 | matrix metalloproteinase 1 (interstitial | Seq ID No 1 & 199 | | |
| | 418007 | M13509 | Hs.83169 | matrix metalloproteinase 1 (interstitial | Seq ID No 2 & 200 | | |
| | 428368 | BE440042 | Hs.83326 | matrix metalloproteinase 3 (stromelysin | Seq ID No 3 & 201 | | |
| | 417866 | AW067903 | Hs.82772 | collagen, type XI, alpha 1 | Seq ID No 4 & 202 | | |
| | 444381 | BE387335 | Hs.283713 | hypothetical protein BC014245 | Seq ID No 5 & 203 | | |
| | 452281 | T93500 | Hs.28792 | Homo sapiens cDNA FLJ11041 fis, clone PL | Seq ID No 6 | | |
| 70 | 428698 | AA852773 | Hs.334838 | KIAA1866 protein | Seq ID No 7 & 204 | | |
| | 452862 | AW378065 | Hs.8687 | ADAMTS2 (a disintegrin-like and metallo | Seq ID No 8 & 205 | | |
| | 432201 | AI538613 | Hs.298241 | Transmembrane protease, serine 3 | Seq ID No 9 & 206 | | |
| | 434206 | AW136973 | Hs.362915 | ESTs, Weakly similar to S69890 mitogen i | Seq ID No 10 & 207 | | |
| | 422260 | AA315993 | Hs.105484 | regenerating gene type IV | Seq ID No 11 & 208 | | |
| 75 | 409041 | AB033025 | Hs.50081 | Hypothetical protein, XP_051860 (KIAA119 | Seq ID No 12 & 209 | | |
| | 443426 | AF098158 | Hs.9329 | chromosome 20 open reading frame 1 | Seq ID No 13 & 210 | | |
| | 443211 | AI128388 | Hs.143655 | ESTs | Seq ID No 14 | | |
| | 428664 | AK001666 | Hs.189095 | similar to SALL1 (sal (Drosophila)-like | Seq ID No 15 & 211 | | |
| | 413278 | BE563085 | Hs.833 | interferon-stimulated protein, 15 kDa | Seq ID No 16 & 212 | | |
| 80 | 452401 | NM_007115 | Hs.29352 | tumor necrosis factor, alpha-induced pro | Seq ID No 17 & 213 | | |
| | 452401 | NM_007115 | Hs.29352 | tumor necrosis factor, alpha-induced pro | Seq ID No 18 & 214 | | |
| | 408380 | AF123050 | Hs.44532 | diubiquitin | Seq ID No 19 & 215 | | |
| | 416209 | AA236776 | Hs.79078 | MAD2 (mitotic arrest deficient, yeast, h | Seq ID No 20 & 216 | | |
| | 409757 | NM_001898 | Hs.123114 | cystatin SN | Seq ID No 21 & 217 | | |

| | | | | | |
|----|--------|-----------|-----------|--|---------------------|
| 5 | 425921 | NM_007231 | Hs.162211 | solute carrier family 6 (neurotransmitter) | Seq ID No 22 & 218 |
| | 452194 | AI694413 | Hs.373599 | olfactory receptor, family 2, subfamily | Seq ID No 23 & 219 |
| | 452194 | AI694413 | Hs.373599 | olfactory receptor, family 2, subfamily | Seq ID No 24 & 220 |
| | 444783 | AK001468 | Hs.62180 | anillin (Drosophila Scars homolog), act | Seq ID No 25 & 221 |
| | 422956 | BE545072 | Hs.122579 | ECT2 protein (Epithelial cell transformi | Seq ID No 26 & 222 |
| | 424905 | NM_002497 | Hs.153704 | NIMA (never in mitosis gene a)-related k | Seq ID No 27 & 223 |
| | 415989 | AI267700 | Hs.351201 | ESTs | Seq ID No 28 |
| | 415989 | AI267700 | Hs.351201 | ESTs | Seq ID No 29 |
| | 424252 | AK000520 | Hs.143811 | hypothetical protein FLJ20513 | Seq ID No 30 & 224 |
| 10 | 424252 | AK000520 | Hs.143811 | hypothetical protein FLJ20513 | Seq ID No 31 & 225 |
| | 432867 | AW016936 | Hs.233364 | ESTs | Seq ID No 32 |
| | 439759 | AL359055 | Hs.67709 | Homo sapiens mRNA full length insert cDN | Seq ID No 33 |
| | 428970 | BE276891 | Hs.194691 | retinoic acid induced 3 (RAIG1); metabo | Seq ID No 34 & 226 |
| | 428953 | AA306610 | Hs.348183 | tumor necrosis factor receptor superfam | Seq ID No 35 & 227 |
| 15 | 428953 | AA306610 | Hs.348183 | tumor necrosis factor receptor superfam | Seq ID No 36 & 228 |
| | 428953 | AA306610 | Hs.348183 | tumor necrosis factor receptor superfam | Seq ID No 37 & 229 |
| | 428953 | AA306610 | Hs.348183 | tumor necrosis factor receptor superfam | Seq ID No 38 & 230 |
| | 428953 | AA306610 | Hs.348183 | tumor necrosis factor receptor superfam | Seq ID No 39 & 231 |
| | 452203 | X57522 | Hs.352018 | transporter 1, ATP-binding cassette, sub | Seq ID No 40 & 232 |
| 20 | 428330 | L22524 | Hs.2256 | matrix metalloproteinase 7 (matrilysin, | Seq ID No 41 & 233 |
| | 436480 | AJ271643 | Hs.87469 | putative acid-sensing ion channel | Seq ID No 42 & 234 |
| | 407603 | AW955705 | Hs.62604 | Homo sapiens, clone IMAGE:4299322, mRNA, | Seq ID No 43 & 235 |
| | 425115 | R44664 | Hs.123956 | downstream of: G protein-coupled recept | Seq ID No 44 & 236 |
| | 435472 | AW972330 | Hs.283022 | triggering receptor expressed on myeloid | Seq ID No 45 & 237 |
| 25 | 418870 | AF147204 | Hs.89414 | chemokine (C-X-C motif), receptor 4 (fus | Seq ID No 46 & 238 |
| | 415511 | AI732617 | Hs.182362 | ESTs | Seq ID No 47 |
| | 440304 | BE159984 | Hs.125395 | hepatitis A virus cellular receptor 1 | Seq ID No 48 & 239 |
| | 423161 | AL049227 | Hs.124776 | downstream of cadherin 6 (by 3.3kb) | Seq ID No 49 & 240 |
| | 423161 | AL049227 | Hs.124776 | downstream of cadherin 6 (by 3.3kb) | Seq ID No 50 |
| 30 | 410153 | BE311926 | Hs.15830 | hypothetical protein FLJ12691 | Seq ID No 51 & 241 |
| | 410153 | BE311926 | Hs.15830 | hypothetical protein FLJ12691 | Seq ID No 52 & 242 |
| | 410153 | BE311926 | Hs.15830 | hypothetical protein FLJ12691 | Seq ID No 53 & 243 |
| | 410153 | BE311926 | Hs.15830 | hypothetical protein FLJ12691 | Seq ID No 54 & 244 |
| | 436895 | AF037335 | Hs.5338 | carbonic anhydrase XII | Seq ID No 55 & 245 |
| 35 | 436895 | AF037335 | Hs.5338 | carbonic anhydrase XII | Seq ID No 56 & 246 |
| | 421471 | U90545 | Hs.327179 | solute carrier family 17 (sodium phospho | Seq ID No 57 & 247 |
| | 428295 | NM_003058 | Hs.183572 | solute carrier family 22 (organic cation | Seq ID No 58 & 248 |
| | 426890 | AA393167 | Hs.41294 | ESTs | Seq ID No 59 & 249 |
| | 437212 | AI765021 | Hs.210775 | ESTs | Seq ID No 60 |
| 40 | 438966 | AW979074 | | gb:EST391184 MAGE resequences, MAGP Homo | Seq ID No 61 |
| | 440311 | AI733079 | Hs.125407 | ESTs, Moderately similar to ALUE_HUMAN ! | Seq ID No 62 |
| | 437100 | AI761073 | Hs.14535 | Homo sapiens cDNA: FLJ22314 fs, clone H | Seq ID No 63 |
| | 437100 | AI761073 | Hs.14535 | Homo sapiens cDNA: FLJ22314 fs, clone H | Seq ID No 64 |
| 45 | 450001 | NM_001044 | Hs.406 | solute carrier family 6 (neurotransmitter) | Seq ID No 65 & 250 |
| | 419080 | AW150835 | Hs.18878 | hypothetical protein FLJ21620 | Seq ID No 66 & 251 |
| | 443595 | AF169312 | Hs.9613 | PPAR(gamma) angiopoietin related protein | Seq ID No 67 & 252 |
| | 443595 | AF169312 | Hs.9613 | PPAR(gamma) angiopoietin related protein | Seq ID No 68 |
| | 410407 | X66839 | Hs.63287 | carbonic anhydrase IX | Seq ID No 69 & 253 |
| 50 | 453496 | AA442103 | Hs.33084 | solute carrier family 2 (facilitated glu | Seq ID No 70 & 254 |
| | 420737 | L08096 | Hs.99899 | CD70 ; tumor necrosis factor (ligand) s | Seq ID No 71 & 255 |
| | 439979 | AW600291 | Hs.6823 | hypothetical protein FLJ10430 | Seq ID No 72 & 256 |
| | 420789 | AI670057 | Hs.199882 | ESTs | Seq ID No 73 |
| | 420789 | AI670057 | Hs.199882 | ESTs | Seq ID No 74 |
| 55 | 441392 | AW451831 | Hs.222119 | ESTs, Weakly similar to S30433 keratin 1 | Seq ID No 75 & 257 |
| | 452431 | U88879 | Hs.29499 | toll-like receptor 3 | Seq ID No 76 & 258 |
| | 431870 | AW449902 | Hs.105500 | ESTs | Seq ID No 77 |
| | 431870 | AW449902 | Hs.105500 | ESTs | Seq ID No 78 |
| | 449523 | NM_000579 | Hs.54443 | chemokine (C-C motif) receptor 5 | Seq ID No 79 & 259 |
| 60 | 409745 | AA077391 | | gb:7B14E12 Chromosome 7 Fetal Brain cDNA | Seq ID No 80 |
| | 438859 | AI559626 | Hs.93522 | Homo sapiens mRNA for KIAA1647 protein, | Seq ID No 81 |
| | 409637 | AA323948 | Hs.55407 | Homo sapiens mRNA; cDNA DKFZp434K0621 (f | Seq ID No 82 & 260 |
| | 409637 | AA323948 | Hs.55407 | Homo sapiens mRNA; cDNA DKFZp434K0621 (f | Seq ID No 83 |
| | 409348 | AI401535 | Hs.146090 | ESTs | Seq ID No 84 |
| 65 | 447269 | NM_004861 | Hs.17958 | cerebroside (3'-phosphoadenylylsulfate:g | Seq ID No 85 & 261 |
| | 453195 | BE241876 | Hs.32352 | hypothetical protein DKFZp434K1210 | Seq ID No 86 & 262 |
| | 428841 | AI418430 | Hs.104935 | ESTs | Seq ID No 87 |
| | 428841 | AI418430 | Hs.104935 | ESTs | Seq ID No 88 |
| | 428841 | AI418430 | Hs.104935 | ESTs | Seq ID No 89 |
| | 409663 | AI743750 | Hs.98306 | KIAA1862 protein | Seq ID No 90 & 263 |
| 70 | 409663 | AI743750 | Hs.98306 | KIAA1862 protein | Seq ID No 91 & 264 |
| | 431939 | AW008061 | Hs.231994 | ESTs | Seq ID No 92 & 265 |
| | 432606 | NM_002104 | Hs.3066 | granzyme K (serine protease, granzyme 3; | Seq ID No 93 & 266 |
| | 411411 | AA345241 | Hs.55950 | ESTs, Weakly similar to KIAA1330 protein | Seq ID No 94 & 267 |
| 75 | 433867 | AK000596 | Hs.3618 | hippocalcin-like 1 | Seq ID No 95 & 268 |
| | 433867 | AK000596 | Hs.3618 | hippocalcin-like 1 | Seq ID No 96 & 269 |
| | 437938 | AI950087 | Hs.369628 | gb:wq05c02.x1 NCL_CGAP_Kid12 Homo sapien | Seq ID No 97 |
| | 432579 | AF043244 | Hs.278439 | nucleolar protein 3 (apoptosis repressor | Seq ID No 98 & 270 |
| | 418526 | BE019020 | Hs.85838 | solute carrier family 16 (monocarboxyic | Seq ID No 99 & 271 |
| | 432196 | AW300888 | Hs.273230 | hypothetical protein FLJ10830 | Seq ID No 100 & 272 |
| 80 | 432196 | AW300888 | Hs.273230 | hypothetical protein FLJ10830 | Seq ID No 101 & 273 |
| | 438929 | AW195515 | Hs.253177 | ESTs | Seq ID No 102 |
| | 410055 | AJ250839 | Hs.58241 | gene for serine/threonine protein kinase | Seq ID No 103 & 274 |
| | 446650 | AB016625 | Hs.15813 | solute carrier family 22 (organic cation | Seq ID No 104 & 275 |

| | | | | | |
|----|--------|-----------|-----------|---|---------------------|
| 5 | 426812 | AF105365 | Hs.172613 | solute carrier family 12 (potassium/chloride) | Seq ID No 105 & 276 |
| | 447131 | NM_004585 | Hs.17466 | retinoic acid receptor responder (Izaro) | Seq ID No 106 & 277 |
| | 449444 | AW818436 | Hs.351306 | solute carrier family 16 (monocarboxylic) | Seq ID No 107 & 278 |
| | 422627 | BE336857 | Hs.118787 | transforming growth factor, beta-induced | Seq ID No 108 & 279 |
| | 444488 | AW192879 | Hs.355660 | ancient conserved domain protein 4 | Seq ID No 109 & 280 |
| | 450931 | N25156 | Hs.25648 | tumor necrosis factor receptor superfamily | Seq ID No 110 & 281 |
| | 409220 | BE243323 | Hs.51233 | tumor necrosis factor receptor superfamily | Seq ID No 111 & 282 |
| | 409220 | BE243323 | Hs.51233 | tumor necrosis factor receptor superfamily | Seq ID No 112 & 283 |
| 10 | 425998 | AU076629 | Hs.165950 | fibroblast growth factor receptor 4 | Seq ID No 113 & 284 |
| | 425998 | AU076629 | Hs.165950 | fibroblast growth factor receptor 4 | Seq ID No 114 & 285 |
| | 425009 | X58288 | Hs.154151 | protein tyrosine phosphatase, receptor I | Seq ID No 115 & 286 |
| | 443987 | AW163123 | Hs.10071 | seven transmembrane protein TM7SF3 | Seq ID No 116 & 287 |
| | 432990 | AL036071 | Hs.279899 | tumor necrosis factor receptor superfamily | Seq ID No 117 & 288 |
| 15 | 436576 | A1458213 | Hs.77542 | ESTs | Seq ID No 118 & 289 |
| | 451527 | AF022813 | Hs.26518 | transmembrane 4 superfamily member 7 | Seq ID No 119 & 290 |
| | 448733 | NM_005629 | Hs.187958 | solute carrier family 6 (neurotransmitter) | Seq ID No 120 & 291 |
| | 410274 | AA381807 | Hs.61762 | hypoxia-inducible protein 2 | Seq ID No 121 & 292 |
| | 125218 | H91923 | Hs.110024 | Empirically selected from AFFX single pr | Seq ID No 122 & 293 |
| 20 | 436961 | AW375974 | Hs.156704 | ESTs | Seq ID No 123 |
| | 431630 | NM_002204 | Hs.265829 | integrin, alpha 3 (antigen CD49C, alpha | Seq ID No 124 & 294 |
| | 431630 | NM_002204 | Hs.265829 | integrin, alpha 3 (antigen CD49C, alpha | Seq ID No 125 & 295 |
| | 419508 | AW997938 | Hs.90786 | ATP-binding cassette, sub-family C (CFTR | Seq ID No 126 & 296 |
| | 431840 | AA534908 | Hs.2860 | POU domain, class 5, transcription factor | Seq ID No 127 & 297 |
| 25 | 442438 | AA995998 | | gbr:os26b03.s1 NCL CGAP_Kd5 Homo sapiens | Seq ID No 128 |
| | 447835 | AW591623 | Hs.164129 | ESTs, Weakly similar to I38022 hypothe | Seq ID No 129 |
| | 429276 | AF056085 | Hs.198612 | G protein-coupled receptor 51 | Seq ID No 130 & 298 |
| | 448595 | AB014544 | Hs.21572 | KIAA0644 gene product | Seq ID No 131 & 299 |
| | 440516 | S42303 | Hs.161 | cadherin 2, type 1, N-cadherin (neuronal | Seq ID No 132 & 300 |
| 30 | 456759 | BE259150 | Hs.127792 | delta (Drosophila)-like 3 | Seq ID No 133 & 301 |
| | 447004 | AW296968 | Hs.157539 | FGENESH predicted secreted protein | Seq ID No 134 & 302 |
| | 425088 | AA663372 | Hs.169395 | hypothetical protein FLJ12015 | Seq ID No 135 & 303 |
| | 409389 | AB007979 | Hs.301281 | Homo sapiens mRNA, chromosome 1 specific | Seq ID No 136 & 304 |
| | 448321 | NM_005883 | Hs.20912 | adenomatous polyposis coli like | Seq ID No 137 & 305 |
| 35 | 426344 | H41821 | Hs.322469 | transcriptional activator of the c-fos p | Seq ID No 138 & 306 |
| | 419704 | AA429104 | Hs.45057 | ESTs | Seq ID No 139 & 307 |
| | 412959 | D87458 | Hs.75090 | KIAA0282 protein | Seq ID No 140 & 308 |
| | 448499 | BE613280 | Hs.77550 | p53-regulated DDA3 | Seq ID No 141 & 309 |
| 40 | 458435 | A1418718 | Hs.144121 | ESTs, Weakly similar to T46916 hypothe | Seq ID No 142 & 310 |
| | 443785 | AW449952 | Hs.190125 | basic-helix-loop-helix-PAS protein | Seq ID No 143 & 311 |
| | 427343 | A1880044 | Hs.176977 | protein kinase C binding protein 2 | Seq ID No 144 & 312 |
| | 416857 | AA188775 | Hs.292453 | FGENESH predicted TM containing protein | Seq ID No 145 & 313 |
| | 429149 | AW193360 | Hs.197962 | Homolog of mouse ADP-ribosylation factor | Seq ID No 146 & 314 |
| | 418030 | BE207573 | Hs.83321 | neuromedin B | Seq ID No 147 & 315 |
| 45 | 457561 | AA331517 | Hs.286055 | chimerin (chimaerin) 2 | Seq ID No 148 & 316 |
| | 457561 | AA331517 | Hs.286055 | chimerin (chimaerin) 2 | Seq ID No 149 & 317 |
| | 430147 | R60704 | Hs.234434 | hair/enhancer-of-split related with YRP | Seq ID No 150 & 318 |
| | 453642 | A1370936 | Hs.34074 | dipeptidylpeptidase VI | Seq ID No 151 & 319 |
| | 453857 | AL080235 | Hs.35861 | Ras-induced senescence 1 (RIS1) | Seq ID No 152 & 320 |
| 50 | 449048 | Z45051 | Hs.22920 | similar to S68401 (cattle) glucose induc | Seq ID No 153 & 321 |
| | 418506 | AA084248 | Hs.372651 | Unknown protein for MGC:29643 (formerly | Seq ID No 154 & 322 |
| | 416636 | N32536 | Hs.42645 | solute carrier family 16 (monocarboxylic | Seq ID No 155 & 323 |
| | 421508 | NM_004833 | Hs.105115 | absent in melanoma 2 | Seq ID No 156 & 324 |
| | 421379 | Y15221 | Hs.103982 | small inducible cytokine subfamily B (Cy | Seq ID No 157 & 325 |
| 55 | 428784 | Y12851 | Hs.193470 | purinergic receptor P2X, ligand-gated ion | Seq ID No 158 & 326 |
| | 431958 | X63629 | Hs.2877 | cadherin 3, type 1, P-cadherin (placenta | Seq ID No 159 & 327 |
| | 417542 | J04129 | Hs.82269 | progesterone-associated endometrial prote | Seq ID No 160 & 328 |
| | 418678 | NM_001327 | Hs.167379 | cancer/testis antigen (NY-ESO-1) | Seq ID No 161 & 329 |
| | 418678 | NM_001327 | Hs.167379 | cancer/testis antigen (NY-ESO-1) | Seq ID No 162 & 330 |
| 60 | 420208 | BE276055 | Hs.95972 | silver (mouse homolog) like | Seq ID No 163 & 331 |
| | 430377 | NM_001922 | Hs.301865 | dopachrome tautomerase (dopachrome delta | Seq ID No 164 & 332 |
| | 438549 | BE386801 | Hs.21858 | trinucleotide repeat containing 3 | Seq ID No 165 & 333 |
| | 412580 | AA113262 | Hs.17901 | similar to CABLES [Homo sapiens] | Seq ID No 166 & 334 |
| | 417166 | AA431323 | Hs.42146 | Paired box protein Pax-3 | Seq ID No 167 & 335 |
| 65 | 428513 | BE220806 | Hs.184697 | plexin C1 | Seq ID No 168 & 336 |
| | 447937 | AL109716 | Hs.20034 | Homo sapiens mRNA full length insert cDN | Seq ID No 169 & 337 |
| | 447937 | AL109716 | Hs.20034 | Homo sapiens mRNA full length insert cDN | Seq ID No 170 & 338 |
| | 446341 | AL040763 | Hs.310735 | FGENESH prediction similar to multidrug | Seq ID No 171 & 339 |
| | 446341 | AL040763 | Hs.310735 | FGENESH prediction similar to multidrug | Seq ID No 172 & 340 |
| 70 | 458079 | A1796870 | Hs.54277 | Homo sapiens similar to RIKEN cDNA 28100 | Seq ID No 173 & 341 |
| | 415668 | AW957684 | Hs.306814 | Homo sapiens lysyl oxidase-like 4 (LOXL4 | Seq ID No 174 & 342 |
| | 447674 | BE270640 | Hs.19192 | cyclin-dependent kinase 2 | Seq ID No 175 & 343 |
| | 447674 | BE270640 | Hs.19192 | cyclin-dependent kinase 2 | Seq ID No 176 & 344 |
| | 440065 | W03476 | Hs.266331 | Homo sapiens Fc receptor homolog express | Seq ID No 177 & 345 |
| 75 | 414945 | BE076358 | Hs.77667 | lymphocyte antigen 6 complex, locus E | Seq ID No 178 & 346 |
| | 440672 | AF083811 | Hs.7345 | MAD1 (mitotic arrest deficient, yeast, h | Seq ID No 179 & 347 |
| | 412609 | Z48804 | Hs.74124 | ocular albinism 1 (Nettleship-Falls) | Seq ID No 180 & 348 |
| | 453837 | AL138387 | Hs.256126 | baculoviral IAP repeat-containing 7 (liv | Seq ID No 181 & 349 |
| | 453837 | AL138387 | Hs.256126 | baculoviral IAP repeat-containing 7 (liv | Seq ID No 182 & 350 |
| 80 | 434276 | AF123659 | Hs.93605 | leucine zipper, putative tumor suppresso | Seq ID No 183 & 351 |
| | 408367 | AK001178 | Hs.44424 | Homo sapiens orphan neurotransmitter tra | Seq ID No 184 & 352 |
| | 444809 | BE207568 | Hs.208219 | oculospasmin | Seq ID No 185 & 353 |
| | 415929 | AA724373 | Hs.304950 | Homo sapiens mucopolin-3 (MCPOLN3) | Seq ID No 186 & 354 |
| | 421666 | AL035250 | Hs.1408 | endothelin 3 | Seq ID No 187 & 355 |

| | | | | |
|--------|-----------|-----------|--|---------------------|
| 424321 | W74048 | Hs.1765 | lymphocyte-specific protein tyrosine kin | Seq ID No 188 & 356 |
| 425535 | AB007937 | Hs.158287 | syndecan 3 | Seq ID No 189 & 357 |
| 451537 | R56631 | Hs.26550 | retinoid X receptor, gamma | Seq ID No 190 & 358 |
| 430280 | AA361258 | Hs.237868 | interleukin 7 receptor | Seq ID No 191 & 359 |
| 418064 | BE387287 | Hs.83384 | S100 calcium-binding protein, beta (neur | Seq ID No 192 & 360 |
| 448610 | NM_006157 | Hs.21602 | nel (chicken)-like 1 | Seq ID No 193 & 361 |
| 432800 | BE391046 | Hs.278962 | AIM-1 protein | Seq ID No 194 & 362 |
| 416350 | AF188625 | Hs.189507 | phospholipase A2, group IID | Seq ID No 195 & 363 |
| 405545 | | | Target Exon | Seq ID No 196 & 364 |
| 414812 | X72755 | Hs.77367 | monokine induced by gamma interferon | Seq ID No 197 & 365 |
| 432874 | W94322 | Hs.279651 | melanoma inhibitory activity | Seq ID No 198 & 366 |

Table 68 lists sequences as described in Table 67

Seq ID NO: 1 DNA sequence

Nucleic Acid Accession #: NM_002421.2

Coding sequence: 1..1409

| | | | | | | |
|------------|-------------|--------------|-------------|------------|-------------|------|
| 1 | 11 | 21 | 31 | 41 | 51 | |
| ATGCACAGCT | TTCTCCACT | GCTGCTGCTG | CTGTTCTGGG | GTGTGGTGTG | ACACAGCTTC | 60 |
| CCAGCGACTC | TAGAAACACA | AGAGCAAGAT | GTGGACTTAG | TCCAGAAATA | CCTGGAAAAA | 120 |
| TACTACAACC | TGAAGAATGA | TGGGAGGCAA | GTTGAAAAGC | GGAGAAATAG | TGGCCAGTGT | 180 |
| GTGAAAAAT | TGAAGCAAAT | GCAGGAATTC | TTTGGGCTGA | AAGTGACTGG | GAAACCAGAT | 240 |
| GCTGAAACCC | TGAAGGTGAT | GAAGCAGCCC | AGATGTGGAG | TGCCTGATGT | GGCTCAGTTT | 300 |
| GTCTCTCACT | AGGGGAACCC | TCGCTGGGAG | CAACACATC | TGACCTACAG | GATTGAAAAAT | 360 |
| TACAAGCCAG | ATTTGCCAAAG | AGCAGATGTG | GACCATGCCA | TTGAGAAAGC | CTTCCAACTC | 420 |
| TGGAGTAATG | TCACACCTCT | GACATTCACC | AAGGTCTCTG | AGGGTCAAGC | AGACATCATG | 480 |
| ATATCTTTTG | TCAGGGGAGA | TCATCGGGAC | AACCTCTCCT | TTGATGGACC | TGGAGGAAAT | 540 |
| CTTGCTCATG | CTTTTCAACC | AGGCCCAAGT | ATTGGAGGGG | ATGCTCATT | TGATGAAGAT | 600 |
| GAAAGGTGGA | CCAACAATTT | CAGAGAGTAC | AACCTTACATC | GTGTTGCGGC | TCATGAACTC | 660 |
| GGCCATTCTC | TTGGACTCTC | CCATTCTACT | GATATCGGGG | CTTTGATGTA | CCCTAGCTAC | 720 |
| ACCTTCAGTG | GTGATGTTCA | GCTAGCTCAG | GATGACATTG | ATGGCATCCA | AGCCATATAT | 780 |
| GGACGTTCCC | AAAATCCTGT | CCAGCCCATC | GGCCCAACAA | CCCCAAAGC | ATGTGACAGT | 840 |
| AAGCTAACCT | TTGATGCTAT | AACCTACGAT | CGGGGAGAAG | TGATGTTCTT | TAAAGACAGA | 900 |
| TTCTACATGC | GCACAAATCC | CTTCTACCCG | GAAAGTTGAGC | TCAATTTTCT | TTCTGTTTTT | 960 |
| TGGCCACAAC | TGCCAAATGG | GCTTGAAGCT | GCTTACGAAT | TTGCCGACAG | AGATGAAGTC | 1020 |
| CGGTTTTTCA | AAGGGAATAA | GTACTGGGCT | GTTCAAGGAC | AGAATGTGCT | ACACGGATAC | 1080 |
| CCCAAGGACA | TCTACAGCTC | CTTTGGCTTC | CCTAGAAGCTG | TGAAGCATAT | CGATGCTGCT | 1140 |
| CTTTCTGAGG | AAAACACTGG | AAAAAACCCTAC | TTCTTTGTTG | CTAACAAATA | CTGGAGGTAT | 1200 |
| GATGAATATA | AACGATCTAT | GGATCCAGGT | TATCCCAAAA | TGATAGCACA | TGACTTTTCT | 1260 |
| GGAAATGGCC | ACAAAGTTGA | TGCAGTTTTT | ATGAAAGATG | GATTTTTCTA | TTTCTTTTCT | 1320 |
| GGAACAAGAC | AATACAAATT | TGATCCTAAA | ACGAAGAGAA | TTTTGACTCT | CCAGAAAGCT | 1380 |
| AATAGCTGGT | TCAACTGCAG | GAAAAATTAG | | | | |

Seq ID NO: 2 DNA sequence

Nucleic Acid Accession #: NM_002421.2

Coding sequence: 1..1409

| | | | | | | |
|------------|-------------|--------------|-------------|------------|-------------|------|
| 1 | 11 | 21 | 31 | 41 | 51 | |
| ATGCACAGCT | TTCTCCACT | GCTGCTGCTG | CTGTTCTGGG | GTGTGGTGTG | ACACAGCTTC | 60 |
| CCAGCGACTC | TAGAAACACA | AGAGCAAGAT | GTGGACTTAG | TCCAGAAATA | CCTGGAAAAA | 120 |
| TACTACAACC | TGAAGAATGA | TGGGAGGCAA | GTTGAAAAGC | GGAGAAATAG | TGGCCAGTGT | 180 |
| GTGAAAAAT | TGAAGCAAAT | GCAGGAATTC | TTTGGGCTGA | AAGTGACTGG | GAAACCAGAT | 240 |
| GCTGAAACCC | TGAAGGTGAT | GAAGCAGCCC | AGATGTGGAG | TGCCTGATGT | GGCTCAGTTT | 300 |
| GTCTCTCACT | AGGGGAACCC | TCGCTGGGAG | CAACACATC | TGACCTACAG | GATTGAAAAAT | 360 |
| TACAAGCCAG | ATTTGCCAAAG | AGCAGATGTG | GACCATGCCA | TTGAGAAAGC | CTTCCAACTC | 420 |
| TGGAGTAATG | TCACACCTCT | GACATTCACC | AAGGTCTCTG | AGGGTCAAGC | AGACATCATG | 480 |
| ATATCTTTTG | TCAGGGGAGA | TCATCGGGAC | AACCTCTCCT | TTGATGGACC | TGGAGGAAAT | 540 |
| CTTGCTCATG | CTTTTCAACC | AGGCCCAAGT | ATTGGAGGGG | ATGCTCATT | TGATGAAGAT | 600 |
| GAAAGGTGGA | CCAACAATTT | CAGAGAGTAC | AACCTTACATC | GTGTTGCGGC | TCATGAACTC | 660 |
| GGCCATTCTC | TTGGACTCTC | CCATTCTACT | GATATCGGGG | CTTTGATGTA | CCCTAGCTAC | 720 |
| ACCTTCAGTG | GTGATGTTCA | GCTAGCTCAG | GATGACATTG | ATGGCATCCA | AGCCATATAT | 780 |
| GGACGTTCCC | AAAATCCTGT | CCAGCCCATC | GGCCCAACAA | CCCCAAAGC | ATGTGACAGT | 840 |
| AAGCTAACCT | TTGATGCTAT | AACCTACGAT | CGGGGAGAAG | TGATGTTCTT | TAAAGACAGA | 900 |
| TTCTACATGC | GCACAAATCC | CTTCTACCCG | GAAAGTTGAGC | TCAATTTTCT | TTCTGTTTTT | 960 |
| TGGCCACAAC | TGCCAAATGG | GCTTGAAGCT | GCTTACGAAT | TTGCCGACAG | AGATGAAGTC | 1020 |
| CGGTTTTTCA | AAGGGAATAA | GTACTGGGCT | GTTCAAGGAC | AGAATGTGCT | ACACGGATAC | 1080 |
| CCCAAGGACA | TCTACAGCTC | CTTTGGCTTC | CCTAGAAGCTG | TGAAGCATAT | CGATGCTGCT | 1140 |
| CTTTCTGAGG | AAAACACTGG | AAAAAACCCTAC | TTCTTTGTTG | CTAACAAATA | CTGGAGGTAT | 1200 |
| GATGAATATA | AACGATCTAT | GGATCCAGGT | TATCCCAAAA | TGATAGCACA | TGACTTTTCT | 1260 |
| GGAAATGGCC | ACAAAGTTGA | TGCAGTTTTT | ATGAAAGATG | GATTTTTCTA | TTTCTTTTCT | 1320 |
| GGAACAAGAC | AATACAAATT | TGATCCTAAA | ACGAAGAGAA | TTTTGACTCT | CCAGAAAGCT | 1380 |
| AATAGCTGGT | TCAACTGCAG | GAAAAATTAG | | | | |

Seq ID NO: 3 DNA sequence

Nucleic Acid Accession #: NM_002422.2

Coding sequence: 64..1497

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| 1 | 11 | 21 | 31 | 41 | 51 | |
| ACAAGGAGGC | AGGCAAGACA | GCAAGGCATA | GAGACAACAT | AGAGCTAAGT | AAAGCCAGTG | 60 |
| GAAATGAAGA | GTCTTCCAAT | CCTACTGTTG | CTGTGCGTGG | CAGTTTGCTC | AGCCTATCCA | 120 |
| TTGGATGGAG | CTGCAAGGGG | TGAGGACACC | AGCATGAACC | TTGTTTCAGAA | ATATCTAGAA | 180 |
| AACCTACTAC | ACCTCAAAAA | AGATGTGAAA | CAGTTTGTTA | GGAGAAAGGA | CAGTGGTCTT | 240 |

| | |
|----|---|
| 5 | GTGTGTA AAAA AATCCGAGA AATGCAGAAG TTCCTTGGAT TGGAGGTGAC GGGGAAGCTG 300 |
| | GACTCCGACA CTCTGGAGGT GATGCGCAAG CCCAGGTGTG GAGTTCCTGA TGTGGTCCAC 360 |
| | TTCAAGAACT TTCTGGCAT CCCGAAGTGG AGGAAAACCC ACCTTACATA CAGGATTGTG 420 |
| | AATTATACAC CAGATTGGCC AAAAGATGCT GTTGATTCTG CTGTTGAGAA AGCTCTGAAA 480 |
| | GTCTGGGAAG AGGTGACTCC ACTCATTTC TCCAGGCTGT ATGAAGGAGA GGCTGATATA 540 |
| | ATGATCTCTT TTGAGTTAG AGAACATGGA GACTTTTACC CTTTGTATGG ACCTGGAAT 600 |
| | GTTTTGGCCC ATGCCATATG CCTGGGCCA GGGATTAAAT GAGATGCCCA CTTTGATGAT 660 |
| | GATGAACAAAT GGACAAAGGA TACAACAGGG ACCAAATTAT TTCTGTTGC TGCTCATGAA 720 |
| 10 | ATTGGCCACT CCCTGGGTCT CTTTCACTCA GCCAACACTG AAGCTTTGAT GTACCCACTC 780 |
| | TATCACTCAC TCACAGACCT GACTCGGTTT CGCTGTCTC AAGATGATAT AAATGGCAAT 840 |
| | CAGTCCCTCT ATGGACCTCC CCTGACTCC CCTGAGACCC CCTTGGTACC CACGGAACCT 900 |
| | GTCCCTCCAG AACCTGGGAC GCCAGCCAACT TGTGATCCTG CTTTGTCTT TGATGCTGTC 960 |
| | AGCACTCTGA GGGGAGAAAT CCTGATCTT AAAGACAGGC ACTTTTGGCG CAAATCCCTC 1020 |
| 15 | AGSAAGCTTG AACCTGAAT GCATTGTATC TCTTCATTTT GGCCATCTCT TCCTTCAGGC 1080 |
| | GTGGATGCCG CATATGAAGT TACTAGCAAG GACCTCGTTT TCATTTTAA AGGAAATCAA 1140 |
| | TTCTGGCCCA TCAGAGGAAA TGAGGTACGA GCTGGATACC CAAGAGGCAT CCACACCTTA 1200 |
| | GGTTTCCCTC CAACCGTAG GAAAATCGAT GCAGCCATTT CTGATAAGGA AAAGAACAAA 1260 |
| | ACATATTCTT TTGTAGAGGA CAAATAGTGG AGATTGTATG AGAAGAGAAA TTCCATGGAG 1320 |
| 20 | CCAGGCTTTC CCAAGCAAAAT AGCTGAAGAC TTTCAGGGA TTGACTCAAA GATTGATGCT 1380 |
| | GTTTTGAAG AATTGGGTT CTTTATTTC TTTACTGGAT CTTCAAGTT GGAGTTTGAC 1440 |
| | CCAAATGCAA AGAAAGTGAC ACACACTTTG AAGAGTAACA GCTGGCTTAA TTGTTGAAAG 1500 |
| | AGATATGTAG AAGGCACAAAT ATGGGCACCTT TAAATGAAGC TCTGTGAAAT TAATAATTCT TCACCTAAGT 1560 |
| 25 | CTCTGTGAAT TGAAATGTTT GTTTTCTCCT GCTGTGCTG TGACTCGAGT CACACTCAAG 1620 |
| | GGAACTGAG CGTGAATCTG TATCTGCGG GTCAATTTTA TGTATTACA GGGCAATCAA 1680 |
| | ATGGGCTGCT GCTTAGCTTG CACCTTGTCA CATAGAGTGA TCTTCCCAA GAGAAGGGGA 1740 |
| | AGCACTCGTG TGCAACAGAC AAGTGACTGT ATCTGTGTAG ACTATTGCT TATTTAATAA 1800 |
| | AGAAGATTG TCAGTTGTT T |
| 30 | Seq ID NO: 4 DNA Sequence |
| | Nucleic Acid Accession #: NM_001854 |
| | Coding sequence: 162..5582 |
| | 1 11 21 31 41 51 |
| 35 | AACCATCAAA TTGTAAGAA AAAGCCCTTT GACTTTTTC CCCTCTCCCT CCCCAATGGC 60 |
| | TGTGTAGCAA ACATCCCTTG CGATACCTTG GAAAGGACGA AGTTGGTCTG CAGTCGCAAT 120 |
| | TTGCTGGGTT GAGTTCACAG TTGTGAGTGC GGGGCTCGGA GATGGAGCOG TGGTCTCTA 180 |
| | GGTGAAAC GAAACGGTGG CTCTGGGATT TCACCGTAAC AACCTCGCA TTGACCTTCC 240 |
| 40 | TCTTCCAGC TAGAGAGGTC AGAGGAGCTG CTCCAGTTGA TGTAATAAAA GCACATAGATT 300 |
| | TTCACAATTC TCAGAGGGGA ATATCAAAAA CACCGGGATT TTGCACAAAC AGAAAGAAAT 360 |
| | CTAAAGGCTC ATGACTGTCT TACAGAGTTT CAAAGCAAGC ACAACTCAGT GCCCAACAAA 420 |
| | AACAGTATT TCCAGGTGGA ACTTTCCTCCAG AAGACTTTTC AATACTATT ACAGTAAAC 480 |
| | CAAAAAAGG AATTCACTCT TTCTTTTAT CTATATATAA TGAGCATGGT ATTCAGCAAA 540 |
| | TTGGTGTGA GGTGGGAGA TCACCTGTTT TTCTGTTGA AGACCACT GGAAAACTG 600 |
| 45 | CCCCAGAGA CTATCCCTTC TTCAGAACTG TTAACATCCG TGACGGGAAG TGGCATCGG 660 |
| | TAGCAATCAG CGTGGAGAAG AAAACTGTGA CAATGATTGT TGATTGTAAG AAGAAAAACA 720 |
| | CGAAACCACT TGATAGAAGT GAGAGAGCAA TTGTGTATAC CAATGGAAATC ACGGTTTTG 780 |
| | GAAACAAGAT TTGTGATGAA GAAGTTTTTG AGGGGACAT TCAGCAGTTT TGTATCAG 840 |
| 50 | GTGATCCCAA GGACGATAT GACTACTGTG AGCATTATAG TCCAGACTGT GACTCTTCAG 900 |
| | CACCCAGGCG TGCTCAAGCT CAGGAACCTC AGATAGATGA GTATGCCCA GAGGATATAA 960 |
| | TGAAATAGA CTATGAGTAT GGGGAAGCAG AGTATAAAGA GGCTGAAAGT GTAACAGAGG 1020 |
| | GACCCACTGT AACTGAGGAG ACAATAGCAC AGACGGAGGC AAACATCGTT GATGATTTTC 1080 |
| | AAGAATACAA CTATGAGACA ATGGAAAGTT ACCAGACAGA AGCTCCTAGG CATGTTCTG 1140 |
| 55 | GGACAATGA GCCAAATCCA GTTGAAGAAA TATTACTGA AGAATATCTA ACGGAGAGG 1200 |
| | ATTATGATT CCAGAGGAAA AATTCTGAGG ATACACTATA TGAAACAAA GAAATAGAG 1260 |
| | GCAGGATTCT TGATCTTCTG GTAGATGGAG ATTTAGGCGA ATATGATTTT TATGAATATA 1320 |
| | AAGAATAGA AGATAAACCA ACAAGCCCC CTAAATGAAGA ATTTGGTCCA GGTGTACCA 1380 |
| | CAGAACTGA TATTACAGAA ACAAGCATAA ATGGCCATGG TGCAATGGA GAGAAAGGAC 1440 |
| | AGAAAGGAGA ACCAGCAGTG GTTGAGCCTG GTATGCTTGT CGAAGGACCA CAGGACCAAG 1500 |
| 60 | CAGGACCTGC AGGTATTATG GGTCTCCAG GTCTACAAG CCCCACTGGA CCCCTGGTG 1560 |
| | ACCCTGGCGA TAGGGCCCC CCAGGACGTC CTGGCTTACC AGGGGCTGAT GGCTACCTG 1620 |
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Seq ID NO: 5 DNA sequence
Nucleic Acid Accession #: XM_057014
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Seq ID NO: 6 DNA Sequence
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Seq ID NO: 7 DNA sequence

Nucleic Acid Accession #: Eos sequence

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| | AGTATCGTCA | GGAGCCTGTC | AGGTTTGGGA | ACATCGGCTT | CGGAACCCCG | TACTACTATG | 5280 |
| | TGGGCTGGTA | CGAGTGTGGG | GTCTCCATCC | CTGGAAGATG | GTAATCACAG | GACCGTCATG | 5340 |
| | CTGCAAGCTT | GCCCTGCCCA | GCCCCACCAA | CTAAGTCGCA | CTAGGGGCTG | TGAGCAAAGA | 5400 |
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| | AATTCCGACA | CTTCAGTATT | TCCAGGAATA | GCATATGCAC | GCTGTTCTTG | CTTCATGGAA | 5700 |
| 60 | TGCTACATGC | TTTCTGTTTT | TCTCATTTTG | GATTCTCCCA | AACTAACTAG | AATTAAAGCT | 5760 |
| | TCAGGTCCCT | TTGTATGCAG | TAGAAAGGAA | TTATTAAGAA | CACCAACAAA | GAAAATAAAT | 5820 |
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Seq ID NO: 8 DNA Sequence
Nucleic Acid Accession #: NM_014244
Coding sequence: 1..3636

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| 75 | AGAGCAGGGG | TACGAGCCCG | CAGGCGCGCC | CGGTCGCGGA | CCCCGAGCTT | CCCCGAGGCG | 300 |
| | AACGAGGAGG | AGCCTGGCAG | TCACTCTTTC | TACAATGTCA | CGGTCTTTGG | CCGAGACCTG | 360 |
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| 80 | CTGATCGGGA | TGGAGGAGGA | GGAGTTCTTC | ATCGAAACCT | TGGAGAAGGG | GCTGGCGGCG | 600 |
| | CAGGAGGCTG | AGCAAGGCGG | TGTGATGTG | GTGTATCGCC | GGCCACCCAC | GTCCCTCTCT | 660 |
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| | CGCGCCCTGG | GGTCTCTAGA | GGAGCAGCGC | AACAGCTCGA | GGCGGAGGGC | ACGACGGCAT | 780 |
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| | |
|----|--|
| 5 | TTCCACGGGA AGGAGCAGT ACAGAAGTAC CTGCTGACAC TCATGAACAT TGTCATGAA 900 |
| | ATCTACCATG ACGAGTCCCT GGGTGCCAC ATCAACGTGG TCCTGGTGGG GATCATCTCT 960 |
| | CTGAGCTATG GAAAGTCCAT GAGCCTCATC GAGATCGGGA ACCCTCTCA GAGCCTGGAG 1020 |
| | AATGTCTGCC GCTGGGCTTA CCTCCAGCAG AAGCCAGACA CGGGCCACGA TGAATACCAC 1080 |
| | GATCACGCCA TCTTCTCTAC ACGGCAGGAC TTTGGGCTT CGGCATGCA AGGCTATGCT 1140 |
| | CCTGTACCG GCATGTGCCA TCCGGTCCGC AGCTGCACCC TGAACCATGA GGACGGCTTC 1200 |
| | TCCTCAGGCT TGTGGTGGC CCATGAGACT GGCCACGTGC TGGCATGGA GCACGACGGG 1260 |
| | CAGGGCAACC GCTGTGGGA CGAGGTGGG CTGGGCAGCA TCATGGGCC CCTGGTGAG 1320 |
| 10 | GCCGCTTCC ACCGCTTCCA CTGGTCCGC TGCAGCCAGC AGGAGCTGAG CCGTACCTG 1380 |
| | CACTCCTATG ACTGCTGTCT GGATGACCCC TTGCCCCAG ACTGGCCGGC GCTGCCCCAG 1440 |
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| | ATGATGTGCA CGGCGTTCGG GACCTTTGAC CCTGCAAGC AGCTGTGGTG CAGCCATCCT 1560 |
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| 25 | ATGTTTGA GA TCCCTGCAG AGCCAGACAC CTGCTCATT AGGAGGTAGA CGCCACCAG 2280 |
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| | GTGGATGCCA GTTCAAAAC CTTCATTGCC ATGGCGTGG AGTGGGAGTA CAGAGACGAG 2400 |
| | GACGGCCGG AGACGCTGCA GACCATGGG CCCCCTCCAG GCACCATCAC CGTTCTGGTC 2460 |
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| 30 | CTGAATGTG ATGACAACAA CGTCTGGAA GAGGACTCTG TGGTCTACGA GTGGGCCCTG 2580 |
| | AAGAAGTGGT CTCCGTGCTC CAAGCCCTGT GCGCGAGGGT CCCAGTTTAC CAAGTATGGC 2640 |
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| 35 | CGCTGCATT AGCGCTACA CCACAACACC ACCCGCTCG TGACGCCAA GCATGCAAT 2880 |
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| | GTAGTTCACT GGCTGTCCG CCGGACCCC GACTCGCCA TCCGGAAGAT CTGCTCAAAG 3180 |
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| | TCATCCAG GCTACAACAA GCTGTCTGC AAGTCTGTG ACCTGTACAA CAACCTCACC 3300 |
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| 45 | CCTACCTCC CAGTGCCAC TGTAGCCATG GAGGTGGCG CATCACCAAG CACCCCTGCT 3420 |
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| 60 | TCAATCCGAT CCGTTTTTGG CCTTGATGAT TTGAAATAA GTCTGTGTC ACCAGATGCA 300 |
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| | GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGT GGGTGGTCTG 540 |
| 65 | AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGGAAGA CCAATGTGTC CGATGACTGG 600 |
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| | CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780 |
| | TGTGCTCTG GCCACGTGGT TACCTTCAG TGCACAGCCT GTGGTCTAG AAGGGGCTAC 840 |
| 70 | AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTGCG AGTGGCCCTG GCAGGCCAGC 900 |
| | CTTCAGTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCTT GTGGATCATC 960 |
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| 75 | CTCACGTTCA ATGAAATGAT CCAGCTGTG TGCTGCCCC ACTCTGAAGA GAACTTCCCC 1200 |
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| | GACAGCTGCC AGGGGACAG CGGGGGGCC CTGGTGTGTC AAGAGAGGAG GCTGTGGAAG 1440 |
| 80 | TTAGTGGGAG CGACCACTT TGGCATCGGC TGCGCAGAGG TGAACAAGCC TGGGGTGTAC 1500 |
| | ACCCGTGTCA CTCCTTCTT GAGCTGGATC CACGAGCAGA TGGAGAGAGA CCTAAAACC 1560 |
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| | GCTGCTTTT GTTTTGTGTT TTTTGTAGGT GGAGTCTCGC TCTGTTGCC AGGCTGGAGT 1800 |
| | GCAGTGGCA AATCCCTGCT CACTGCAGCC TCCGCTTCCC TGGTTCAAGC GATTCTCTG 1860 |

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Seq ID NO: 10 DNA Sequence
Nucleic Acid Accession #: AK092195
Coding sequence: 1..2034

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CTTTGGTGGG AACAGAAGCA TTGCTGGCTT CTGAAAAACC ACTGGACCTT GGACAAATAT 240
GGGGTCCAGG CAGATGCAAA GCTTCTCTTC ACCCTCAGC ATAAATGCT GCGCCTTCGT 300
CTGCCGAATT TGAAGATGGT GAGGTTGCGA GTGAGCTTCT CAGCTGTGGT TTTTAAAGCT 360
GTGAGTGATA TCTGCAAAAT CTTGAATATT AGAAGATCAG AAGAGCTTTC CTGTGTTAAG 420
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GTTGATAAAG CCAAGCTCAA TGCAGGTTGG CTAGACTCCT CAGCTCTCCT TATGGAACAA 780
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Seq ID NO: 11 DNA Sequence
Nucleic Acid Accession #: NM_032044
Coding sequence: 182..658

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Seq ID NO: 12 DNA Sequence
Nucleic Acid Accession #: XM_051860.2
Coding sequence: 261..4346

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| 5 | AGAGGGAGCA | CAGTGGCAG | ATGGGAGCTG | CTGGGAGGCA | GGACTTCCTC | TTCAAGGCCA | 300 |
| | TGCTGACCAT | CAGCTGGCTC | ACTCTGACCT | GCTTCCCTGG | GGCCACATCC | ACAGTGGCTG | 360 |
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| 15 | TGACCCCAA | ATCAGGCACA | GTCAATCCAT | CTGACCGGTT | TGACACCTAT | AGATCCAAGA | 900 |
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| 40 | GATTTTGGTT | TATTTTTCAC | CACGTACCAA | CGGGCCCTCT | CGTGGGAATG | TACTCCCCAG | 2400 |
| | GTTATTTCAG | GCACATTCCA | CTGGGAAAAT | TCTATAACAA | CCGAGCACAT | TCCAACTACC | 2460 |
| | GGGCTGGCAT | GATCATAGAC | AACGGAGTCA | AAACCAACGA | GGCCTCTGCC | AAGGACAAGC | 2520 |
| | GGCCGTCTCT | CTCAATCATC | TCTGCCAGAT | ACAGCCCTCA | CCAGGACGCC | GACCCGCTGA | 2580 |
| | AGCCCCGGGA | GCCGGCCATC | ATCAGACACT | TCATTGCCCTA | CAAGAACCAG | GACCAACGGG | 2640 |
| 45 | CCTGGCTGCG | CGGCGGGGAT | GTGTGGCTGG | ACAGCTGCGG | GTTTGTGAGC | AATGGCATTG | 2700 |
| | GCCTGACCCCT | GGCCAGTGGT | GGAACTTTCC | CGTATGACGA | CGGCTCCAAG | CAAGAGATAA | 2760 |
| | AGAACAGCTT | GTTTGTGGCG | GAGAGTGGCA | ACGTGGGGAC | GGAAATGATG | GACAAATAGGA | 2820 |
| | TCTGGGGCCC | TGGCGGCTTG | GACCATAGCG | GAAGGACCCCT | CCCTATAGGC | CAGAAATTTT | 2880 |
| | CAATTAGAGG | AATTTCAGTTA | TATGATGGCC | CAATCAACAT | CCAAAATGTC | ACTTTCCGAA | 2940 |
| 50 | AGTTTGTGGC | CCTGGAGGGC | CGGCACACCA | GCGCCCTGGC | CTTCCGCTG | AATAATGCCT | 3000 |
| | GGCAGAGCTG | CCCCATAAAC | AAAGTGACCG | GCAATTGCCCT | TGAGGAGGTT | CCGATTACTT | 3060 |
| | CCAGAGTGTT | GTTTGTGGCG | CCTGGGCCCT | GGTTCAACCA | CTGGGACATG | GATGGGGATA | 3120 |
| | AGACATCTGT | GTTTCAATGAC | GTGCGCGGCT | CCGTGTGCGA | GTACCTGGGC | TCTTACCTCA | 3180 |
| | CGAAGAATGA | CAACTGGCTG | GTCCGGCACC | CAGACTGCAT | CAATGTTCCC | GACTGGAGAG | 3240 |
| 55 | GGGCCATTG | CAGTGGGTGC | TATGCACAGA | TGTACATTCA | AGCCTACAAG | ACCAGTAACC | 3300 |
| | TGCGAATGAA | GATCATCAAG | AATGACTTCC | CCAGCCACCC | TCTTTACCTG | GAGGGGGCGC | 3360 |
| | TCACCAAGGAG | CACCCATTAC | CAGCAATACC | AACCGGTTGT | CACCCCTGCA | AAGGGCTACA | 3420 |
| | CCATCCACTG | GGACAGAGCG | GCCCCCGCCG | AACTCGCCAT | CTGGCTCATC | AACCTCAACA | 3480 |
| | AGGGGAGACT | GATCCGAGTG | GGGCTCTGCT | ACCCGCGAGG | CACCACTTCT | TCCATCTCTT | 3540 |
| 60 | CGGATGTTCA | CAATGCGCTG | CTGAAGCAAA | CGTCCAAGAC | GGGCGTCTTC | GTGAGGACCT | 3600 |
| | TGCAGATGGA | CAAAATGGAG | CAGAGCTACC | CTGGCAGGAG | CCACTACTAC | TGGGACGAGG | 3660 |
| | ACTCAGGGCT | GTTGTTCTCT | AAGCTGAAAG | CTCAGAACGA | GAGAGAGAA | TTTGCTTTCT | 3720 |
| | GCTCCATGAA | AGGCTGTGAG | AGGATAAAGA | TTAAAGCTCT | GATTCCAAAG | AACGCAGGCG | 3780 |
| | TCAGTGACTG | CACAGCCACA | GCTTACCCCA | AGTTCAACGA | GAGGGCTGTC | GTAGACGTGC | 3840 |
| 65 | CGATGCCCAA | GAAGCTCTTT | GGTTCTCAGC | TGAAACAAAA | GGACCATTTT | TTGGAGGTGA | 3900 |
| | AGATGGAGAG | TTCCAAGCAG | CACCTCTTCC | ACCTCTGGAA | CGACTTGGCT | TACATTGAAG | 3960 |
| | TGGATGGGAA | GAAGTACCCC | AGTTGGAGGG | ATGGCATCCA | GGTGGTGGTG | ATTGACGGGA | 4020 |
| | ACCAAGGGCG | CGTGGTGAGC | CACACGAGCT | TCAGGAATCT | CATTCTGCAA | GGCATACCAT | 4080 |
| | GGCAGCTTTT | CAACTATGTG | GCGACCATCC | CTGACAATTC | CATAGTGCTT | ATGGCATCAA | 4140 |
| 70 | AGGGAAGATA | CGTCTCCAGA | GGCCCATGGA | CCAGAGTGCT | GGAAAAGCTT | GGGGCAGACA | 4200 |
| | GGGGTCTCAA | GTTGAAAGAG | CAAAATGGCAT | TGGTTGGCTT | CAAAAGGAGC | TTCCGGCCCA | 4260 |
| | TCTGGGTGAC | ACTGGACACT | GAGGATCACA | AAGCCAAAAT | CTTCCAAGTT | GTGCCCATCC | 4320 |
| | CTGTGGTGAA | GAAGAAGAAG | TTGTGAGGAC | AGCTGCCGCC | CGGTGCCACC | TCGTGGTAGA | 4380 |
| | CTATGACGGT | GACTCTTGGC | AGCAGACCCAG | TGGGGGATGG | CTGGGTCCCC | CAGCCCCCTG | 4440 |
| 75 | CAGCAGCTGC | CTGGGAAGGC | CGTGTTCAG | CCCTGATGGG | CCAAGGGAAG | GCTATCAGAG | 4500 |
| | ACCCTGGTGC | TGCCACCTGC | CCCTACTCAA | GTGTCTACCT | GGAGCCCTCT | GGGCGGTGCT | 4560 |
| | GGCCAATGCT | GGAAACATTC | ACTTCTCTGC | AGCCTCTTGG | GTGCTTCTCT | CCTATCTGTG | 4620 |
| | CCTCTTCAGT | GGGGGTTTGG | GGACCATATC | AGGAGACCTG | GTTTGTGCTG | ACAGCAAAAG | 4680 |
| | TCCACTTTGG | CAGGAGCCCT | GACCCAGCTA | GGAGGTAGTC | TGGAGGGCTG | GTCAATCACA | 4740 |
| 80 | GATCCCCATG | GTCTTCAGCA | GACAAAGTGA | GGTGGTAAAT | GTAGGAGAAA | GAGCCTTGGC | 4800 |
| | CTTAAGGAAA | TCTTTACTCC | TGTAAGCAAG | AGCCAACTCT | ACAGGATTAG | GAGCTGGGGT | 4860 |
| | AGAATCTGGT | ATCCTTGGGG | AAGAGGCAAG | CCCTGCCCTCT | GGCCGTGTCC | ACCTTTCAGG | 4920 |
| | AGACTTTGAG | TGGCAGGTTT | GGACTTGGAC | TAGATGACTC | TCAAAGGCCCT | TTTATGTTCT | 4980 |
| | GAGATTCCAG | AAATCTGCTG | CATTTACAT | GGTACCTGGA | ACCCCAACAGT | TCATGGATAT | 5040 |
| | CCACTGATAT | CCATGATGCT | GGGTGCCCCA | GCGCACACGG | GATGGAGAGG | TGAGAACTAA | 5100 |

634

| | | | | | | | |
|----|--|-------------|-------------|-------------|-------------|-------------|------|
| | ACTCTCACCC | TCTCCCCAAC | TTTTTTTAAA | AATTTTAACC | AGAAAAATAA | GATAGTTAAA | 2760 |
| | TCCTAAGATA | GAGATTAAGT | CATGTTTTAA | ATGAGGAACA | ATCAGTAAAT | CAGATTCTGT | 2820 |
| | CCTCTTCTCT | GCATACCGTG | AATTTATAGT | TAAGGATCCC | TTTGCTGTGA | GGGTAGAAAA | 2880 |
| 5 | CCTCACCAAC | TGCACCAAGT | AGGAAGAAAG | CTGCTGGAT | TCATGGGGAG | CCTCACAGCA | 2940 |
| | GCCACGCAGC | AGGCTCTGGG | TGGGGCTGCC | GTTAAGGCAC | GTTCTTCTCT | TACTGGTGCT | 3000 |
| | GATAACAACA | GGGAACCGTG | CAGTGTGCAT | TTTAAGACCT | GGCCTGGAAT | AAATACGTTT | 3060 |
| | TGCTTTTCCC | TC | | | | | 3072 |
| 10 | Seq ID NO: 14 DNA Sequence | | | | | | |
| | Nucleic Acid Accession #: Eos sequence | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| | ATTCTTGGAG | ATGGCTCCTC | TGGAACATAT | GCATCTCTCC | TGATACTTGG | ATGCTTTTCC | 60 |
| 15 | TCTGACTGAT | GAAGATCCCTG | AATACCAAAG | AGGGCCGCTG | AAAGGGCTCT | AGGAGTACAC | 120 |
| | CTTCTAGGAA | CCCTAAGCCA | GAGAGAGGCT | TCACTACATC | ATGCTTCTCTG | ACATCTCTCC | 180 |
| | CTTTGAAGAG | CAGTCAGACT | CCTGCTTTGC | TCTTCAGACT | TAATTTGGGG | GTTTAAACAGG | 240 |
| | TGAGGTGTCT | GGGGAACTC | TTTTACAACA | TCTCTCTGAA | AGAATCCGGG | CTGCCAGTTT | 300 |
| | CATTTGGTTT | GGGTGTCACT | AGCATGATGG | AAAGACAAA | AAACCAACT | TGACATCTGC | 360 |
| 20 | AGAAATGGGT | TCAAATTTTA | CCTGCAACTC | ACCAATTCTG | TGGCTTGGT | TCAGCAATTA | 420 |
| | AATCCCTCAA | AATTCAGTTT | TTTCTTTGTA | AAATGGGGTT | ATGAACAGTA | CCTACTTCAA | 480 |
| | AATGTGTTTG | TGAAGATTAA | AAAAGTTAAC | ATAAGAGATT | TAGAAGAGTG | TCTGGCATAT | 540 |
| | TGTGCTCAAT | AAGTGTATT | TTATTTATTG | CTGAATAAAC | CAGTAATTTA | ATTAGTAT | 598 |
| 25 | Seq ID NO: 15 DNA Sequence | | | | | | |
| | Nucleic Acid Accession #: Eos sequence | | | | | | |
| | Coding sequence: 63..3224 | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| 30 | CAGGAATTTG | TGGCGGAGAG | GGCAATAAAC | TGCGGCTCTC | CCGGCGCCCC | GATGCTCGCA | 60 |
| | CCATGTGAG | GGCAAGCAG | GGCAAAACCC | AGCACATCAA | CTCGGAGGAG | GACCAAGGCG | 120 |
| | AGCAGACAGC | GCAGCAGCAG | ACCCCGAGT | TTGCAGATGC | GGCCCAAGCG | GGCCCGCGCG | 180 |
| | CGGGGAGGCT | GGGTGCTCCA | GTGAACCAAC | CAGGGAATGA | CGAGGTGGCG | AGTGAGGATG | 240 |
| | AAGCCACAGT | AAAGCGGCTT | CCTCGGGAGG | AGACGCACGT | CTGTGAGAAA | TGCTGTGCGG | 300 |
| 35 | AGTTCCTCAG | CATCTCTGAG | TTCTTGGAAC | ATAAGAAAAA | TTGCACTAAA | AATCCACCTG | 360 |
| | TCCTCATCAT | GAATGACAGC | GAGGGGCGCTG | TGCCTTCAGA | AGACTTCTCC | GGAGCTGTAC | 420 |
| | TGAGCCACCA | CCCAACCACT | CCCGGCAGTA | AGGACTGTCA | CAGGGAGAAT | GGCGGCAGCT | 480 |
| | CAGAGGACAT | GAAGGAGAAG | CCGGATGCGG | AGTCTGTGGT | GTACCTAAAG | ACAGAGACAG | 540 |
| | CCCTGCCACC | CACCCCCCAG | GACATAAGCT | ATTTAGCCAA | AGGCAAAAGTG | GCCAACACTA | 600 |
| 40 | ATGTGACCTT | GCAGGCACTA | CGGGGCACCA | AGGTGGCGGT | GAATCAGCGG | AGCGCGGATG | 660 |
| | CACCTCCCTG | CCCGGTGCTC | GGTGCCAACA | GCATCCCGTG | GGTCTCTGAG | CAGATCTTGT | 720 |
| | GTCTGCAGCA | CAGCAGATCC | AGCTCACCGA | GCAGATCCGC | ATCCAGGTGA | | 780 |
| | ACATGTGGGC | CTCCACGCC | CTCCACTCAA | CGCGGGCAGG | GGCCGACACT | CTGAAGACCT | 840 |
| | TGGGCAGCCA | CATGTCTCAG | CAGGTTTCTG | CAGCTGTGGC | TTTGCTCAGC | CAGAAAGCTG | 900 |
| 45 | GAAGCCAAAG | TCTGTCTCTG | GATGCCCTGA | AACAAGCCAA | GCTACCTCAC | GCCAACATCC | 960 |
| | CTTCTGCCAC | CAGCTCCCTG | TCCCGAGGGC | TGGCACCCCT | CACTCTGAAG | CCGGATGGGA | 1020 |
| | CCCGGAGTCT | CCGAAACGTC | ATGTCCCGCC | TCCCGAGCGC | TTTGCTTCTC | CAGGCCCGCG | 1080 |
| | GCTCGGTGCT | CTTCAGAGC | CTTTTCTCCA | CTGTGGCGCT | AGACACATCC | AAGAAAGGGA | 1140 |
| | AGGGGAAGCC | ACCGAACATC | TCGCGGTGG | ATGTCAAAAC | CAAAGACGAG | GGCGCCCTCT | 1200 |
| 50 | ACAAGCACAA | GTGTAAGTAC | TGTAGCAAGG | TTTTTGGGAC | TGATAGCTCC | TTGCAGATCC | 1260 |
| | ACCTCGCTC | CCACTCTGGA | GAGAGACCCT | TGCTGTGCTC | TGCTGTGGT | CATCGCTTCA | 1320 |
| | CCACCAAGGG | AGCCTCAAG | GTGCACTTTC | ACCGACATCC | CCAGGTGAAG | GCAAAACCCC | 1380 |
| | AGCTGTTTGC | CGAGTTCAG | GACAAAGTGG | CGCGCGGCAA | TGGCATCCCC | TATGCACTCT | 1440 |
| | CTGTACTTGA | CCCATAGAT | GAACCGAGTC | TTTCTTTAGA | CAGCAAACTT | GTCTTGTAA | 1500 |
| 55 | CCACCTCTGT | AGGCTACCT | CAGAACTTTT | CTTCGGGGAC | TAATCCCAAG | GACCTCAGCG | 1560 |
| | GTGGCTCTCT | GGCGGTGAC | CTGCAGCCTG | GGCCTTCTCC | AGAAAGTGAG | GGTGGACCCA | 1620 |
| | CACCTCCCTG | GGTGGGACCA | AACTATAATT | CCCCAAGGGC | TGGTGGCTTC | CAAGGGAGTG | 1680 |
| | GGACCCCTGA | GCCAGGGTCA | GAGACCCCTGA | AATTGCAGCA | GTGTGTGGAG | AACATTGACA | 1740 |
| | AGGCCACCAC | TGATCCCAAC | GAATGTCTCA | TTTGCCACCG | AGTCTTAAGC | TGTGAGAGCT | 1800 |
| 60 | CCCTCAAGAT | GCATTATGCG | ACCCACACCG | GGGAGAGACC | GTTCAGTGT | AAGATCTGTG | 1860 |
| | GCGAGGCCTT | TTCTACCAAA | GGTAACCTGA | AGACACACCT | TGGGTTCCAC | CGAAACCAACA | 1920 |
| | CATCCATTAA | GACGCAGCAT | TGTCGCCCA | TCTGCCAGAA | GAAGTTCACT | AATGCCGTGA | 1980 |
| | TGCTGCAGCA | ACATATTGCG | ATGCACATGG | GGGTTCAGAT | TCCCAACACG | CCCTGCCAG | 2040 |
| | AGAATCCCTG | TGACTTTACG | GGTTCTGAGC | CAATGACCGT | GGGTGAGAAC | GGCAGCACCG | 2100 |
| 65 | GGCTATCTG | CCATGATGAT | GTCTATGAAA | GCATCGATGT | AGAGGAAGTC | AGCTCCAGG | 2160 |
| | AGGCTCCAG | CAGCTCTCTC | AAGGTCCCCA | CGCTCTTCTC | CAGCATCCAC | TCGGCATCAC | 2220 |
| | CCACGCTAGG | GTTTGCCATG | ATGGCTTCCT | TAGATGCCCC | AGGGAAAGTG | GGTCTGCCCC | 2280 |
| | CTTTTAACT | GCAGCGCCAG | GGCAGCAGAG | AAAAAGGTTT | CGTGGAGAGC | GATGGCTTGA | 2340 |
| | CCAAAGACTC | ATCTCTGCTG | ATGGGAGACC | AGGAGTATCA | GAGCCGAAGC | CCAGATATCC | 2400 |
| 70 | TGAAACCCAC | ATCCTTCCAG | GCACTCTCCC | CGGCCAATAG | TCAAGCCGAA | AGCATCAAGT | 2460 |
| | CAAGGTCTCC | CGATGCTGGG | AGCAAAGCAG | AGAGCTCCGA | GAACAGCCGC | ACTGAGATGG | 2520 |
| | AAGGTCCGAG | CAGTCTCCCT | TCCACGTTTA | TCCGAGCCCC | GGCGACCTAT | GTCAAGGTTG | 2580 |
| | AAGTCTCTGG | CACATTTGTG | GGACCCCTCGA | CATTGTCCCC | AGGGATGACC | CCTTTGTTAG | 2640 |
| | CAGCCCAAGC | ACGCCGACAG | GCCAAAGCAAC | ATGGCTGCAC | ACGGTGTGGG | AAGAAGTTCT | 2700 |
| 75 | CGTCTGTAG | CGCTCTTCAG | ATCCACGAGC | GGACTCACAC | TGGAGAGAAG | CCTTTTGTGT | 2760 |
| | GCAACATTGG | TGGCGAGCT | TTTACCACCA | AAGGCAACTT | AAAGTTTCAC | TACATGACAC | 2820 |
| | ACGGGCGGAA | CAATAACTCA | GCCCGCCGTG | GAAGGAAGTT | GGCCATCGAG | AACACCATGG | 2880 |
| | CTCTGTAGG | TACGGACGGA | AAAAGAGTCT | CAGAAATCTT | TCCCAAGGAA | ATCTGGCCCC | 2940 |
| | CTTCAGTAA | TGTGGACCTT | GTTGTGTGGA | ACCAATACAC | CAGCATGCTC | AATGGCGGTC | 3000 |
| 80 | TGGCGGTGAA | GACCAATGAG | ATCTCTGTGA | TCCAGAGTGG | GGGGTTTCTT | ACCTCCCGG | 3060 |
| | TTCTCTGGG | GGCCACCTCC | GTTGTGAATA | ACGCCACTGT | CTCCAAGATG | GATGGCTCCC | 3120 |
| | AGTCCGGTAT | CAGTGCAGAT | GTGGAAAAAC | CAAGTGTCTAC | TGACGGCGTT | CCCAACACCC | 3180 |
| | AGTTTCTCTA | CTTCTGGAA | GAAAAACAAG | TTGCGGTGAG | CTAAGGGAGA | ACTTGGGTGG | 3240 |
| | AAGGAGCAAT | GCAGACACAG | TGAAATCTCT | AGAATCTGCT | TTGTTTGTGA | AGAACTCATC | 3300 |
| | TCTCTGCTT | TTCTTTTCT | TACTGATATG | CAAAATGATG | TTACTACGTT | GGTTGTGACC | 3360 |

ACAACCTCAG GCAAGTGCTA CAATCAGAT TGTGTCTATG CTGCTTTGCA AAAAGTTG 3418

Seq ID NO: 16 DNA Sequence

Nucleic Acid Accession #: NM_005101

Coding sequence: 76..573

5
1 11 21 31 41 51
| | | | |
CGGCTGAGAG GCAGCGAACT CATCTTTGCC AGTACAGGAG CTTGTGCCGT GGCCACAGC 60
CCACAGCCCA CAGCCATGGG CTGGGACCTG ACGGTGAAGA TGCTGGCGGG CAACGAATTC 120
10 CAGGTGTCCC TGAGCAGCTC CATGTCCGTG TCAGAGCTGA AGGCGCAGAT CACCCAGAAG 180
ATTGGCGTGC ACGCTTCCA GCAGGCTCTG GCTGTCCACC CGAGCGGTGT GCGCTGCAG 240
GACAGGGTCC CCCTTGCCAG CCAGGGCCTG GGCCCTGGCA GCAAGGTCTT GCTGGTGGTG 300
GACAAATGCG ACGAACCTCT GAGCATCTCT GTGAGGAATA ACAAGGGCCG CAGCAGCACC 360
TACGAGGTCC GGCTGACGCA GACCGTGGCC CACCTGAAGC AGCAAGTGAG CGGCTGGAG 420
15 GGTGTGCAGG ACGACCTGTT CTGGCTGACC TTCGAGGGGA AGCCCCCTGA GGACAGCTC 480
CGCTGGGGG AGTACGGCCT CAAGCCCCTG AGCACCCTGT TCATGAATCT GCGCTCGCG 540
GGAGGCGGCA CAGAGCCTGG CCGGCGGAGC TAAGGGCCTC CACCAGCATC CGAGCAGGAT 600
CAAGGGCCCG AAATAAAGGC TGTGTGAAGA GAAT 634

Seq ID NO: 17 DNA sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 62..895

25
1 11 21 31 41 51
| | | | |
CACTGCTCTG AGAATTGTG AGCAGCCCCC AACAGGCTGT TACTTCACTA CAACTGACGA 60
TATGATCATC TTAATTTACT TATTTCTCTT GCTATGGGAA GACACTCAAG GATGGGGATT 120
CAAGGATGGA ATTTTTCATA ACTCCATATG GCTTGAACGA GCAGCCGGTG TGTACCACAG 180
AGAAGCACGG TCTGCAAAAT ACAAGCTCAC CTACGCAGAA GCTAAGGCGG TGTGTGAATT 240
TGAAGGCGGC CATCTCGCAA CTTACAAGCA GCTAGAGGCA GCCAGAAAAA TTGGATTTC 300
30 TGTCTGTGCT GCTGGATGGA TGGCTAAGGG CAGAGTTGGA TACCCCATTT TGAAGCCAGG 360
GCCCAACTGT GGATTTGAA AAAGTGGCAT TATTGATTAT GGAATCCGT TCAATAGGAG 420
TGAAAGATGG GATGCTATT GCTACAACCC ACACGCAAG GAGTGTGGTG GCGTCTTTAC 480
AGATCCAAG CAAATTTTAA ATCTCCAGG CTTCCTCAAT GAGTACGAAG ATAACCAAT 540
CTGCTACTGG CACATTAGAC TCAAGTATGG TCAGCGTATT CACCTGAGTT TTTTAGATT 600
35 TGACCTTGAA GATGACCCAG GTTGTCTGGC TGATTATGTT GAAATATATG ACAGTTACGA 660
TGATGTCCAT GGCCTTTGGG GAAGATACTG TGGAGATGAG CTTCAGATG ACATCATCAG 720
TACAGGAATG TCATGACCT TGAAGTTTCT AAGTGATGCT TCAGTGACAG CTGAGGTTT 780
CCAAATCAAA TATGTTGCAA TGGATCCTGT ATCCAAATCC AGTCAAGGAA AAAATACAAG 840
TACTACTCTCT ACTGGAATA AAAACTTTTT AGCTGGAAGA TTTAGCCACT TATAAAAAA 900
40 AAAAAAAGGA TGATCAAAAC ACACAGTGT TATGTTGGAA TCTTTTGAA CCCTTTGAT 960
CTCACTGTTA TTATTAACAT TTATTTATTA TTTTCTTAAA TGTGAAAGCA ATACATAAT 1020
TAGGGAAAT TGGAAATAT AGGAACTTT AAACGAGAAA ATGAAACCTC TCATAATCCC 1080
ACTGCATAGA AATAACAAGC GTTAACATTT TCATATTTTT TTCTTTCAGT CATTTTCTA 1140
TTTGTGGTAT ATGTATATAT GTACCTATAT GTATTTGCAT TTGAAATTTT GGAATCCTGC 1200
45 TCTATGTACA GTTTTGTATT ATACTTTTAA AATCTTGAAC TTTATAAACA TTTTCTGAAA 1260
TCATTGATTA TTCTACAAA ACATGATTTT AAACAGCTGT AAAATATTCT ATGATATGAA 1320
TGTTTATGC ATTATTAAG CCTGTCTCTA TTGTGGAAT TCAGGTTCAT TTTCAATAAT 1380
ATTGTTGCAA TAAATATCTT TGAACACACA AAAAAA AA

Seq ID NO: 18 DNA sequence

Nucleic Acid Accession #: NM_007115.1

Coding sequence: 69..902

55
1 11 21 31 41 51
| | | | |
GAATTGCGAC TGCTCTGAGA ATTTGTGAGC AGCCCTTAAC AGGCTGTTAC TTCCTACAA 60
CTGACGATAT GATCATCTTA ATTTACTTAT TTCTCTTGCT ATGGGAAGAC ACTCAAGGAT 120
GGGATTTCAA GGTGGAATT TTTCAAACT CCATATGGCT TGAACGAGCA GCGGTGTGT 180
ACCACAGAGA AGCAGCGTCT GGCAAAATACA AGCTCACCTA CCGAGAAGCT AAGCGGTGT 240
GTGAATTTGA AGCGGCCCAT CTCGCAACTT ACAAGCAGCT AGAGGCAGCC AGAAAAATTG 300
60 GATTTCATGT CTGTGCTGCT GGATGGATGG CTAAGGGCAG AGTTGGATAC CCCATTGTGA 360
AGCCAGGGCC CAATGATGA TTTGGAAAAA CTGGCATTAT TGATTATGGA ATCCGTCTCA 420
ATAGGAGTGA AAGATGGGAT GCCTATTGCT ACAACCCACA CGCAAAGGAG TGTGGTGGCG 480
TCTTTACAGA TCCAAAGCGA ATTTTAAAT CTCCAGGCTT CCCAATGAG TACGAAGATA 540
ACCAATCTGT CTACTGGCAC ATTAGACTCA AGTATGGTCA GCGTATTAC CTGAGTTT 600
65 TAGATTTTGA CCTTGAAGAT GACCCAGGTT GCTTGGCTGA TTATGTTGAA ATATATGACA 660
GTTACGATGA TGTCCATGGC TTTGTGGGAA GATAGTGTGG AGATGAGCTT CCAGATGACA 720
TCATCAGTAC AGGAAATGTC ATGACCTTGA AGTTTCTAAG TGATGCTTCA GTGACAGCTG 780
GAGGTTTCCA AATCAAATAT GTTGCAATGG ATCTCTGTAT CAAATCCAGT CAAGGAAAAA 840
ATACAAGTAC TACTTCTACT GGAATAAATA ACTTTTATAG TGAAGATT 900
70 AAAAAAAGGA AAGGATGATC AAAACACACA GTGTTTATGT TGAATCTTT TGGAACTCCT 960
TTGATCTCAC TGTATTATTT AACATTTATT TATTATTTTT CTAAATGTGA AAGAAATACA 1020
TAATTTAGGG AAAATGGGAA AATATAGGAA ACTTTAAACG AGAAAAATGAA ACCTCTCATA 1080
ATCCCACTGC ATAGAAATAA CAAGCGTTAA CATTTTCATA TTTTTCCTT TCAGTCATTT 1140
TTGTATTTGT GGTATATGTA TATATGTACC TATATGTATT TGCAATTTGAA ATTTTGGAA 1200
75 CCGTCTCTAT GTACAGTTTT GTATTACTT TTTTAAATCT TGAACCTTAT GAACATTTTC 1260
TGAATCATTT GATTATTTCT CAAAACATG ATTTTAAACA GCTGTAAAT ATTCTATGAT 1320
ATGAATGTTT TATGCATTAT TTAAGCCTGT CTCTATTGTT GGAATTCAG GTCATTTTCA 1380
TAAATATTGT TGCAATAAAT ATCCTTCGGA ATTC

Seq ID NO: 19 DNA Sequence

Nucleic Acid Accession #: NM_006398.1

Coding sequence: 19..516

1 11 21 31 41 51
| | | | |

| | | | | | | | |
|----|---------------------------------------|-------------|------------|------------|-------------|-------------|------|
| | GGCCCCCTTGT | CTGCAGAGAT | GGCTCCCAAT | GCTTCCTGCC | TCTGTGTGCA | TGTCGGTTCC | 60 |
| | GAGGAATGGG | ATTTAATGAC | CTTTGATGCC | AACCCATATG | ACAGCGTGAA | AAAAATCAAA | 120 |
| | GAACATGTCC | GGTCTAAGAC | CAAGGTTCC | GTGCAGGACC | AGGTTCTTTT | GCTGGGCTCC | 180 |
| 5 | AAGATCTTAA | AGCCACGGAG | AAGCCTCTCA | TCTTATGGCA | TTGACAAAGA | GAAGACCATC | 240 |
| | CACCTTACCC | TGAAAGTGGT | GAAGCCCACT | GATGAGGAGC | TGCCCTTGTT | TCTTGTGGAG | 300 |
| | TCAGGTGATG | AGGCAAGAG | GCACCTCCTC | CAGGTGCGAA | GGTCCAGCTC | AGTGGCACAA | 360 |
| | GTGAAAGCAA | TGATCGAGAC | TAAGACGGGT | ATAATCCCTG | AGACCCAGAT | TGTACTTGC | 420 |
| | AATGGAAGA | GACTGGAAGA | TGGGAAGATG | ATGGCAGATT | ACGGCATCAG | AAAGGGCAAC | 480 |
| 10 | TTACTCTTCC | TGGCATCTTA | TGTATTGGA | GGGTGACCAC | CCTGGGGATG | GGGTGTTGGC | 540 |
| | AGGGGTCAAA | AAGCTTATTT | CTTTTAACT | CTTACTCAAC | GAACACATCT | TCTGATGATT | 600 |
| | TCCCAAAAT | AATGAGAATG | AGATGAGTAG | AGTAAGATTT | GGGTGGGATG | GGTAGGATGA | 660 |
| | AGTATATTGC | CCAACCTCTAT | GTTTCTTTGA | TTCTAACACA | ATTAATTAAG | TGACATGATT | 720 |
| | TTTACTAATG | TATTACTGAG | ACTAGTAAAT | AAATTTTTAA | GGCAAAATAG | AGCATTTC | 777 |
| 15 | Seq ID NO: 20 DNA Sequence | | | | | | |
| | Nucleic Acid Accession #: NM_002358.2 | | | | | | |
| | Coding sequence: 75..692 | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| 20 | GGGAAGTGCT | GTGGAGCCG | CTGTGGTTGC | TGTCCGCGGA | GTGGAAGCGC | GTGCTTTTGT | 60 |
| | TTGTGTCCCT | GGCCATGGCG | CTGCAGCTCT | CCCGGAGCA | GGGAATCACC | CTGCGCGGGA | 120 |
| | GGCGCGAAT | CGTGGCCGAG | TTCTTCTCAT | TCGGCATCAA | CAGCATTTTA | TATCAGCGTG | 180 |
| | GCATATATCC | ATCTGAAACC | TTTACTCGAG | TGCAGAAATA | CGGACTCACC | TTGCTTTGTA | 240 |
| 25 | CTACTGATCT | TGAGCTCATA | AAATACCTAA | ATAATGTGGT | GGAACTACTG | AAAGATTGGT | 300 |
| | TATACAAAGT | TTAGTTTCAG | AAACTGGTTG | TAGTTATCTC | AAATATTGAA | AGTGGTGAGG | 360 |
| | TCCTGGAAG | ATGGCAGTTT | GATATTGAGT | GTGACAAGAC | TGCAAAAGAT | GACAGTGCAC | 420 |
| | CCAGAGAAA | GTCTCAGAAA | GCTATCCAGG | ATGAAATCCG | TTCACTGATC | AGACAGATCA | 480 |
| | CAGCTACGGT | GACATTTCTG | CCACTGTTGG | AAGTTTCTTG | TTCAITTTGAT | CTGCTGATT | 540 |
| 30 | ATACAGACAA | AGATTGTGGT | GTACCTGAAA | AATGGGAAGA | GTCCGGACCA | CAGTTTATTA | 600 |
| | CCAATTTCTGA | GGGAAGTCCG | CTTCGTTTCT | TTACTACTAC | AATCCACAAA | GTAATATAGCA | 660 |
| | TGGTGGCCTA | CAAAATTCCT | GTCAATGACT | GAGGATGACA | TGAGGAAAAT | AATGTAATTG | 720 |
| | TAATTTTGAA | ATGTGGTTTT | CCTGAAATCA | GGTCATCTAT | AGTTGATATG | TTTATTTTCA | 780 |
| | TTGGTTAAT | TTTACATGGA | GAAAACCAAA | ATGATACTTA | CTGAACTGTG | TGTAATTGTT | 840 |
| 35 | CCTTTATTTT | TTTGGTACCT | ATTTGACTTA | CCATGGAGTT | AACATCATGA | ATTTATTGCA | 900 |
| | CATTGTTCAA | AAGGAACCCG | GAGGTTTTTT | TGTCAACATT | GTGATGTATA | TTCTTTTGAA | 960 |
| | GATAGTAACT | GTAGATGGAA | AAACTTGTGC | TATAAAGCTA | GATGCTTTCC | TAAATCAGAT | 1020 |
| | GTTTTGTGCA | AGTAGTTTGA | CTCAGTATAG | GTAGGGAGAT | ATTTAAGTAT | AAAATACAAC | 1080 |
| | AAAGGAAGTC | TAAATATTCA | GAATCTTTGT | TAAAGTCTGT | AAAGTAACCT | ATAATCTATA | 1140 |
| 40 | AACAATGAAA | TATTGCTGTA | TAGCTCCTTT | TGACCTTCAT | TTCAATGATA | GTTTTCCCTA | 1200 |
| | TTGAATCAGT | TTCCAATTAT | TTGACTTTAA | TTTATGTAA | TTGAACCTAT | GAAGCAATGG | 1260 |
| | ATATTGTGAC | TGTTTAAATG | TCTGTGATAC | AGAACTCTTA | AAAATGTTTT | TTATGTGTT | 1320 |
| | TTATAAAATC | AAGTTTTTAA | TGAAAGTGAG | GAAATAAAGT | TAAAGTTGTT | TTAAAAAATA | 1380 |
| | AAAAAAAAAA | | | | | | 1390 |
| 45 | Seq ID NO: 21 DNA sequence | | | | | | |
| | Nucleic Acid Accession #: NM_001898.1 | | | | | | |
| | Coding sequence: 57..482 | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| 50 | GGCTCTCACC | CTCCTCTCCT | GCAGCTCCAG | CTTTGTGCTC | TGCCCTGAG | GAGACCATGG | 60 |
| | CCCAGTATCT | GAGTACCCCT | CTGCTCCTGC | TGGCCACCTC | AGCTGTGGCC | CTGGCCTGGA | 120 |
| | GGCCCAAGGA | GGAGGATAGG | ATAATCCCGG | GTGGCATCTA | TAACGCAGAC | CTCAATGATG | 180 |
| | AGTGGGTACA | CGCTGCCCTT | CACCTCCGCA | TCAGCGAGTA | TAACAAGGCC | ACCAAGATG | 240 |
| 55 | ACTACTACAG | CGCTCCGCTG | CGGGTACTAA | GAGCCAGGCA | ACAGACCGTT | GGGGGGGTGA | 300 |
| | ATTACTTCTT | CGACGTAGAG | GTGGGCGGCA | CCATATGTAC | CAAGTCCCAG | CCCAACTTGG | 360 |
| | ACACCTGTGC | CTTCCATGAA | CAGCCAGAAC | TGCAGAAAGA | ACAGTTGTGC | TCTTTGAGA | 420 |
| | TCTACGAAGT | TCCTGGGAG | AACAGAAAGT | CCCTGGTGAA | ATCCAGGTGT | CAAGATCTCT | 480 |
| | AGGGATCTGT | GCCAGGCCAT | TCCGACCAGC | CACCAACCAC | TCCCACCCCT | TGTAGTGCTC | 540 |
| 60 | CCACCCCTGG | ACTGGTGGCC | CCCACCCCTG | GGGAGGCGCT | CCCATGTGCT | TGGCCCAAGA | 600 |
| | GACAGACAGA | GAAGGCTGCA | GGAGTCCCTT | GTTGCTCAGC | AGGGCGCTCT | GCCTCCCTC | 660 |
| | CTTCTCTCTT | GCTTCTAATA | GCCCTGGTAC | ATGGTACACA | CCCCCCCACC | TCTGCAATT | 720 |
| | AAACAGTAGC | ATCGCC | | | | | |
| 65 | Seq ID NO: 22 DNA sequence | | | | | | |
| | Nucleic Acid Accession #: NM_007231.1 | | | | | | |
| | Coding sequence: 89..2017 | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| 70 | TAGGAACAGG | GGAGAGTGCA | CCTGCTACCA | GTCAAGCTCA | GCCAGACTGC | AAGAGGAGGC | 60 |
| | GAGGCGGAGC | CAGCCGAGGG | AGTGAACCAT | GGACAAGTTG | AAATGCCCGA | GTTTCTTCAA | 120 |
| | GTGCAGGGAG | AAGGAGAAAG | TGTGGGCTTC | ATCAGAGAAT | TTCCATGTTG | GTGAAAATGA | 180 |
| | TGAGAATCAG | GACCGTGGTA | ACTGGTCCAA | AAAATGGGAT | TATCTTCTAT | CTATGATTGG | 240 |
| | ATACGCACTG | GGATTAGGAA | ATGTGTGGAG | ATTTCCATAT | CTGACCTACA | GCAATGGTGG | 300 |
| 75 | AGGCGCTTCT | TTGATACCTT | ATGCAATTAT | GTTAGCATTG | GCTGGTTTAC | CTTTGTTCTT | 360 |
| | TCTGGAGTGT | TCACTGGGAG | AATTTGCTAG | CTTAGGTCCA | GTTTCAGTTT | GGAGGATTCT | 420 |
| | TCCATTGTTT | CAAGGTGTGG | GAATTACAA | GGTCCTGATC | TCCATTTTGT | TGACAACTCA | 480 |
| | TTACAAATGTC | ATAATTGCTC | ATAGTCTTTA | CTACATGTTT | GCTTCTTTTC | AAAGTGAAC | 540 |
| | ACCATGGAAA | AATTTGTTCT | CGTGGTCAGA | TAAAAACTGT | AGCAGATCAC | CAATAGTAAC | 600 |
| 80 | TCACTGTAAT | GTGAGTACAG | TGAATAAAGG | AATACAAGAG | ATCATCCAAA | TGAATAAAGG | 660 |
| | CTGGGTAGAC | ATCAACAATT | TTACCTGCAT | CAACGGCAGT | GAAATTTATC | AGCCAGGGCA | 720 |
| | GCTTCCCAAT | GAAACAATAT | GGAATAAAGT | GGCGCTCCAA | CGGTCAAGTG | GAATGAATGA | 780 |
| | GACTCGAGTA | ATTGTTTGGT | ATTTAGCACT | TTGTCTTCTT | CTGGCTTGGC | TCATAGTTGG | 840 |
| | AGCAGCACTA | TTTAAAGGAA | TCAAATCGTC | TGGCAAGGTG | GTATATTTTA | CAGCTCTTTT | 900 |
| | CCCTATGTG | GTCCTACTCA | TCTGTTAGT | ACGAGGTGCA | ACTCTGGAGG | GTGCTTCAAA | 960 |

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AGGCATTTC TACTATATTG GAGCCCAGTC AAATTTTACA AAACCTAAGG AAGCTGAGGT 1020
ATGGAAGAGT GCTGCCACTC AGATATTTTA CTCCTTTTCA GTGGCTTGGG GTGGCTTAGT 1080
TGCTCTATCA TCTTACAATA AGTTCAAAAA CAACTGCTTC TCTGATGCCA TTGTGGTTTG 1140
TTTGACAAAC TGTCTCACTA GCGTGTGTTG TGGATTGCTT ATTTTCTCTA TATTGGGACA 1200
CATGGCCCAT ATATCTGGAA AGGAAGTTTC TCAAGTTGTA AAATCAGGTT TTGATTGGGC 1260
ATTCAATTGC TATCCAGAGG CTCTAGCCCA ACTCCCAGGT GGTCCATTTT GGTCCATATT 1320
ATTTTCTTTC ATGCTTTTAA CTTTGGGTCT CGATTCTCAG TTTGCTTCGA TTGAAACGAT 1380
CACAAACACA ATTCAGATT TATTTCCCAA AGTGATGAAG AAAATGAGGG TTCCCATAAC 1440
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TTACTGGGTT CATCTGATTG ACCACTTCTG TGCTGGATGG GGCATTTTAA TTGCAGCTAT 1560
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AATGATGATT GGAGCAAAGA GGTGGATATT CTGGCTATGG TGGAGAGCTT GCTGGTTTGT 1680
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TGCAATATAA AAATGTGAAT CTCTTAATTC TCAGCCATGT GCTTATTATA TTTCTTTTAA 2220
GATTGTCTAT GTGTATAACA CACACACACA CACCTAAGAG TCTCTATTTC ACAATTATAT 2280
TTTGTAAAT AGTATATGCA TTTTAAATAC ATTGGAGGCT TTTATTTGAA CTAATTTCTT 2340
AGAGAAATAG TATATTTTCT ATTACACAAG TTTAAAAATA TTATTAACCT GTATTTCTTT 2400
AATATACAA CTATCTTTTC CACAAATATG AGTGGGAAAT AAATCAGCAC ATTTGAAAGA 2460
AAGTGTAAAC ACTGAAGGCC TCACCTTAAT AGAAACGTGA TAAATATATG GACAAATGGA 2520
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TCGTGCAATT GTTACAGCTC ATGTTTCTTA TATGAACCTA GTCATTAAAT TCTTTTATAA 2640
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TTGAGTTTGT AGTACCTCTT TTCCCATATA CAATCTTCTT TCCTTAGGTA ATTTGGAAGA 2760
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GCTTTAATCA ATTCTAGCAT TTTATTAAGT TAATACAGGG CTGATAGAGT GATTTTGTCT 2940
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CAAACTGTGC AAGAATGAGA AAAGCCAAAT TAGAAAAATC TATGCTCTAG TTTCTTACC 3060
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CTTGTCTGTG TGCTGGGCTT GGAGTGCACT GGCATGATCT CAGCTCACTG CAACCTCTGC 3720
CTTCTGGAAT CAAGTGATTG TCCTGCCTCA GCCTCTTGAG TAGCTGGGAC TACAGGTGCC 3780
CGCCACCACA CCAGCTAATT TTTGTATTT TAGTAGAGGC GAAGTTTCCC CATGTTGGCC 3840
AGGCTGGTCT TGAACCTCCG ACCTCAAGTG ATCTGTCTAC CTCGGCTCTC TAAAGTGCTG 3900
AGATTACAGG GTGTAGCCAC CGTGCCCGGC CCATTCTAAG GGTTTTCTTT GAAGACAGGT 3960
CAATGCTGTT TAGTAAGTTT CAGGAGATTG TTAATCTCTC AGTTATACCA GATTTTATAA 4020
AATATTGAG AATAGATGGC TAACAAGAGG TTAGAAATAC TTTTCTTAA TTTTAACTCA 4080
CAGTATGTTA CATGCATCTT ACCACTACAT TTTGGTGCTA TTTAAGGTGT GCAATTTTCT 4140
ATAGGTGACT TTTGCAATTC AGGGAAGATT TGGGCATATT AAATGAAAGA ATATCTAATT 4200
GGGGAGGTG TGAAGGGAAA GAAATCTTT TCAAAAGCTG ACCACAAAGA GTAGTTAAAA 4260
GTTTGTGCTA CTATCTTAC AAGTGTGTAA AGCAGAGATT TCAACAGAGT GCTTGGCATA 4320
TTGTAGGGTG CTCAAATGGT GTTTTATTA TTATTACTCA GATTCCACAG TGGCAAGAAA 4380
CATCATTCTA CATAATGCAA AACATTTACA TCAAAATCCA CTTACTTAA TGCGAACTTG 4440
GAGATAATTT ATGTTATTGT ATTGTAAACC ATTAATGAAA ACTTTTTCAC AGTTGAGTGA 4500
AATTAAAACT ACTATATCTC

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Seq ID NO: 23 DNA sequence

Nucleic Acid Accession #: NM_006398.1

Coding sequence: 19..516

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1 11 21 31 41 51
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GGCCCCCTGT CTGCAGAGAT GGCTCCCAAT GCTTCTGCTC TCTGTGTGCA TGTCCGTTCC 60
GAGGAATGGG ATTTAATGAC CTTTGATGCC AACCCATATG ACAGCGTGAA AAAAATCAAA 120
GAACATGTCC GGTCTAAGAC CAAGGTTTCT GTGCAGGACC AGGTTCTTTT GCTGGGCTCC 180
AAGATCTTAA AGCCACGGAG AAGCCTCTCA TCTTATGGCA TTGACAAAGA GAAGACCATC 240
CACCTTACCC TGAAGTGGT GAAGCCCACT GATGAGGAGC TGCCCTTGTT TCTTGTGGAG 300
TCAGGTGATG AGGCAGAGAG GCACCTCCTC CAGGTGCGAA GGTCCAGCTC AGTGGCACA 360
GTGAAGCAA TGATCGAGAC TAAGACGGGT ATAATCCCTG AGACCCAGAT TGTGACTTGC 420
AATGGAAGA GACTGGAAGA TGGGAAGATG ATGGCAGATT ACGGCATCAG AAAGGGCAAC 480
TTACTCTTCC TGGCATCTTA TTGTATTGGA GGGTGACCAC CCTGGGATG GGGTGTGGC 540
AGGGGTCAA AAGCTTATTT CTTTAACTCT CTTACTCAAC GAACACATCT TCTGATGATT 600
TCCCAAAATT AATGAGAATG AGATGAGTAG AGTAAGATT GGGTGGGATG GGTAGGATGA 660
AGTATATTGC CCAACTCTAT GTTCTTTTGA TTCTAACACA ATTAATTAAG TGACATGATT 720
TTTACTAATG TATTACTGAG ACTAGTAAAT AAATTTTAA GGCAAAATAG AGCATTTC

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Seq ID NO: 24 DNA sequence

Nucleic Acid Accession #: XM_094741.1

Coding sequence: 1..948

1 11 21 31 41 51

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| | 1 | 11 | 21 | 31 | 41 | 51 | |
| | ATGAAGGCCA | ACTACAGCGC | AGAGGAGCGC | TTTCTCCTGC | TGGGTTTCTC | CGACTGGCCT | 60 |
| | TCCCTGCAGC | CGGTCTCTTT | CGCCCTTGTC | CTCCTGTGCT | ACCTCCTGAC | CTTGACGGGC | 120 |
| 5 | AACTCGGCGC | TGGTGTCTGT | GGCGGTGCGC | GACCGCGGCC | TGCACACGCC | CATGTACTAC | 180 |
| | TTCTCTTGCC | ACCTGGCCTT | GGTAGACGCG | GGCTTCACTA | CTAGCGTGGT | GCGCGCGCTG | 240 |
| | CTGGCCAACC | TGCGGGGACC | AGCGCTCTGG | CTGCCGCGCA | GCCACTGCAC | GGCCCACTG | 300 |
| | TGCGCATCGC | TGGTCTGGG | TTGGGCGGAA | TGGTCTCTCC | TGGCGGTGAT | GGCTCTGGAC | 360 |
| | CGCGGGGCGC | CAGTGTGCGC | CCGCTGCGC | TATGCGGGGC | TGCTCTCCCC | GCGCTATGT | 420 |
| 10 | CGCAGCTGG | CCAGCGCCTC | CTGGCTAAGC | GGCCTCACCA | ACTCGGTTGC | GCAAAACCGC | 480 |
| | CTCTTGGCTG | AGCGGCGCCT | GTGCGCGCCC | CGCCTGTGG | ACCACTTCAT | CTGTAGAGCTG | 540 |
| | CGCGGCTTGC | TCAAAGCTGG | CTGCGGAGGC | GAACGAGACA | CTACCGAGAA | CCAGATGTTT | 600 |
| | GCGCGCCGCG | TGGTCTATCT | GCTGCTGCGG | TTTGGCGTCA | TCTTGGCCTC | CTACGGTGCC | 660 |
| | GTGGCCCGAG | CTGTCTGTTC | CATGCGTTT | AGCGGAGGCC | GGAGGAGGGC | GGTGGCCACG | 720 |
| 15 | TGTGGGTCCC | ACCTGACAGC | CGTCTGCTGG | TTCTACGGCT | CGGCCATCTA | CACCTACCTG | 780 |
| | CAGCCCGCGC | AGCGCTACAA | CCAGGCACGG | GGCAAGTTTG | TATCGCTCTT | CTACACCGTG | 840 |
| | GTCAACACTG | CTCTCAACCC | GCTCATCTAC | ACCCTCAGGA | ATAAGAAAGT | GAAGGGGGCA | 900 |
| | GCGAGGAGGC | TGCTGCGGAG | TCTGGGAGAG | GGCCAGGCTG | GGCAGTGA | | |
| 20 | Seq ID NO: 25 DNA Sequence | | | | | | |
| | Nucleic Acid Accession #: NM_018685.1 | | | | | | |
| | Coding sequence: 156..3533 | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| 25 | CTGGAAGCCG | AGAGGAGAGG | ACAGCTGGTT | GTGGGAGAGT | TCCCCCGCCT | CAGACTCCTG | 60 |
| | GTTTTTTTCA | GGAGACACAC | TGAGCTGAGA | CTCACTTTTC | TCTTCTTGAA | TTTGAACCTC | 120 |
| | CGTTTCCATC | GTCTCGTAGT | CCGACGCTTG | GGGCGATGGA | TCCGTTTACG | GAGAAACTGC | 180 |
| | TGGAGCGAAC | CCGTGCCAGG | CGAGAGAATC | TTAGAGAGAA | AATGGCTGAG | AGGCCACAG | 240 |
| | CAGCTCCAAG | GTCTATGACT | CATGCTAAGC | GAGCTAGACA | GCCACTTTCA | GAAGCAAGTA | 300 |
| 30 | ACCAGCAGCC | CTCTCTCGTT | GGTGAAGAGA | AATCTTGATC | AAAACCATCG | CCATCAAAAA | 360 |
| | AACGCTGTTT | TGACAACACT | GAAGTAGAAG | TTTCTAACTT | GGAAAAATAA | CAACCAAGTTG | 420 |
| | AGTGACATCT | TGCAAAATCT | TGTTCTCCAA | GTCTGTGTGC | TCTCAGGTG | CAGCCACAAG | 480 |
| | CAGCAGATAC | CATCAGTGAT | TCTGTTGCTG | TCCCGGCATC | ACTGCTGGGC | ATGAGGAGAG | 540 |
| | GGCTGAACCT | AAGATTGGAA | GCAACTGCAG | CCTCTCTCAGT | TAAACACAGT | ATGCAAAAC | 600 |
| 35 | TTGCAGAGCA | AGCGCGCCTG | TGGGATAATG | ATGATATGAC | AGATGACATT | CCTGAAAGCT | 660 |
| | CACCTCTTCT | ACCAATGCCA | TCAGAGGAAA | AGGCTGCTTC | CCCTCCCAAA | CCTCTGCTTT | 720 |
| | CAAAATGCCT | GCCAACTCCA | GTTGGCAGAA | GGGGCGGTCT | GGCCAATCTT | GCTGCAACTA | 780 |
| | TTTGCTCCTG | GGAAGATGAT | GTAAATCACT | CATTGTGCAA | ACAAAACAGT | GTACAAGAAC | 840 |
| | AGCCTGGTAT | CGCTTGTGTT | TCCAAATTTT | CCTCTGCAAG | TGGAGCATCT | GCTAGGATCA | 900 |
| 40 | ATAGCAGCAG | TGTTAAGCAG | GAAGCTACAT | TCTGTTCCCA | AAGGGATGGC | GATGCCTCTT | 960 |
| | TGAATAAAGC | CCATCTCTCA | AGTGCTGATG | ATGCGTCTTT | GGTTAATGCC | TCAATTTCCA | 1020 |
| | GCTCTGTGAA | AGCTACTTCT | TCTCCAGTGA | AATCTACTAC | ATCTATCACT | GATGCTAAAA | 1080 |
| | GTTGTGAGGG | ACAAATCTCT | GAGCTACTTC | CAAAAACCTCC | TATTAGTCCT | CTGAAAACGG | 1140 |
| | GGGTATCGAA | ACCAATTGTG | AAGTCAACTT | TATCCCAGAC | AGTTCATCC | AAGGGAGAAT | 1200 |
| 45 | TAAGTAGAGA | AATTTGTCTG | CAATCTCAAT | CTAAAGACAA | ATCTACGACA | CCAGGAGGAA | 1260 |
| | CAGGAATTAA | GCCTTTCTCT | GAAAGCTTTG | GAGAGCGTTG | TCAAGAACAT | AGCAAAAGAA | 1320 |
| | GTCCAGCTCG | TAGCAGACCC | CACAGAACCC | CCATTATTAC | TCCAAATACA | AAGGCCATCC | 1380 |
| | AAGAAAGATT | ATTCAAGCAA | GACACATCTT | CATCTACTAC | CCATTAGACA | CAACAGCTCA | 1440 |
| | AGCAGGAAGC | TCAAAAGAA | CTAGCATGTC | TTCTGGGCGG | ATTTGACAAG | GGCAATATAT | 1500 |
| 50 | GGAGTCAGCA | AAAAGCGGCA | AACTCAAAAA | GCAAAACAACT | AGAAACCAAA | CAGGAACTC | 1560 |
| | ACTGTGAGAG | CACCTCCCTC | AAAAAACACC | AAGGTGTTTC | AAAAACTCAG | TCACTTCCAG | 1620 |
| | TAACAGAAAA | GGTGACGAAA | AACAGATAC | CAGCAAAAAA | TTCTAGTACA | GAACCTAAAG | 1680 |
| | GTTTCACTGA | ATGCGAAATG | ACGAAATCTA | GCCCTTTGAA | AATAACATTG | TTTTTAGAAG | 1740 |
| | AGGACAAATC | CTTAAAGATA | ACATCAGACC | CAAAGGTGTA | GCAGAAATTT | GAAGTGATAC | 1800 |
| 55 | GTGAAATGGA | GATGAGTGTG | GATGATGATG | ATATCAATAG | TTGAAAGATA | ATTAATGACC | 1860 |
| | TCTTCAGTGA | TGTCCTAGAG | GAAGGTGAAC | TAGATATGGA | GAAGAGCCAA | GAGGAGATGG | 1920 |
| | ATCAAGCAAT | AGCAGAAAGC | AGGAAGATGC | ACTGAATATC | TCCTCAATGT | | 1980 |
| | CTTTACTTGC | ACCATGGGCA | CAAACAGTTG | GTGTGGTAAG | TCCAGAGAGT | TTAGTGTTCA | 2040 |
| | CACCTAGACT | GGAAATGAAA | GACACCAGCA | GAAGTGATGA | AAGTCCAAAA | CCAGGAAAAA | 2100 |
| 60 | TCCAAAGAAC | TGCTGTCCTC | CGAGCTGAAT | CTGGTGATAG | CCTTGGTTCT | GAAGATCGTG | 2160 |
| | ATCTTCTTTA | CAGCATTGAT | GCATATAGAT | CTCAAGATT | CAAGAAACAA | GAACGTCCTA | 2220 |
| | CAATAAAGCA | GGTGATTGTT | CGGAAGGAAG | ATGTTACTTC | AAAACTGGAT | GAAAAAAATA | 2280 |
| | ATGCCTTTCC | TTGTCAAGTT | AATATCAAAC | AGAAAAAGCA | GGAATCAAT | AACGAAATAA | 2340 |
| | ATATGCAACA | GACAGTGATC | TATCAAGCTA | GCCAGGCTCT | TAACTGCTGT | GTGTATGAAG | 2400 |
| 65 | AACATGGAAA | AGGGTCCCTA | GAAGAAGCTG | AAGCAGAAAG | ACTTCTTCTA | ATTGCAACTG | 2460 |
| | GGAAGAGAAC | ACTTTTGATT | GATGAATTGA | ATAAATTGAA | GAACGAAGGA | CCTCAGAGGA | 2520 |
| | AGAATAAGGC | TAGTCCCAAA | AGTGAATTTA | TGCCATCCAA | AGGATCAGTT | ACTTTGTGAG | 2580 |
| | AAATCCGCTT | GCCTCTAAAA | GCAGATTTTG | TCTGCAGTAC | GGTTCAGAAA | CCAGATGCAG | 2640 |
| | CAAAATTAATA | TTACTTAATTT | ATACTAAAAG | CAGGAGCTGA | AAATATGSTA | GCCACACCAT | 2700 |
| 70 | TAGCAAGTAC | TTCAAACTCT | CTTAAACGGT | ATGCTCTGAC | ATTCATCTAC | ACATTTACTC | 2760 |
| | TGCAAGATGT | ATCCAAATGAC | TTTGAAATAA | ATATTGAAGT | TTACAGCTTG | GTGCAAAAGA | 2820 |
| | AAGATCCCTC | AGGCCTTGAT | AAGAAGAAAA | AAACATCCAA | GTCCAAGGCT | ATTACTCCAA | 2880 |
| | AGCGACTCCT | CACATCTATA | ACCACAAAAA | GCAACATTCA | TTCTTCAGTC | ATGGCCAGTC | 2940 |
| | CAGGAGGTCT | TAGTGCTGTG | CGAACCAGCA | ACTTCGCCCT | TGTTGGATCT | TACACATTAT | 3000 |
| 75 | CATTGTCTTC | AGTAGGAAAT | ACTAAGTTTG | TTCTGGACAA | GGTCCCTTTT | TTATCTTCTT | 3060 |
| | TGGAAGGTCA | TATTTATTTA | AAAATAAAAT | GTCAAGTGAA | TTCCAGTGTT | GAAGAAAGAG | 3120 |
| | GTTTTCTAAC | CATATTTGAA | GATGTTAGTG | GTTTGTGTGC | CTGSCATCGA | AGATGGTGTG | 3180 |
| | TTCTTTCTGG | AAACTGTATA | TCTTATTGGA | CTTATCCAGA | TGATGAGAAA | CGCAAGAAATC | 3240 |
| | CCATAGGAAG | GATAAATCTG | GCTAATTGTA | CCAGTCGTCA | GATAGAACCA | GCCACACAGG | 3300 |
| | AATTTTGTGC | AAGACGCAAC | ACTTTTGAAT | TAATTAAGTG | CCGACCACAA | AGAGAAGATG | 3360 |
| 80 | ACCGAGAGAC | TCTTGTGAGC | CAATGCAGGG | ACACACTCTG | TGTTACCAAG | AACTGCTGTG | 3420 |
| | CTGCAGATAC | TAAAGAAAGG | CGGATCTCTT | GGATGCAAAA | ACTCAATCAA | GTTCCTTGTG | 3480 |
| | ATATTTCGCT | TGGCAACCTT | GATGCTTGCT | ACAAACCTAT | TGGAAAGCCT | TAAACCGGGA | 3540 |
| | AATTTCCATG | CTATCTAGAG | GTTTGTGATG | TCACTTAAG | AAACACACTT | AAGAGCATCA | 3600 |
| | GATTTACTGA | TGCAATTTTA | TGCTTTAAGT | ACGAAAGGGT | TTGTGCCAAT | ATTCACTACG | 3660 |

| | | | | | | | |
|----|---------------------------------------|------------|------------|-------------|------------|-------------|------|
| | TATTATGCAG | TATTTATATC | TTTTGTATGT | AAAACTTTAA | CTGATTTCTG | TCATTTCATCA | 3720 |
| | ATGAGTAGAA | GTAAATACAT | TATAGTTGAT | TTTGCTAAAT | CTTAATTTAA | AAGCCTCATT | 3780 |
| | TTCTAGAA | TCTAATTATT | CAGTTATTCA | TGACAATATT | TTTTTAAAG | TAAGAAATTC | 3840 |
| | TGAGTTGTCT | TCTTGGAGCT | GTAGGTCTTG | AAGCAGCAAC | GTCTTTCAGG | GGTTGGAGAC | 3900 |
| 5 | AGAAACCCAT | TCTCCAATCT | CAGTAGTTTT | TTTCAAAGGC | TGTGATCATT | TATTGATCGT | 3960 |
| | GATATGACTT | GTACTAGGG | TACTGAAAA | AATGTCTAAG | GCCTTTACAG | AAACATTTTT | 4020 |
| | AGTAATGAGG | ATGAGAACTT | TTTCAAATAG | CAAAATATATA | TTGGCTTAAA | GCATGAGGCT | 4080 |
| | GTCTTCAGAA | AAGTGATGTG | GACATAGGAG | GCAATGTGTG | AGACTTGGGG | GTTCATATT | 4140 |
| | TTATATAGAA | GAGTTAATA | GCACATGGTT | TACATTTACT | CAGCTACTAT | ATATGCAGTG | 4200 |
| 10 | TGGTGACAT | TTTCACAGAA | TTCTGGCTTC | ATTAAGATCA | TTATTTTTCG | TGCGTAGCTT | 4260 |
| | ACAGACTTAG | CATATTAGTT | TTTTCTACTC | CTACAAGTGT | AAATGAAAA | ATCTTTATAT | 4320 |
| | TAAAAAGTA | AACTGTTATG | AAGCTGCTAT | GTACTAATAA | TACTTTGCTT | GCCAAAGTGT | 4380 |
| | TTGGGTTTGG | TTGTTGTTTG | TTTGTGTTT | TGTTTTGGT | TCATGAACAA | CAGTGTCTAG | 4440 |
| | AAACCCATT | TGAAAGTGA | AAATTATTA | GTACCTATC | ACCTTTAAAC | GCCTTTTTTT | 4500 |
| 15 | AAAAATTATA | AATATTGTAA | AGCAGGGTCT | CAACTTTTAA | ATACACTTTG | AACCTCTTCT | 4560 |
| | CTGAATTATT | AAAGTTCTTT | ATGACCTCAT | TTATAAACAC | TAAATTCGT | CACCTCCTGT | 4620 |
| | CATTTTATT | TTTATTCA | CAAAATGATT | TTTTCTGTG | CATATTATAA | AAATATATT | 4680 |
| | TATGAGCTCT | TACTCAAATA | AATACCTGTA | AATGCTAAAA | GG | | 4722 |
| 20 | Seq ID NO: 26 DNA Sequence | | | | | | |
| | Nucleic Acid Accession #: NM_018098.4 | | | | | | |
| | Coding sequence: 29..2680 | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| 25 | AGAGTGCTGA | TTTGAAGAA | TACAAATCAT | GGCTGAAAT | AGTGATTAA | CATCCACTAC | 60 |
| | GGGAGGACT | AGCTTGGCAG | ACTCTTCCAT | TTTTGATTCT | AAAGTTACTG | AGATTTCCAA | 120 |
| | GGAAACTTA | CTTATTGGAT | CTACTTCATA | TGTAGAAGAA | GAGATGCCTC | AGATTGAAAC | 180 |
| | AAGAGTGATA | TTGGTTCAAG | AAGCTGGA | ACAAGAAGAA | CTTATAAAG | CCTTAAAGGA | 240 |
| | CATTAAAGTG | GGCTTTGTAA | AGATGGAGTC | AGTGAAGAA | TTTGAAGGTT | TGGATTCTCC | 300 |
| 30 | GGAAATTGAA | AATGTATTGT | TAGTCACGGA | CTTTCAGGAT | TCTGTCTTTA | ATGACCTCTA | 360 |
| | CAAGGCTCAT | TGTAGAGTTA | TTGGACCCAC | AGTTGTATTA | AATTGTTTCA | AAAAAGGAGA | 420 |
| | GCCTTGGCA | TTTTCATGTC | GCCGTTGTA | TTGTACAAGT | ATGATGAATC | TAGTACTATG | 480 |
| | CTTTACTGGA | TTTAGGAAAA | AAGAAGAACT | AGTCAGGTTG | GTGACATTGG | TCCATCACAT | 540 |
| | GGGTGGAGTT | ATTGCGAAAG | ACTTTAAATC | AAAAGTTACA | CATTTGGTGG | CAAAATGTAC | 600 |
| 35 | ACAAAGGAGAA | AAATTTCAGG | TTGCTGTGAG | TCTAGTACT | CCAATTATGA | AGCCAGAAATG | 660 |
| | GATTATATAA | GCTTGGGAAA | GGCGGAATGA | ACAGGATTTT | TATGCAGCAG | TTGATGACTT | 720 |
| | TAGAAATGAA | TTTAAAGTTC | TCTCAATTCA | AGATTGTATT | TTAAGTTTCC | TGGGATTTTC | 780 |
| | AGATGAAGAG | AAAACCAATA | TGGAAGAAAT | GACTGAAATG | CAAGGAGGTA | AATATTTACC | 840 |
| | GCTTGGAGAT | GAAAGATGCA | CTCACCTTGT | AGTTGAAGAG | AATATAGTAA | AAGATCTTCC | 900 |
| 40 | CTTTGAACCT | TCAAAGAAAC | TTTATGTTGT | CAAGCAAGAG | TGGTTCTGGG | GAAGCATTCA | 960 |
| | AATGGATGCC | CGAGCTGGAG | AAACTATGTA | TTTATATGAA | AAGGCAATA | CTCTGAGCT | 1020 |
| | CAAGAATACA | GTGCTCAATG | TTTCTCTAAA | TACCCCTAAC | AGCAATCGCA | AACGACGTGG | 1080 |
| | TTTAAAGAA | ACACTTGCTC | AGCTTTCAAG | AGAGACAGAC | GTGTCACCAT | TCCACCCCG | 1140 |
| | TAAGCGCCCA | TCAGCTGAGC | ATTCCTTTTC | CATAGGGTCA | CTCCTAGATA | TCTCCAACAC | 1200 |
| 45 | ACCAGAGTCT | AGCATTAACT | ATGGAGACAC | CCCAAAGTCT | TGTACTAAGT | CTTCTAAAAG | 1260 |
| | CTCCACTCCA | GTTCCTTCAA | AGCAGTCAGC | AAGGTGGCAA | GTTCGAAAAG | AGCTTTATCA | 1320 |
| | AACTGAAAGT | AATTATGTTA | ATATATTGGC | AACAATTATT | CAGTATTTC | AAGTACCATT | 1380 |
| | GGAAAGGGAA | GGACAACGTG | GTGGACCTAT | CCTTGCAACA | GAGGAGATTA | AGACTATTTT | 1440 |
| | TGGTAGCATC | CCAGATATCT | TTGATGTACA | CACTAAGATA | AAGGATGATC | TTGAAGACCT | 1500 |
| 50 | TATAGTTAAT | TGGGATGAGA | GCAAAAGCAT | TGGTGACATT | TTTCTGAAAT | ATTCAAAAGA | 1560 |
| | TTTGGTAAAA | ACCTACCTCT | CCTTTGTAAA | CTTCTTTGAA | ATGAGCAAGG | AAACAATTAT | 1620 |
| | TAAATGTGAA | AAACAGAAAC | CAAGATTTC | TGCTTTTCTC | AAGATAAAC | AAGCAAAACC | 1680 |
| | AGAAATGTGA | CGGCAGAGCC | TTGTTGAATC | TCTTATCCGA | CCAGTACAGA | GGTTACCCAG | 1740 |
| | TGTTGCATTA | CTTTAAATG | ATCTTAAGAA | GCATACAGCT | GATGAAAATC | CAGACAAAAG | 1800 |
| 55 | CACCTTAGAA | AAAGCTATTG | GATCACTGAA | GGAAAGTAAT | ACGCATATTA | ATGAGGATAA | 1860 |
| | GAGAAAACA | GAGCTCAAA | AGCAAAATTT | TGATGTTGTT | TATGAAGTAG | ATGGATGCC | 1920 |
| | AGCTAATCTT | TTATCTTCTC | ACCGAAGCTT | AGTACAGCGG | GTGAAACAA | TTTCTCTAGG | 1980 |
| | TGAGCACCCC | TGTGACAGAG | GAGAACAAAT | AATCTCTTCT | CTCTTCAATG | ATTGCCCTAGA | 2040 |
| | GATAGCAAGA | AAACGGCACA | AGGTTATTGG | CACCTTTAGG | AGTCCTCATG | GCCAAACCCG | 2100 |
| 60 | ACCCCGAGCT | TCTCTTAAGC | ATATTCACT | AATGCCCTCT | TCTCAGATTA | AGAAGGTATT | 2160 |
| | GGACATAAGA | GAGACAGAAG | ATTGCCATAA | TGCTTTTGCC | TTGCTTGTA | GGCCACCAAC | 2220 |
| | AGAGCAGGCA | AATGTGCTAC | TCAGTTTCCA | GATGACATCA | GATGAACCTC | CAAAAGAAAA | 2280 |
| | CTGGCTAAAG | ATGCTGTGTC | GACATGTAGC | TAACACCATT | TGTAAGCAG | ATGCTGAGAA | 2340 |
| | TCTTATTTAT | ACTGCTGATC | CAGAATCCTT | TGAAGTAAAT | ACAAAAGATA | TGGACAGTAC | 2400 |
| 65 | ATTGAGTAGA | GCATCAAGAG | CAATAAAAAA | GACTTCAAAA | AAGGTTACAA | GAGCAATCTC | 2460 |
| | TTTCTCCAAA | ACTCCAAAAA | GAGCTCTTCG | AAGGGCTCTT | ATGACATCCC | ACGGCTCAGT | 2520 |
| | GGAGGGAAGA | AGTCTTCCA | GCAATGATAA | GCATGTAATG | AGTCGTCTTT | CTAGCACATC | 2580 |
| | ATCATTAGCA | GGTATCCCTT | CTCCCTCCCT | TGTCAGCCTT | CCTTCCTTCT | TTGAAAGGAG | 2640 |
| | AAGTCATACG | TAAAGTAGAT | CTACAATCA | TTGATATGA | AGCGTTACCA | AAATCTTAAA | 2700 |
| 70 | TTATAGAAT | GTATAGACAC | CTCATACTCA | ATAAGAAAC | TGACTTAAAT | GGTACTTGTA | 2760 |
| | ATTAGCACTT | GGTGAAGCT | GGAAGGAAGA | TAAATAACAC | TAAACTATGC | TATTGATTT | 2820 |
| | TTCTTCTTGA | AAGAGTAAGG | TTTACCTGTT | ACATTTTCAA | GTTAATTCAT | GTAAAAATG | 2880 |
| | ATAGTGAATT | TGATGTAATT | TATCTCTTGT | TTGAATCTGT | CATTCAAAGG | CCAATAATTT | 2940 |
| | AAGTTGCTAT | CAGCTGATAT | TAGTAGCTTT | GCAACCCGTA | TAGAGTAAAT | AAATTTTATG | 3000 |
| 75 | GGCGGGTGCC | AAATCTGCT | GTGAATCTAT | TTGTATAGTA | TCCATGAATG | AATTTATGGA | 3060 |
| | AATAGATATT | TGTGCAGCTC | AATTTATGCA | GAGATTAAT | GACATCATAA | TACTGGATGA | 3120 |
| | AAACTTGCA | AGAAATCTGA | TTAAATAGTG | GGTCTGTTTC | ACATGTGCAG | TTTGAAGTAT | 3180 |
| | TTAAATAACC | ACTCCTTTCA | CAGTTTATTT | TCTTCTCAAG | CGTTTTCAAG | ATCTAGCATG | 3240 |
| | TGGATTTTAA | AAGATTGGCC | CTCATTAACA | AGAATAACAT | TTAAAGGAGA | TTGTTTCAAA | 3300 |
| 80 | ATATTTTTCG | AAATTGAGAT | AAGGACAGAA | AGATTGAGAA | ACATTGTATA | TTTTGCAAAA | 3360 |
| | ACAAGATGTT | TGTAGCTGTT | TCAGAGAGAG | TACGGTATAT | TTATGGTAA | TTTATCCACT | 3420 |
| | AGCAAACTCT | GATTTAGTTT | GATAGTGTGT | GGAAATTTAT | TTTGAAGGAT | AAGACCATGG | 3480 |
| | GAAAAATTGG | GTAAAGACTG | TTTGTACCCT | TCATGAAATA | ATTCTGAAGT | TGCCATCAGT | 3540 |
| | TTTACTAATC | TCTGTGAAA | TGCATAGATA | TGCGCATGTT | CAACTTTTAA | TTTGGTCTT | 3600 |

5 ATAATTAAT GTAAATTTGA AATTCATTT GCTGTTTCAA AGTGTGATAT CTTTCACAAT 3660
 AGCCTTTTTT TAGTCAGTAA TTCAGAAATA TCAAGTTTAT ATGGATAAAT GCATTTTTAT 3720
 TTCCTATTTT TTTAGGGAGT GCTACAAATG TTTGTCACTT AAATTTCAAG TTTCTGTTTT 3780
 AATAGTTAAC TGACTATAGA TTGTTTTCTA TGCCATGTAT GTGCCACTTC TGAGAGTAGT 3840
 AAATGACTCT TTGCTACATT TTAAAAGCAA TTGTATTAGT AAGAACTTTG TAAATAAATA 3900
 CCTAAAACCC AAGTGT 3916

Seq ID NO: 27 DNA Sequence

Nucleic Acid Accession #: NM_002497.1

Coding sequence: 135..1472

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1 11 21 31 41 51
 | | | | |
 GGCACGAGTA GGGGTGGCGG GTCAGTGTCT CTCGGGGGCT TCTCCATCCA GGTCCCTGGA 60
 GTTCTTGCTC CTTGGAGCTC CGCACTTGGC GCGCAACCTG CGTGAGGCAG GCGCACTCTG 120
 GCGACTGGCC GGCCATGCTT TCCCGGGCTG AGGACTATGA AGTGTGTAC ACCATTGGCA 180
 CAGGCTCCTA CGGCCGCTGC CAGAAGATCC GGAGGAAGAG TGATGGCAAG ATATTAGTTT 240
 GGAAAGAACT TGACTATGGC TCCATGACAG AAGCTGAGAA ACAGATGCTT GTTCTGAAG 300
 TGAATTTGCT TCGTGAACCTG AAACATCCAA ACATCGTTCT TTAATATGAT CGGATTATTG 360
 ACCGGACCAA TACACACTG TACATTGTAA TGAATATTG TGAAGGAGGG GATCTGGCTA 420
 GTGTAATTAC AAAGGGAACC AAGGAAAGGC AATACTTAGA TGAAGAGTTT GTTCTCGAG 480
 TGATGACTCA GTTGACTCTG GCGCTGAAGG AATGCCACAG ACGAAGTGAT GGTGGTCATA 540
 CGGTATTGCA TCGGATCTT AAACAGCCA ATGTTTTCTT GGATGGCAAG CAAAACGTCA 600
 AGCTTGGAGA CTTTGGGCTA GCTAGAATAT TAAACCATGA CACGAGTTT GCAAAAACAT 660
 TTGTTGGCAC ACCTTATTAC ATGCTCTCTG AACAAATGAA TCGCATGTCC TACAATGAGA 720
 AATCAGATAT CTGGTCAATT GGCTGCTTGC TGTATGAGT ATGTGCATTA ATGCTCCAT 780
 TTACAGCTT TAGCCAGAAA GAACCTGCTG GGAATACTAG AGAAGGCAAA TTCAGGCGAA 840
 TTCCATACCG TTACTCTGAT GAATGAATG AAATTATTAC GAGGATGTTA AACTTAAAGG 900
 ATTACCATCG ACCTTCTGTT GAAGAAATTC TTGAGAACCC TTTAATAGCA GATTGGTTG 960
 CAGACGAGCA AAGAAGAAAT CTTGAGAGAA GAGGCGGACA ATTAGGAGAG CCAGAAAAAT 1020
 CGCAGGATTC CAGCCCTGTA TTGAGTGAGC TGAACCTGAA GGAATTCAG TTACAGGAGC 1080
 GAGAGCGAGC TCTCAAAGCA AGAGAAGAAA GATTGGAGCA GAAAGAACAG GAGCTTTGTG 1140
 TCGTGAGAG ACTAGCAGAG GACAACTGG CTAGAGCAGA AAATCTGTG AAGAAGTACA 1200
 GCTTGCTAAA GGAACGGAAG TTCTGTCTC TGGCAAGTAA TCCAGAACTT CTTAATCTTC 1260
 CATCTCAGT AATTAAGAAG AAAGTTCATT TCAGTGGGGA AAGTAAAGAG AACATCATGA 1320
 GGAGTGAGAA TTCTGAGAGT CAGCTCACAT CTAAGTCCAA GTGCAAGGAC CTGAAGAAAA 1380
 GGCTTCAAGC TGCCAGCTG CGGCTCAAG CCCTGTGAGA TATTGAGAAA AATTACCAAC 1440
 TGAAAGCAG ACAGATCCTG GGCATGGCT AGCCAGGTAG AGAGACACAG AGCTGTGTAC 1500
 AGGATGTAAT ATTACCAACC TTTAAGACT GATATTCAAA TGCTGTAGTG TTGAATACCT 1560
 GGCCCATGA GCCATGCCTT TCTGTATAGT ACACATGATA TTTGGAAAT GGTTTTACTG 1620
 TTCTTCAGCA ACTATTGTAC AAAATGTTCA CATTTAATTT TCTTTCTTC TTTTAAAGAA 1680
 ATATTATAAA AAGAATACTT TCTTGGTTGG GCTTTAATC CTGTGTGTGA TTAAGTAGT 1740
 GAACATGAGA TGTGACATTC TAAATCTTGG GAGAAAAAT AATATTAGGA AAAAATATT 1800
 TATGCAGGAA GAGTAGCACT CACTGAATAG TTTTAAATGA CTGAGTGGTA TGCTTACAAT 1860
 TGTCATGTCT AGATTTAAAT TTTAAGTCTG AGATTTTAAA TGTTTTGTAG CTTGAAAAAC 1920
 CCAGTTAGAT GCAATTTGGT CATTAAATACC ATGACATCTT GCTTATAAAT ATTCCATTCG 1980
 TCTGTAGTTC AAATCTGTTA GCTTTGTGAA AATTCATCAC TGTGATGTTT GTATTCTTTT 2040
 TTTTCTCTG TTTAACAGAA TATGAGCTGT CTGTCAATTA CTTACTTCTT TCCCACTAAA 2100
 TAAAGAATT CTTCACTTA 2119

Seq ID NO: 28 DNA Sequence

Nucleic Acid Accession #: Eos sequence

55
 60
 65
 70
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1 11 21 31 41 51
 | | | | |
 GGGAGCTACA ATGTTTGTG ATTATTCAT CTGATGTGAA AAAGGCAGTG AATTTAATAG 60
 AAAATAACTT CGTAGAGCAA AATCTCAGGT GTGTTTTTTT AGTGCCGAG TCTTGGATGA 120
 TGGGTTCTTA GAAGCTCTCA ACATCTCTTC TTAATTGGAG AAAGTGTAA GCCCCAAAGT 180
 AGCTGGAGCA GTACATCTTC AATTTTGTAC AAGAAAAACAG GAACCTGATT ACTTTGAGTG 240
 CTATTCTTCA GTTCTGCTT TCAATTGAGAA TGCAACAAAA GCCAAGTAGG CTGCTGTCAA 300
 CTCTTGCTNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN 360
 CTAGGAGTCT TTTCATCTTG AGTGAGTCT GCACAAATGA TCTTCAAAGC ATTTAGCCCA 420
 CCAGAGGAAT TCTCTGAAA TACCCAAAAT CCATCAGTAT CTTGAATCAT GCTGGATTTT 480
 GAAGATTTCT TAACAAGCCA TGTAAGGGGG GCTCTCTGGC CTTGAAATAG TGATGTTTTT 540
 TATACAGAAA GGAGAATGCA GAATGGTCAG ACTACCATGC ACTGTTAAAT TTGATTTCAA 600
 GAAATTACAG GAAAACTTTC CAAAGTTCCA TCTCACAGAA ATTATTTTAA CAAAGAATTC 660
 CAAGATAAGT TTAGTTTTAT GGAAGACTTT TATGTGGTTT TTACTCACTC TTACTCTCAG 720
 ACATCAACAG ATGATTACAT CACTTATTTA GCTAGTAAAT TTATTAATAT AAAAAGTCTG 780
 AGACATTTCA ATATCCACAT TGCTTACACC ATTAGGCATA GATTCAAGTG CAGCTATGAC 840
 AATTGAAAAA AAGCTGTTTT GTGATTTAAA GGTTTAAAT TCTCTAACCA AACTGCTTGA 900
 TCCAGATGCA GGACTGCAAA TGTTAATATT TGTCTCGAA GAACAATCAA ATAAGACTTA 960
 AGAGGAAAAG GAATGGCCAC AATCCACCTG AAATTTTTTT TTAAGAAAGTG TGCAGCTTAC 1020
 TAAATCAGAA TGAATAAGTA AGTACAAGAT TATAACAAAA ATGCAATCAA ACTTTTCTTA 1080
 AGCTTACCTA AAGTTATTTT ATCTGAAAAT TTCAAGCAAC TTTGTTCAAC ATTAATTTGA 1140
 CAATCTAAAC TAACAAGTCT TTTGAATTTA TGCAATGGTAG TAAACATTTT CTCTATTAAAC 1200
 TGTATTACCT AAGGCTAAAC CTAAAATTTT TAAGCAAAAT TAGAAAAATA GTCTTCACTC 1260
 ATCAAAAAAT AAAGTTTGTG ACATTTAGTA TTTTCCCAAG AAAAAAATAA GTCTTCACTC 1320
 AAAAAAATAA AGAGTCTGTG CAAAATGTCA CTAATAATTA ATTAGCACTA GAAATTATTT 1380
 CTAATAATCA AAAAAAATAA AAATTTGAGA TGGGTTTCCC AAGGAAAAACA CTCGCAATCA 1440
 AACACAAAAA ACAAGAGACA AAAAAGAATA GACAAAAAGA 1480

Seq ID NO: 29 DNA Sequence

Nucleic Acid Accession #: Eos sequence

1 11 21 31 41 51
 | | | | |
 TCCCTGCAGC TGTGTTTGA CAGGTCAATT ACCATGCTGT CCTCCAGGTT CAACAGTATG 60

5 GCTCCAAAGG ATGAAATTTT ATTCTGATTT TCTGGCTGAA GACTATTCTC TTTGTGTATG 120
 TCCACCACAG TTACTTTATC CTTTCATCTG TGGATGGGCA GGAACCTCCA AACTGTCCAA 180
 GGAGATAGTT CTGTTGTGAT TACTTCATTG AGAAATTTAA CTTATGAGCA GTTGAAAGGA 240
 ATGCAAGTTG CTGCAAAATC AGAATGAAGA GTGCAAAACG ASSRAGCTAC AATGTTTGT 300
 CATTATTCAC TCTGATGTGA AAAAGGCAGT GAATTTAATA GAAAAAATC TCGTAGAGYA 360
 AAATCTCAGG TGTGTTTITT TAGTGCCGCA GTCTTGGATG ATGGGTTCCT AGAAGCTCTC 420
 AAACATCTCT TCTTAATTGG AGAAAGTGTT AAGCCCCAAA GTAGCTGGAG CAGTACATCT 480
 TCAATTTTTC ACAAGAAAGC AGGAACTTGA TTACTTTGAG TGCTATTCTAT TAGTTTCTGC 540
 10 TTTCAATTGAG AATGCAACAA AAGCCAATA GGTCTGCTGT AACTCCTTGC TGGACTTCTT 600
 CTGCCACTGT CACAGGAATC GTAATCTCAC TGGACAATTA ACTAGGGAGT CTTTCATCTT 660
 GAGTGACTGC TGCACAAATG ATCTTCAAGG CATTTTAGCC ACCAGAGGAA TTCTCTTGAA 720
 ATACCCAAAG TCCATCAGTA TCTTGAATCA TGCTGGATTT TGAAGAATTC TTAACAAGCC 780
 ATGTAAAGGG GGCTCTCTGG CCTTGAATA GTGATGTTTT TTATACAGAA AGGAGAATGC 840
 15 AGAATGGTCA GACTACCATG CACTGTTAAA TTTGATTTCA AGAAATTACA GGAAGAACTT 900
 CCAAGTTCCT ATCTCAGAGA AATTATTTTT ACAAGAATTT CCAAGATAAG TTTAGTTTAA 960
 TGGAGAGACT TTATGTGTTT TTTACTCACT CTTCATCTCA GACATCAACA GATGATTACA 1020
 TCACTTATTT AGCTAGTAAA TTTATTAATA TAAAAACTCA GAGACATTCC AATATCCACA 1080
 TTGCTTACAC CATTAGGCAT AGATTCACTG TCAGCTATGA CAATTGAAAA TAAGCTGTTT 1140
 20 TGTGATTTAA AGGTTTAAAT TTCTCTAACC AAAGTCTTGC ATCCAGATGC AGGACTGCAA 1200
 ATGTTAATAT TTGTTCTGGA AGAACAAATCA AATAAGACTT AAGAGGAAAA GGAATGGCCA 1260
 CAATCCACCT GAAAAATTTT TTTTAAAAAG TGTGCAGCCT ACTAAATCAG AATGAAAAATA 1320
 GAAGTACAGG ATTATAAACA AAATGCAATC AAACCTTTCT TAAGCTTACC TAAAGTTATT 1380
 TCATCTGAAA ATTTCAAGCA ACTTTGTCTA ACATTAAATT GACAATCTAA ACTAACAAGT 1440
 25 CTTTGAATT TATGCAATGT AGTAAACATT CTCTCTATTA ACTTTATTAC CTAAGGCTAA 1500
 ACCTAAATTT TTTAAGCAAA ATTAGAAAAA TAGTCTTCTC TCATCAAAAA ATAAAGTTTG 1560
 TTACATTAG TATTTTCCCA AT 1582

Seq ID NO: 30 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: ..817

30 1 11 21 31 41 51
 | | | | |
 AGATATATCA TACGAAAAATG AAAATTATAA TTCTTCTTGG ATTCTTGGGA GCCACATTGT 60
 35 CAGCCCCAGT TTACTTCTTA ATCTTAATAA TGGTCAACTT TTGCCACTAC AACTTCAGGG 120
 CCCACTTAAT TCATGGAATTC CACTTTCTC TGGAAATTTA CAACAGCAGC AGCAGGCTCA 180
 AATTCCAGGA CTCTCCCACT TCTCTTATC AGCTCTAGAC CAGTTTGCTG GACTGTCTCC 240
 AAATCAGATA CCCTTAAACAG GAGAGGCCAG TTTTGCCCAA GGAGCCCAAG CAGGCCAAGT 300
 TGATCCCTTA CAGCTTCAAA CACCGCCTCA GACACAACCA GGCCCCAGTC ACGTGATGCC 360
 40 CTATGTATTC TCCCTCAAAA TGCTCAAGA GCAAGGACAG ATGTTTCAAT ACTATCCAGT 420
 TTACATGGTC CTACCTCGGG ACAACCTCA GCAAAACAGT CCAAGGTCAC CTCACAAAC 480
 AAGACAGCAA CAGTATGAGG AGCAGATACC ATTCTATGCT CAATTGAGT ACATTCCACA 540
 ACTAGCAGAA CCTGCTATAT CAGGAGGACA GCAGCAACTA GCTTTGATC CCCAACTAGG 600
 CACAGCTCCT GAAATGCTG TGATGTCAAC AGGAGAAGAG ATACCATATT TACAAAAAGA 660
 45 AGCGATCAAC TTTAGACATG ACAGTGACAG AGTTTTCATG CCCTCAACTT CACCAAAACC 720
 CAGCACAAAC AATGTTTTCA CTTCTGCTGT AGACCAAACT ATTACCCAG AGCTCCCAAG 780
 AGAGAAGGAC AAGACTGACA GCCTAAGGGA ACCATAA 817

Seq ID NO: 31 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: ..917

50 1 11 21 31 41 51
 | | | | |
 AGAGAGGAAA AGAACACAGA TCTCGCATGG TTCAGATTTT TCTTTTATAG TCCAGGAGTA 60
 55 AGATATATCA TACGAAAAATG AAAATTATAA TTCTTCTTGG ATTCTTGGGA GCCACATTGT 120
 CAGCCCCAGT TATCCACAGC GCTCTCATGT CTGCCAGCAA TAGCAATGAG TTACTTCTTA 180
 ATCTTAATAA TGGTCAACTT TTGCCACTAC AACTTCAGGG CCCACTTAAT TCATGGATTC 240
 CACCTTCTC TGGAAATTTA CAACAGCAGC AGCAGGCTCA AATTCCAGGA CTCTCCCACT 300
 60 TCTCTTATC AGCTCTAGAC CAGTTTGCTG GACTGTCTCC AAATCAGATA CCCTTAACAG 360
 GAGAGGCCAG TTTTGCCCAA GGAGCCCAAG CAGGCCAAGT TGATCCCTTA CAGCTTCAAA 420
 CACCGCCTCA GACACAACCA GGCCCCAGTC ACGTGATGCC CTATGTATTC TCTTCAAAA 480
 TGCTCAAGA GCAAGGACAG ATGTTTCAAT ACTATCCAGT TTACATGGTC CTACCTCGGG 540
 65 AACAACTCA GCAACAGATT CCAAGGTCAC CTCACAAAC AAGACAGCAA CAGTATGAGG 600
 AGCAGATACC ATTCTATGCT CAATTGAGT ACATTCCACA ACTAGCAGAA CCTGCTATAT 660
 CAGGAGGACA GCAGCAACTA GCTTTGATC CCCAACTAGG CACAGCTCCT GAAATGCTG 720
 70 TGATGTCAAC AGGAGAAGAG ATACCATATT TACAAAAAGA AGCGATCAAC TTTAGACATG 780
 ACAGTGACAG AGTTTTCATG CCCTCAACTT CACCAAAACC CAGCACAAAC AATGTTTTCA 840
 CTTCTGCTGT AGACCAAACT ATTACCCAG AGCTCCCAAG AGAGAAGGAC AAGACTGACA 900
 GCCTAAGGGA ACCATAA 917

Seq ID NO: 32 DNA Sequence

Nucleic Acid Accession #: Eos sequence

70 1 11 21 31 41 51
 | | | | |
 TTTTITTTTT TTTTGTAGA GATGGGGTCT CACTTTGTTG CCCATGCTTT GGCTGCTCTT 60
 75 CAAGATTTAG CACTTCTGAG CTGTTGCTTT TGTCTCCAGT CTACCTCGAG CAGTTCCTTA 120
 GGTGTTTGAA GCAGAAGAAA GAGAAAAGAG GCTTAGGTTA TACTGCTTAG AACCTCCTCT 180
 TCAACTAACC TACCGACCCA CCTACCCATA AATCCATACC TACACACACA CCCCCTTCTCT 240
 TTCTCTGCC CTGGTTTTCG CTGCGCTGCT TTCAATTGCA CGTGTGTTGA GTATAGCCTT 300
 80 TGCTCTGCC TACTCAGCTC CTGGAAGTGA GGGTGAATTT GAGACCCAGA GGAATGGGAT 360
 TTACAGCTTC TTGCTTTCTT CTTGCTTGT CTAGAACTG AAGTACAAAT GGGAGAAGGC 420
 TTTGATGAAG GAAGACCCCC ATCCAAGAAC ATCTAGTTTT CAGGTGCCAT AACAGCAGAG 480
 CAAGTTCA 488

Seq ID NO: 33 DNA Sequence

Nucleic Acid Accession #: Eos sequence

| | 1 | 11 | 21 | 31 | 41 | 51 | |
|----|-------------|------------|-------------|------------|-------------|-------------|------|
| 5 | CTCCCAGAGT | GCTAGGATTA | CAGGCATGAG | CCACTGCTCC | CAGCCTTCCA | GAGGAATTTT | 60 |
| | AAGCCCATGT | CCAAACATTC | TGTTTGTATA | AATATATTCT | AAATTTTAAA | TAAATAGTTT | 120 |
| | CTACTTTTCT | GAACCTTATA | TTTTTCTTG | CTATAATGGA | TTTTCATAAT | CAGAAAAGAT | 180 |
| | TAAATTAGTA | ATCATGAATT | GCCTTCAATA | TTTGGCAGTA | AGTCAATGAA | ATAATAAGGC | 240 |
| | ACTTATATAC | CATCTTTGAC | ATCATTAAAA | GTATCAAATC | CCATTAACT | AAAACTTCTT | 300 |
| 10 | TAAGCATTTT | GAAGACAGAA | AATGTTTACA | TGTTTCTTTC | AGTTCTCTAG | GCTTTTGTGC | 360 |
| | TAATGATGCG | TGACTTAGGA | TAAGATTGGA | ATTAAGTGCC | CAGCTTGAAA | CATAATAATT | 420 |
| | TTTCTGTATA | AGCCACAGAT | CCTCTACCTC | CTTTGTGTTA | AAGCCTTTAT | ATGAAACAAT | 480 |
| | TAAGTAGAAG | CATTCAATAG | TGTGTCAATTA | ACTGTTTATA | CTAATAAATG | GATACAGCAC | 540 |
| | ATTTTCATGG | CCTGTAATGT | AGAACATACT | ATATAAGTT | CTCAGTTTGG | GGATGACTAG | 600 |
| 15 | GTITCTGGAA | GGAATAGAAT | GCTAAATCAA | TGGATGGCAT | TGGGCTGAGA | AACACTGCTG | 660 |
| | CTACTAATCA | GCCTTGAATG | TGTAATGTGA | ACATGCAAAA | GAGAACATGC | ATACACTCAA | 720 |
| | ATTGTIACAA | TGCTATAACT | GGAAGTTGAA | GGACTTGAAT | TTTTATATTG | TGCTATTGTT | 780 |
| | ATGTTTCTG | TAATGTGTTA | TATCTAAGGA | ATTTTGTAGG | TAATATAAAA | GAAAAAGAGA | 840 |
| | ATAATGAACA | ATGATGTAC | TGGAGGGTTT | TTACATTAAA | TTAGATCATT | TTTCTTCTTA | 900 |
| 20 | TTCAATAA | TAATCTTAAT | CTTTAAGAAT | TAATATAAT | TTAATATTAT | AATTCATAAT | 960 |
| | CTTTAAGAAT | TAATAATTAT | AATTTAATAT | TATAATTAAT | AATCTTTAAG | AATTAATAAT | 1020 |
| | ATAATTTAAT | ATTATAATTA | ATAATCTTTA | AGAATTAATA | ATTACAATTA | ATAATTAATA | 1080 |
| | ATAATCTTAA | TCTTTAAGAA | TTAATAATAA | TCCTTAATCG | CAATAATAAT | CGCAAGGAGG | 1140 |
| | AGAAGTAAAT | CCCTCTCTCT | TCTGTATGAA | CTTTTCTCCC | ACATGCTGCT | GTATGGTTTA | 1200 |
| 25 | GTGAGAGTGA | AGTTCTAAAG | AACATCAATA | TGATTGGTGG | GATAATCCAA | AGACATTTT | 1260 |
| | TCAGAAATCAA | ATGCAATGTC | GAAGGTTTGT | TTCTTGATCA | TGTATTACT | GGTCCACAGC | 1320 |
| | ACAAATATAA | GTGACCAAT | ATACATAGGA | AAGTTGAAT | TGTACACATA | CAGCATCTGA | 1380 |
| | AATGTATCTG | ATGTTACGCA | TCAAGATTTC | ACTGAACATT | GTAGAAATGT | GTATCTTTTG | 1440 |
| | CATGTATATT | TTACATTGAT | TTTCTATTTA | TGTACATCTA | GAAAGTTTAA | ACCCTAATAA | 1500 |
| 30 | ATAGTTTTGT | AATTTTGAAT | AATAGTGTCA | GTTTATATGT | GAGGGAGTAG | AGACAGAGAG | 1560 |
| | GTTAGCACTG | GATAATAATT | AGTAAGGCCA | AAGGAGAAAA | TTTCATAGAA | AATATTGTGT | 1620 |
| | TTGTCAATA | GAGTACAGCA | TGAAAGGCTT | CCTCTACAAG | ACACTAGTCA | AAGAGTTGAG | 1680 |
| | AGCTGCGGTT | TCTAATCTTT | GTCCATTACT | CCCTTACTCC | CTATGAGACT | GTGGACCTGT | 1740 |
| | CACITGGCCT | CTCTGGTCTT | CAGTTTTCTC | ACCAGTAAAA | CAAGGAACCT | GAACCAAAATG | 1800 |
| 35 | ACCTCTAGTG | TTCCCTTGG | GTTTAAATGT | CTATAAATGT | TCAATGACTA | GAATGTATTG | 1860 |
| | CGTTTTTCTT | TATTTCTTTT | GCTTTGAGAA | AAGAGAATGT | GATTTAAGAG | TAATAATTGT | 1920 |
| | AATACCAATT | ATCCACATTA | AAATTGTGTC | CTCTATGTGT | AAGGCATAGC | ACATTATAGCA | 1980 |
| | CACATACATA | AGCACACTAA | GCACCTTACA | AATATCTCTA | TTTATTCTTT | ACATAATCTT | 2040 |
| | TTGAAATGGA | TTATGTAATA | CACACTGTTT | TTGAACAATT | GGTGACTTCC | AGCTGTTTAA | 2100 |
| 40 | AACAACTAC | AGTATGCTGC | TTGAGTACTG | ACTTAGGAGG | TCAGCAATTGG | TTTCACTAGG | 2160 |
| | AGCTTCTCAA | AGCACGCTGC | CAACATGCT | CCAGTCTCAT | TGTCAAGGCC | TTAGACCAGG | 2220 |
| | CAATCAATTAC | GAGTATGCTG | CTTCAACTTC | AGCAGCAGCA | AAACGATCTG | GCGGGGCTT | 2280 |
| | GGTGAAACAG | ACTGCTGGGC | TGCACCACTA | GAATTTCTCA | TTCAGAGGGT | CTGGCCTGAT | 2340 |
| | CACITGCATT | TCTAATCACT | TCCAGGTGA | TGCAGATGTT | TCTGGTCCAG | GGACCCCAAT | 2400 |
| 45 | TTGAGAACCA | CTGTATTAAA | ATTTCTTTCA | TCTCTATAGA | AATGGAAAGA | TTTTTTATAA | 2460 |
| | GTCTCTAAT | TGCTTTAAG | ATAAATGAGA | TTTCACTTAA | TTCTGTTGGA | GAAATTTGTT | 2520 |
| | TAAAAATTTT | TGTAAGAAG | CGAAATCAC | TTTATGTTAA | GGCTCTATT | ATAGCAAGTG | 2580 |
| | AACTTTTTCA | GAGTTAATAA | AGGCTTACAA | AAATAATTTT | GACTGTGAAA | CTAATTAATA | 2640 |
| | TCTCTGTGTT | TCAATTAAG | CATAAACATA | TTTGAATAAA | AATAGGTTAA | CAATAATTGT | 2700 |
| 50 | GGACATGTAT | TCAGTATAAT | TTTAAGATAA | TTTACAAAA | TATATGTAAC | ATTGCAATTG | 2760 |
| | TTTCTGTAAA | ATATCTTCGG | AAAAAGCCTT | GTTTTCCCTA | GTGTGTTATT | TGTTGAATTT | 2820 |
| | CTTGTATAAT | GTATTTTTTT | CCATTGAAAA | AAATGTTTTT | AATCAATGTG | ATCAATACAG | 2880 |
| | CTATCTATAT | GCCTGCTTT | CACGTGA | | | | 2907 |

Seq ID NO: 34 DNA Sequence
Nucleic Acid Accession #: NM_003979.2
Coding sequence: 254..1357

| | 1 | 11 | 21 | 31 | 41 | 51 | |
|----|------------|-------------|-------------|------------|------------|------------|------|
| 60 | ATAACAGCAT | GAAGTGCCGT | GGAAGTGGAA | TAGGGGTGTC | CTCTCCCTCG | ACCCTCCCCC | 60 |
| | TCCTTGTCCT | TCTGCTCACC | CCTCGCTCGT | TCCCTCCCTC | CGGCGAGGGC | CGCCTTTATA | 120 |
| | ACAACTGTCT | AGAGTGGGAG | GGCGGGATAG | CTGTCCAAGG | TCTCCCCCAG | CAGTGAGGAG | 180 |
| | CTCGCTGCT | GCCTCTTGC | GCGCGGGAAG | CAGCACCAAG | TTCAACGGCA | ACGCTTGGC | 240 |
| | ACTAGGGTCC | AGAAATGGCTA | CAACAGTCCC | TGATGGTTGC | CGCAATGGCC | TGAAATCCAA | 300 |
| 65 | GTAATACAGA | CTTTGTGATA | AGGCTGAAGC | TTGGGGCATC | GTCTAGAAAA | CGGTGGCCAC | 360 |
| | AGCCGGGGTT | GTGACCTCGG | TGGCCTTCAT | GCTCACTCTC | CCGATCCTCG | CTCTCAAGGT | 420 |
| | GCAGGACTCC | AACAGGCGAA | AAATGCTGCC | TACTCAGTTT | CTCTTCTCTC | TGGGTGTGTT | 480 |
| | GGGCATCTTT | GGCCTCACTT | TGCTCTTTC | CATCTGCTTC | TCTTGCCTGC | TGGCTCATGC | 540 |
| | AGCTTCTTTC | CTCTTTGGGA | TGCTCTTTC | CATCTGCTTC | TCTTGCCTGC | TGGCTCATGC | 600 |
| 70 | TGTGAGCTG | ACCAAGCTCG | TCCGGGGGAG | GAAGCCCTTT | TCCCTGTGTT | TGATTTCTGG | 660 |
| | TCTGGCCGTG | GGCTTCAGCC | TAGTCCAGGA | TGTTATCGCT | ATTGAATATA | TTGTCTTGAC | 720 |
| | CATGAATAGG | ACCAACGTCA | ATGTCTTTTC | TGAGCTTTCC | GCTCCTCGTC | GCAATGAAGA | 780 |
| | CTTTGTCTCT | CTGCTCACTT | ACGTCTCTCT | CTTGATGGCG | CTGACCTTCC | TCAATGCTCT | 840 |
| | CTTCACTTTC | TGTGGTTTCT | TCAACGGGCTG | GAAGAGACAT | GGGGCCACCA | TCTACCTCAC | 900 |
| 75 | GATGCTCTCT | TCCATTGCCA | TCTGGGTGGC | CTGGATCACC | CTGCTCATGC | TTCTGACTT | 960 |
| | TGACCGCAGG | TGGSATGACA | CCATCCTCAG | CTCCGCTTGT | GCTGCCAATG | GCTGGGTGTT | 1020 |
| | CCTGTTGGCT | TATGTTAGTC | CCGAGTTTTG | GCTGCTCACA | AAGCAACGAA | ACCCCATGGA | 1080 |
| | TTATCTGTTT | GAGGATGCTT | TCTGTAAACC | TCAACTCGTG | AAGAAGAGCT | ATGGTGTGGA | 1140 |
| | GAACAGAGCC | TACTCTCAAG | AGGAAATCAC | TCAAGTTTTT | GAAGAGACAG | GGGACACGCT | 1200 |
| 80 | CTATGCCCCC | TATTCACAC | ATTTTCAGCT | GCAGAACACC | CCTCCCCCAA | AGGAATTCTC | 1260 |
| | CATCCACGG | CCCCACGCTT | GGCCGAGCCC | TTACAAAGAC | TATGAAGTAA | AGAAAGAGGG | 1320 |
| | CAGCTAACTC | TGTCCTGAGT | AGTGGGACAA | ATGCAGCCGG | GCGGCAGATC | TAGCGGGAGC | 1380 |
| | TCAAAGGGAT | GTGGGCGAAA | TCTTGAGTCT | TCTGAGAAAA | CTGTACAGA | CACATCGGGA | 1440 |
| | ACAGTTTGCC | TCCCTCCAG | CCTCAACCAC | AATTCTTCCA | TGCTGGGGCT | GATGTGGGCT | 1500 |
| | AGTAAGACTC | CAGTTCTTAG | AGGCGCTGTA | GTATTTTTTT | TTTTTTGTCT | CATCCTTTGG | 1560 |

| | | | | | | | |
|----|------------|------------|------------|------------|-------------|-------------|------|
| | ATACCTCTTT | TAAGTGGGAG | TCTCAGGCAA | CTCAAGTTTA | GACCCCTTACT | CTTTTTGTTT | 1620 |
| | GTITTTTGAA | ACAGGATCTT | GCTCTGTAC | CCAGGCTTGA | GTGCAGTGGT | GCGATCACAG | 1680 |
| | CCAGTGCAG | CCTCGACCAC | CTGTGCTCAA | GCAATCCTCC | CATCTCCATC | TCCCAAAGTG | 1740 |
| | CTGGGATGAC | AGGCGTGAGC | CACAGCTCCC | AGCCTAGGCC | CTTAATCTTG | CTGTTATTTT | 1800 |
| 5 | CCATGGACTA | AAGGTCTGGT | CATCTGAGCT | CACGCTGGCT | CACACAGCTC | TAGGGGCCCTG | 1860 |
| | CTCCTCTAAC | TCACAGTGGG | TTTGTGAGG | CTCTGTGGCC | CAGAGCAGAC | CTGCATATCT | 1920 |
| | GAGCAAAAT | AGCAAAAGCC | TCTCTCAGCC | CACTGGCCTG | AATCTACACT | GGAAGCCAAAC | 1980 |
| | TGCTGGCAC | CCCCGCTCCC | CAACCCCTCT | TGCTGGGTA | GGAGAGGCTA | AAGATCACCC | 2040 |
| | TAAATTTACT | CATCTCTCTA | GTGCTGCCTC | ACATTGGGCC | TCAGCAGCTC | CCCAGCACCA | 2100 |
| 10 | ATTACAGAGT | CACCCCTCTC | TTCTTGCACT | GTCCCAAAAC | TTGCTGTCAA | TTCCGAGATC | 2160 |
| | TAATCTCCCC | CTACGCTCTG | CCAGGAATTC | TTTCAGACCT | CACCTAGCAC | AGCCCGGTG | 2220 |
| | CTCCTTGTC | AGAGAAATTG | TAGATCATTC | TCACCTCAAA | TTCTGGGGC | TGATACTTCT | 2280 |
| | CTCATCTTGC | ACCCCAACCT | CTGTAAATAG | ATTTACCGCA | TTTACGGCTG | CATTCTGTAA | 2340 |
| | GTGGGCATGG | TCTCTAATG | GAGGAGTGT | CATTGTATAA | TAAATTATTC | ACCTGAGTAT | 2400 |
| 15 | GCAATAAAG | TGTGTGGCC | ACTCTTCAT | GGTGGTGGA | GCAAAAAA | AAAAA | 2456 |

Seq ID NO: 35 DNA Sequence

Nucleic Acid Accession #: NM_032957.1

Coding sequence: 1..4203

| | | | | | | | |
|----|-------------|------------|-------------|------------|-------------|-------------|------|
| 20 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| | ATGCCCAAGA | TAGTCTGTAA | TGGTGTGACC | GTAGACTTCC | CTTCCAGGCC | CTACAAATGC | 60 |
| | CAACAGAGT | ACATGACCAA | GGTCTGTGAA | TGTCTGCAGC | AGAAGGTGAA | TGGCATCTCG | 120 |
| 25 | GAGAGCCCTA | CGGTACAGG | GAAGACGCTG | TGCTGTCTGT | GCACCACGCT | GGCCTGGCGA | 180 |
| | GAACACCTCC | GAGACGGCAT | CTCTGCCGCG | AAGATTGCOG | AGAGGGCGCA | AGGAGAGCTT | 240 |
| | TTCCCGGATC | GGGCTGTGTC | ATCTGGGGGC | AACGCTGCTG | CTGCTGTGGG | AGACCCCAATA | 300 |
| | GCTTGTCTACA | CGGACATCCC | AAAGATTATT | TACGCTTCCA | GGACCCCACTC | GCAACTCACA | 360 |
| | CAGGTCAATCA | ACGAGCTTCG | GAACACCTCC | TACCGGCTTA | AGGTGTGTGT | GCTGGGCTCC | 420 |
| 30 | CGGGAGCAGC | TGTGCATCCA | TCCTGAGGTG | AAGAAACAAG | AGAGTAACCA | TCTACAGATC | 480 |
| | CACCTTGTGCT | GTAAGAAGGT | GGCAAGTGGC | TCCTGTCTAT | TCTACAACAA | CGTAGAAGAA | 540 |
| | AAAAGCCTGG | AGCAGGAGCT | GGCCAGCCCC | ATCCTGGACA | TTGAGGAGCTT | GGTCAAGAGC | 600 |
| | GGAGGCAAGC | CACAGGTGTG | CCCTTACTAC | CTGTCCCGGA | ACCTGAAGCA | GCAAGCCGAC | 660 |
| | ATCATATTCA | TGCCGTACAA | TTACTTGTGT | GATGCCAAGA | GCCGAGAGC | ACACAACATT | 720 |
| | GACCTGAAGG | GGACAGTGGT | GATCTTTGAC | GAAGCTCACA | ACGTGGAGAA | GATGTGTGAA | 780 |
| 35 | GAATCGGCAT | CCTTTGAGCT | GACTCCCAT | GACCTGGCTT | CAGGACTGGA | CGTCATAGAC | 840 |
| | CAGGTGTCTG | AGGAGCAGAC | CAAGGCAGCG | CAGCAGGGTG | AGCCCCACCC | GGAGTTGAGC | 900 |
| | GGGACTCCCC | CCAGCCAGGG | GCTGAACATG | GAGCTGGAAG | ACATTGCAAA | GCTGAAGATG | 960 |
| | ATCCTGCTGC | GCCTGGAGGG | GGCCATCGAT | GCTGTTGAGC | TGCTGGAGAA | CGACAGCGGT | 1020 |
| 40 | GTCAACCAAGC | CAGGAGGCTA | CATCTTTGAG | CTGTTTGTCT | AAGCCAGAT | CAGTTTCAG | 1080 |
| | ACCAAGGGCT | GCACTCTGGA | CTCGCTGAGC | CAGATCATCC | AGCACCTGGC | AGGACGTGCT | 1140 |
| | GGAGTGTCTA | CCAACAAGGC | CGGACTGCAG | AAGCTGGGGG | ACATTATCCA | GATTGTGTTT | 1200 |
| | AGTGTGCAAC | CCTCCGAGGG | CAGCCCTGGT | TCCCAAGCAG | GGCTGGGGGC | CTTACAGTCC | 1260 |
| | TATAAGGTGC | ACATCCATCC | TGATGCTGGT | CACCGGAGGA | CGGCTCAGCG | GTCTGATGCC | 1320 |
| | TGGAGCACCA | CTGCAGCCAG | AAAGCGAGGG | AAGGTGCTGA | GCTACTGGTG | CTTCAGTCCC | 1380 |
| 45 | GGCCACAGCA | TGCACGAGCT | GGTCCGCGAG | GGCGTCCGCT | CCCTCATCCT | TACCAAGCGC | 1440 |
| | ACGCTGGCCC | CGGTGTCTTC | CTTTGCTCTG | GAGATGCAGA | TCCCTTTCCC | AGTCTGCCTG | 1500 |
| | GAGAAACCAAC | ACATCATCGA | CAAGCACCAAG | ATCTGGGTGG | GGGTGCTCCC | CAGAGGCCCC | 1560 |
| | GATGGAGGCC | AGTTGAGCTC | CGGTTTGAC | AGACGGTTTT | CCGAGGAGTG | CTTATCTCTC | 1620 |
| | CTGGGGGAAG | CTCTGGGCAA | CATCGCCCGC | GTGGTGGCCT | ATGGGTCTCT | GATCTTCTTC | 1680 |
| 50 | CCTTCTATC | CTGTCTATGA | GAAGAGCCTG | GAGTTCTGGC | GGGCGCGCGA | CTTGGCCAGC | 1740 |
| | AAGATGGAGG | CGCTGAAGCC | GCTGTTTGTG | GAGCCAGGGA | GCAAGAGGAG | CTTCTCGAG | 1800 |
| | ACCATCAGTG | CTTACTATGC | AAGGGTTGCC | GCCCTGGGT | CCACCGGCGC | CACCTTCTCT | 1860 |
| | GCGGTCTGCC | GGGGCAAGGC | CAGCGAGGGG | CTGGACTTCT | CAGACACGAA | TGGCCGTGGT | 1920 |
| 55 | GTGATTGTGA | CGGGCTCCCC | GTACCCCCCA | CGCATGGACC | CCCGGTTGCT | CCTCAAGATG | 1980 |
| | CAGTTCTCTG | ATGAGATGAA | GGGCCAGGGT | GGGCTGGGGG | GCCAGTTCTCT | CTCTGGGCAG | 2040 |
| | GAGTGGTACC | GGCAGCAGGC | GTCCAGGGCT | GTGAACCAAG | CCATCGGGCG | AGTATCCCGG | 2100 |
| | CACCGCCAGG | ACTACCGAGC | TGCTTCTCTC | TGTGACCACA | GGTTGCGCTT | TGCCGACGCA | 2160 |
| | AGAGCCCAAC | TGCCCTCTCT | GGTGCCTCCC | CAGCTCAGGG | TGTATGACAA | CTTTGGCCAT | 2220 |
| 60 | GTCTCCGAG | ACGTGGCCCA | GTTCTTCCGT | GTTCGCGAGC | GAACATATGCC | AGCGCCGGCC | 2280 |
| | CCCCGGGCTA | CAGCACCCAG | TGTGCGTGGG | GAAGATGCTG | TCAGCGAGGC | CAAGTCGCTC | 2340 |
| | GGCCCCCTCT | TCTCCACCAG | GAAGCTAAG | AGTCTGGACC | TGCATGTCCC | CAGCCTGAAG | 2400 |
| | CAGAGGTCTT | CAGGCTCACC | AGCTGCCGGG | GACCCGAGGA | GTAGCCTGTG | TGTGGAGTAT | 2460 |
| | GAGCAGGAGC | CAGTTCTTGC | CCGGCAGAGG | CCAGGGGGGC | TGCTGGCCGC | CCTGGAGCAC | 2520 |
| 65 | AGCGAACAGC | GGGCGGGGAG | CCCTGGCGAG | GAGCAGGCCC | ACAGCTGCTC | CACCTGTGCC | 2580 |
| | CTCCTGTCTG | AGAAGAGGCC | GGCAGAAGAA | CCGCGAGGAG | GGAGGAAGAA | GATCCGGCTG | 2640 |
| | GTCAAGCAAC | CGGAGGAGCC | CGTGGCTGGT | GCACAGACGG | ACAGGGCCAA | GCTCTTCATG | 2700 |
| | GTGGCCGTGA | AGCAGGAGTT | GAGCCAAGCC | AACCTTGCCA | CCTTCACCCA | GGCCCTGCAG | 2760 |
| | GACTACAAGG | GTCCGATGGA | CTTCGCGGCC | CTGGCCGCTC | GTCTCGGCCC | CCTCTTGTCT | 2820 |
| 70 | GAGGACCCCA | AGAAGACAAA | CCTGCTCCAA | GGCTTCTACC | AGTTTGTGCG | GCCTCCACAT | 2880 |
| | AAGCAGCAGT | TTGAGGAGGT | CTGTATCCAG | CTGACAGGAC | GAGGCTGTGG | CTATCGGCTC | 2940 |
| | GAGCAGCAGA | TTCCCGAAG | GCAGCGGGCA | CAGCCGGTCC | TGGACCCCAAC | TGGAAGAAAG | 3000 |
| | GCGCCGGATC | CCAAGCTGAC | CGTGTCCAGG | GCTGCAGCCC | AGCAGCTGGA | CCCCCAAGAG | 3060 |
| | CACCTGAACC | AGGGCAGGCC | CCACCTGTGC | CCAGGCCAAC | CCCCAACAGG | AGACCTTGGC | 3120 |
| | AGCCAAACAC | AGTGGGGGTC | TGGAGTGCCC | AGAGCAGGGA | AGCAGGGCCA | GCACCGCGTG | 3180 |
| 75 | AGCGCTTACC | TGGCTGATCG | CCGCAAGGCC | CTGGGGTCCG | CGGGCTGTAG | CCAACTCTTG | 3240 |
| | GCAGCGCTGA | CAGCCTATAA | GCAAGACGAC | GACCTCGACA | AGGTGCTGGC | TGTGTTGGCC | 3300 |
| | GCCTGTACCA | CTGCAAGGCC | AGAGGACTTC | CCCTCTGCTC | ACAGGTTTCT | CATGTTTGTG | 3360 |
| | CGTCCACACC | ACAAGCAGCG | CTTCTCACAG | ACGTGACACG | ACCTGACCCG | CCGGCCCTAC | 3420 |
| | CCGGGCTATG | AGCCACCGGG | ACCCCAAGGAG | GAGAGGCTTG | CCGTGCTCTC | TGTGCTTACC | 3480 |
| 80 | CACAGGGCTC | CCCAAGCAGG | CCCTCAAGG | TCCGAGAAGA | CCGGGAAGAG | CCAGAGCAAG | 3540 |
| | ATCTCGTCTC | TCCTTAGACA | GAGGCCAGCA | GGGAGCTGGG | GGGCGGGCGG | TGAGGATGCA | 3600 |
| | GGTCCAGAGC | AGTCTCTCAG | ACCTCCCCAC | GGGCTGTCAG | CATCTGAGTG | GGGTGAGCCT | 3660 |
| | CATGGGAGAG | ACATGCTCTG | GCAGCAGGCC | ACGGGAGGTC | CGGGCGGGCC | CCTCTCAGCA | 3720 |
| | GGCTGTGTGT | GCCAGGGCTG | TGGGGCAGAG | GACGTGGTGC | CCTTCCAGTG | CCCTGCTGCT | 3780 |

| | | | | | | | |
|----|------------|------------|------------|------------|------------|------------|------|
| 5 | GACTTCCAGC | GCTGCCAAGC | CTGCTGGCAA | CGGCACCTTC | AGGCCTCTAG | GATGTGCCCA | 3840 |
| | GCCTGCCACA | CCGCTCCAG | GAAGCAGAGC | GTCTATCAGG | TCTTCTGGCC | AGAGCCCCAC | 3900 |
| | AAGGACCATG | ATGGCCGTGG | AGGGGCCAGG | CCTGTGCTGG | CTGTGCTGGG | TGTTGGCGCT | 3960 |
| | GCCTGCCCTG | CTGCCGGTGC | CGCTGTACG | CGGAGTGGCA | GAAACACCCA | CCTACCCCTG | 4020 |
| | GCGGGAAGCA | GAGACAGGGG | AGCGGCTGGT | GTGTGCCCAG | TGCCCCCCAG | GCACCTTTGT | 4080 |
| | GCAGCGGCGG | TGCCGCGGAG | ACAGCCCCAC | GACGTGTGGC | CGGTGTCCAC | CGGCCCACTA | 4140 |
| | CACGCACTTC | TGGAACATCC | TGGAGCGCTG | CGCTACTGTC | AACGTCTCT | GCGGGGAGCG | 4200 |
| | TGAGGAGGAG | GCACGGGCTT | GCCACGCCAC | CCACAACCGT | GCCTGCGGCT | GCGCACCGGG | 4260 |
| 10 | CTTCTTGGCG | CACGCTGGTT | TCTGCTTGA | GCACGCATCG | TGTCCACCTG | GTGCCGGCGT | 4320 |
| | GATTGCCCGG | GGCACCACCA | GCCAGAACAC | GCAGTGCCAG | CGGTGCCCCC | CAGGCACCTT | 4380 |
| | CTCAGCCAGC | AGCTCCAGCT | CAGAGCAGTG | CCAGCCCCAC | CGCACTGCA | CGGCCCTGGG | 4440 |
| | CCTGGCCCTC | AATGTGCCAG | GCTCTTCTCT | CCATGACACC | CTGTGCACCA | GCTGCACTGG | 4500 |
| | CTTCCCCCTC | AGCACCAGGG | TACCAGGAGC | TGAGGAGTGT | GAGCGTGCCG | TCATCGACTT | 4560 |
| 15 | TGTGGCTTTC | CAGGACATCT | CCATCAAGAG | GCTGCAGCGG | CTGCTGCAGG | CCCTCGAGGC | 4620 |
| | CCCGGAGGGC | TGGGGTCCGA | CACCAAGGGC | GGGCCGCGCG | GCCTTGACAG | TGAAGCTGGG | 4680 |
| | TGCGCGGCTC | TGGGGGCTCC | TGGGGGCGCA | GGAAGGGGCG | CTGCTGGTGC | GGCTGCTGCA | 4740 |
| | GGCGCTGGCG | GTGGCCAGGA | TGCCCGGGCT | GGAGCGGAGC | GTCCGTGAGC | GCTTCTCTCC | 4800 |
| | TGTGCACTGA | TCTTGGCCCC | CTCTTATTTA | TCTACATCC | TGGCACCCCC | ACTTGCACTG | 4860 |
| 20 | AAAGAGGCTT | TTTTTTAAAT | AGAAGAAATG | AGGTTTCTTA | AAGCTTATTT | TTATAAAGCT | 4920 |
| | TTTTCATAAA | ACTGGTGTGA | GTTC | | | | 4945 |

Seq ID NO: 36 DNA Sequence

Nucleic Acid Accession #: NM_016434.1

Coding sequence: 828..4487

| | | | | | | | |
|----|------------|------------|------------|------------|-------------|------------|------|
| 25 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| | AGTCAGCCCT | GCTGCCAGCC | AGTGCAGGGT | GCTGGGGACT | CAGGAGAGGCC | CGCCGGGACC | 60 |
| | ACTGCGGGAC | AGTGAGCCGA | GCAGAAGCTG | GAACGCAGGA | GAGGAAGGAG | AGGGGGCGGT | 120 |
| 30 | CAGGGCTCTC | AGGAGCCGGG | TCCTGGGCAA | GGCGCAGCGG | TTTTCAAATT | TTACAGAAAG | 180 |
| | CGGTGCGCTC | ACACTCGAGC | AGTAAAAAGA | TGCTCTCTGG | GAGGAGGGCC | GTGCAGCTCT | 240 |
| | CGGGCAATAG | TGTGTGGCTC | GGCTTAGAGA | GGCGGTAGTG | GAACGCAGAC | CTGTGGTGGG | 300 |
| | GAATGACATC | AAGGGAGGAG | ACGGGCGGGA | CCCCAGATT | CTGCTGTGG | GCGATGGAAG | 360 |
| | TGAGGTTTAC | TGCCCAGCGG | AGCCGACAC | AGAAGCGCA | AAACGCCGTG | TAGGCTTGGG | 420 |
| 35 | GGAGCCGAG | AGCAGGCGGA | CCOCTCCGC | GGGGAAACAG | TTTCGCGCG | GAGCACAAAG | 480 |
| | CAACGGACCG | GAAGTGGGGG | CGGGAAGTGC | AGTGGGCTCA | GCGCGGAGCT | GCGCCCTCTG | 540 |
| | CCCGGAAAA | CTCTGAGCTC | GCTGACAGCT | GGGACCGGGT | GCGGCCCTC | GACTGGAGTC | 600 |
| | GGTTGAGTTC | CTGAGGGACC | CGGTTCTGG | AAGGTTCCGC | CGGAGACAA | GTGAGCAGTC | 660 |
| | TGTGCCATAG | GGATTCTCGA | AGAGAACAGC | GTTGTGTCCC | AGTGCAATG | CTCGCATCGC | 720 |
| 40 | TTACCAAGAG | TGCCCGAGAC | CCTAAGATGT | TGGAGTGGT | TTTTTCGCAC | AGACCCGAAT | 780 |
| | AGCCTGCCCC | TCAGCCACGC | TCTGTGCCCT | TCTGAGAAC | GGCTGATATG | CCCAAGATAG | 840 |
| | TCTCTGAATG | TGTGACCTGA | GACTTCCCTT | TCCAGCCCTA | CAATGCCAA | CAGGAGTACA | 900 |
| | TGACCAAGGT | CCTGGAATGT | CTGCAGCAGA | AGGTGAATGG | CATCTGGAG | AGCCCTACGG | 960 |
| | GTACAGGGAA | GACGCTGTGC | CTGCTGTGCA | CCACGCTGGC | CTGGGAGAA | CACCTCCGAG | 1020 |
| 45 | ACGGCATCTC | TGCCCGCAAG | ATTGCCGAGA | GGGCGCAAGG | AGAGCTTTTC | CCGATCGGG | 1080 |
| | CCTGTGATC | CTGGGGCAAC | GCTGCTGCTG | CTGCTGGAGA | CCCATAGCT | TGCTACACGG | 1140 |
| | ACATCCCAAA | GATTATTATC | GCCTCCAGGA | CCCACTCGCA | ACTCACACAG | GTATCAACG | 1200 |
| | AGCTTCGGAA | CACCTCTTAC | CGGCTTAAGG | TGTGTGTGCT | GGGCTCCCGG | GAGCAOCTGT | 1260 |
| | GCATCCATCC | TGAGGTGAAG | AAACAAGAGA | GTAACCATCT | ACAGATCCAC | TTGTGCCGTA | 1320 |
| 50 | AGAAGGTGGC | AAGTGCCTCC | TGTCTTTTCT | ACAACAACGT | AGAAGAAAAA | AGCCTGGAGC | 1380 |
| | AGGAGCTGGC | CAGCCCCATC | CTGGACATTG | AGGACTTGGT | CAAGAGCGGA | AGCAAGCACA | 1440 |
| | GGGTGTGCCC | TACTACCTG | TCCCGGAACC | TGAAGCAGCA | AGCCGACATC | ATATTCTATG | 1500 |
| | CGTACAATTA | CTTGTGTGAT | GCCAAAGAGC | GCAGAGCACA | CAACATTGAC | CTGAAGGGGA | 1560 |
| | CAGTGTGTAT | CTTTGACGAA | GCTCACAACG | TGGAGAAGAT | GTGTGAAGAA | TGGCATCCT | 1620 |
| 55 | TTGACCTGAC | TCCCCATGAC | CTGGCTTCAG | GACTGGAGCT | CATAGACCAG | GTGCTGGAGG | 1680 |
| | AGCAGACCAA | GGCAGCGCAG | CAGGGTGAGC | CCCAACCCGA | GTTGAGCGCG | GACTCCCCCA | 1740 |
| | CGCCAGGGCT | GAAATGAGAG | CTGGAAGACA | TTGCAAGCT | GAAGATGATC | CTGCTGCGCC | 1800 |
| | TGGAGGGGGC | CATCGATGCT | GTTGAGCTGC | CTGAGAGCGA | CAGCGGTGTC | ACCAAGCCAG | 1860 |
| | GGAGCTACAT | CTTTGAGCTG | TTTGCTGAAG | CCCAGATCAC | GTTTCAGACC | AAGGGCTGCA | 1920 |
| 60 | TCCTGGACTC | GCTGGACCAG | ATCATCCAGC | ACCTGGCAGG | ACGTGCTGGA | GTGTTACCCA | 1980 |
| | ACACGGCGCG | ACTGCAGAA | CTGGCGGACA | TTATCCAGAT | TGTGTTCAAT | GTGGACCCCT | 2040 |
| | CCGAGGGCGG | CCCTGGTTCC | CCAGCAGGGC | TGGGGGCCCT | ACAGTCTTAT | AAGGTGCACA | 2100 |
| | TCCATCTCTA | TGCTGGTTC | CGGAGGACGG | CTCAGCGGTC | TGATGCTGG | AGCACCCTG | 2160 |
| | CAGCCAGAAA | GCGAGGGAAG | GTGCTGAGCT | ACTGGTGTCT | CAGTCCCGGC | CACAGCATGC | 2220 |
| 65 | ACGAGCTGGT | CCGCCAGGGC | GTCCGCTCCC | TCATCCTTAC | CAGCGGCACG | CTGGCCCCGG | 2280 |
| | TGTCTCTCTT | TGCTCTGGAG | ATGCAGATCC | CTTTCCCACT | CTGCTGGAG | AACCCACACA | 2340 |
| | TCATCGACAA | GCACCAGATC | TGGGTGGGGG | TGCTCCCCAG | AGGCCCCGAT | GGAGCCCACT | 2400 |
| | TGAGCTCCGC | GTTTGACAGA | CGGTTTTCCG | AGGAGTGCTT | ATCCTCCCTG | GGGAAGGCTC | 2460 |
| | TGGGCAACAT | CGCCCGGCTG | GTGCCCTATG | GGCTCTCTAT | CTTCTTCCCT | TCCTATCCTG | 2520 |
| 70 | TCATGGAGAA | GAGCCTGGAG | TTCTGGCGGG | CCCGGACATT | GGCCAGGAAG | ATGGAGGCGC | 2580 |
| | TGAAGCCGCT | GTTTGTGGAG | CCAGGAGCA | AAGGCAGCTT | CTCCGAGACC | ATCAGTGCTT | 2640 |
| | ACTATGCAAG | GATTGCGGCC | CCTGGGTCCA | CGGGCGCCAC | CTTCTGGCG | GTCTGCGGGG | 2700 |
| | GCAAGGGCCG | CGAGGGGCTG | GACTTCTCAG | ACACGAATGG | CGGTGCTGTG | ATTGTACCGG | 2760 |
| | GCCTCCCGTA | CCCCCAGCG | ATGGACCCCC | GGGTTGTCTT | CAAGATGCAG | TTCTGGATG | 2820 |
| 75 | AGATGAAGGG | CCAGGGTGGG | GCTGGGGGCC | AGTTCTCTCT | TGGGCAGGAG | TGGTACCGGC | 2880 |
| | AGCAGGGCTG | CAGGGCTGTG | AACCAGGCCA | TGGGGCGAGT | GATCCGCGAC | CGCCAGGACT | 2940 |
| | GGTCACCAAG | CTTCTCTGT | GACCAAGGT | TGCTCTTTC | CGAAGCAAGA | GCCCACTGTC | 3000 |
| | CCTCTCTGGT | GCGTCCCGAC | GTGAGGCTGT | ATGACAACCT | TGGCATGTCT | ATCCGAGACG | 3060 |
| | TGGCCAGTGT | CTTCCGTGTT | GCCGAGCGAA | CTATGCCAGC | GCCGGCCCCC | CGGGCTACAG | 3120 |
| 80 | CACCCAGTGT | GCGTGGAGAA | GATGCTGTCA | GCGAGGCCAA | GTGCGCTGGC | CCCTTCTTCT | 3180 |
| | CCACCAGGAA | AGCTAAGAGT | CTGGACCTGC | ATGTCCCGAG | CCTGAAGCAG | AGGTCCTCAG | 3240 |
| | GGTCACCAAG | TGCCGGGGAG | CCCGAGAGTA | GCCTGTGTGT | GGAGTATGAG | CAGGAGCCAG | 3300 |
| | TTCTCTCCCG | GCAAGGGCCC | AGGGGGCTGC | TGGCCGCGCT | GGAGCACAGC | GAACAGCGGG | 3360 |
| | CGGGGAGCCC | TGGCGAGGAG | CAGGCCACCA | GCTGCTCCAC | CCTGTCCCTC | CTGTCTGAGA | 3420 |
| | AGAGGCCCGC | AGAAGAACC | CGAGGAGGGA | GGAAGAAGAT | CCGGCTGGTC | AGCCACCCGG | 3480 |

5 AGGAGCCCGT GGCTGGTGCA CAGACGGACA GGGCCAAGCT CTTTCATGGT GCCGTGAAGC 3540
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 CCGATGACTT CCGCGCCCTG GCGCCTCTGC TCGGCCCCCT CTTTGTCTGAG GACCCCAAGA 3660
 AGCACAACCT GCTCCAAGGC TTCTACAGT TTGTGGGGCC CCACATAAG CAGCAGTTTG 3720
 AGGAGGTCTG TATCCAGCTG ACAGGACGAG GCTGTGGCTA TCGGCTGAG CACAGCATT 3780
 CCGGAAGGCA GCGGGCAGAG CCGGTCCTGG ACCCACTGG AAGAAGCGCG CCGGATCCCA 3840
 AGCTGACCGT GTCCACGGCT GCAGCCAGC AGCTGGAGCC CCAAGAGCAC CTGAACCAAG 3900
 GCAGGCCCCA CTGTGCGCC AGGCCACCC CAACAGGAGA CCTGGCAGC CAACCAAGT 3960
 GGGGTCTGG AGTGCCCAAG GCAGGGAAGC AGGGCCAGCA GCGGTGAGC GCCTACTGG 4020
 10 CTGATGCCCG CAGGGCCCTG GGTTCGCGG GCTGTAGCCA ACTCTGGCA GCGCTGACAG 4080
 CCTATAAGCA AGACGACGAC CTGACAAGG TGCTGGCTGT GTTGGCCGCC CTGACCACTG 4140
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 AGCAGCGCTT CTACAGAGC TGACAGACC TGACGGCGG GCCCTACCG GGCATGGAGC 4260
 CACCGGAGC CCAGGAGGAG AGGCTTGGG TGCTCTGTG GCTTACCCAC AGGGCTCCCC 4320
 15 AACGAGGCC CTACGCGTCC GAGAAGACG GGAAGACCCA GAGCAAGAT TCGTCTCTCC 4380
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 TGCCACACCG CTCCAGGAA GCAGAGCTC ATGCAGGTCT TCTGGCCAGA GCCCAGTGA 4560
 GTGCCACCG AGGCCCCAG CACACCAAC GTGGCTTGAT CACTGCTGT TCCAGCTCTG 4620
 20 GTGGGCCAAG AACCCACCCA ACAGAAATAG CCAGCCCATG CCAGCCGGCT TGGCCCGCTG 4680
 CAGGCTCAG GCAGGCGGG CCCATGGTTG GTCTCTGCGG TGGGACCGGA TCTGGGCTGT 4740
 CCTCTGAGAA GCACTTCCCT ACCTTGGGGT CTGGGGTGGG TTTCTGGAA AGTGCTTCCC 4800
 CAGAACTTCC CTGGCTCTG GCTGTGAGT GGTGCCACAG GGGCACCCA GCTGAGCCCC 4860
 25 TCACCGGAAA GGAGGAGACC CCGTGGGCA CGTGTCCACT TTAATCAGG GACAGGGCT 4920
 CTCTAATAAA GCTGCTGGCA GTGCC 4946

Seq ID NO: 37 DNA Sequence
 Nucleic Acid Accession #: NM_015647.2
 Coding sequence: 246..1883

30 1 11 21 31 41 51
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 35 GGTTCGCTT TCGCAGCGA AGAGCCCAAC TGCCCTCTG GGTGCTGCC CAGCTCAGG 180
 TGTATGACAA CTTTGGCCAT GTCATCCGAG ACGTGGCCCA GTTCTTCCG GTTGGCGAGC 240
 GAACTATGCC AGCGCGGGC CCCCGGGCTA CAGCACCCAG TGTGCTGGA GAAATGCTG 300
 TCAGCGAGGC CAAGTGCCT GGCCTTCTT TCTCCACAG GAAAGCTAAG AGTCTGGACC 360
 TGCACTGCCC CAGCCTGAAG CAGAGTCTC CAGGCTCAC AGCTGCCGG GACCCGAGA 420
 40 GTAGCTGTG TGTGGAGTAT GAGCAGGAG CAGTTCTGC CCGCAGAGG CCCAGGGGC 480
 TGCTGGCCGC CTGTGGAGC AGCGAACAG GCGCGGGAG CCTTGGCGAG GAGCAGGCC 540
 ACAGCTGCTC CACCTGTCC CTCTGTCTG AGAAGAGGCC GGCAGAAAG CCGGAGGAG 600
 GGAGGAGAA GATCCGGCT GTACGCCAC CGAGGAGCC GGTGGCTGT GCACAGACG 660
 ACAGGCCCAA GCTCTTCAT GTGGCGTGA AGCAGGAGT GAGCCAAAG AACTTTGCCA 720
 45 CCTTACCCA GGCCTGCGA GACTACAAG GTTCCGATG CTTGCGCGC CTGCGCGCT 780
 GTCTGGCCGC CTTCTTGTG GAGGACCCA AGAAGCACAA CTTGCTCAA GGCTTCTAC 840
 AGTTTGTGG GCGCCACCA AAGCAGCAG TTGAGGAGT CTGTATCCAG CTGACGGGAC 900
 GAGGCTGTG CTATCGGCT GAGCACAGCA TCCCCGAAG GCAGCGGCA CAGCGGTCC 960
 TGGACCCAC TGGAGAAGC GCGCGGATC CCAAGCTGAC CGTGTCCAG GCTGCAGCCC 1020
 50 AGCAGCTGA CCCCCAAGAG CACTGAACC AGGGCAGGCC CCACCTGTG CCCAGGCCAC 1080
 CCCCACAGG AGACCTTGC AGCCAAACAC AGTGGGGTC TGGAGTGC CAGAGCAGGA 1140
 AGCAGGCCA GCAGCGCTG AGCGCTACC TGGCTGATG CCGCAGGGCC CTGGGCTCG 1200
 GCGGCTGTG CCAACTCTG CAGCGCTGA CAGCTTATA GCAAGACGAC GACCTGACA 1260
 AGGTGTGGC TGTGTGGCC GCCCTGACA CTGCAAGGC AGAGGACTT CCCCTGCTG 1320
 55 ACAGGTTAG CATGTTTGT GTTCCACAC ACAAGCAGC CTTCTCACAG ACGTGACAG 1380
 ACCTGACCG CCGGCCCTAC CCGGCTATG AGCCACCGG ACCCCAGGAG GAGAGGCTT 1440
 CCGTGCTCC TGTGCTTAC CACAGGCTC CCAACACAG CCCCTCACG TCCGAGAAGA 1500
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 60 CATCTGAGT GGTGTAGCT CATGGAGAG ACATCGTGG GCAGCAGGCC ACGGAGCTC 1680
 CCGGCGGGC CCTCTCAGA GGTGTGTGT GCCAGGGCTG TGGGCGAGG GACGTGTGT 1740
 CCTTCAGT CCGTGCCTG GACTTCCAG GCTGCCAAG CTGCTGGCA CCGCACCTT 1800
 AGGCCTTAG GATGTGCCA CGCTGCCCA CCGGAGGAG GAAGCAGAG GTCATGAGG 1860
 TCTTCTGGC AGAGCCCGC TGAGTGCCA CCGAGGGCCC CAGCACACC AACGTGGCT 1920
 65 GATCACTGC CTGTCCAGT CTGTTGGCC AAGAACCAC CCAACAGAA AGGCCAGCC 1980
 ATGCCAGCG GCTTGGCCG CTGCAGGCT CAGGCAGGC GGGCCCATG TTGGTCCCT 2040
 GGTGTGGAC GGTCTGGGC CTGCCTCTG GAAAGCTGA GCTACCTTG GGTCTGGGT 2100
 GGGTTTCTG GAAAGTCTT CCCAGAACT TCCCTGGCT CTGGCTGTG AGTGTGCCA 2160
 CAGGGGACC CCACTGAGC CCTCACCG GAAGGAGGAG ACCCCCGTG GCACGTGCT 2220
 70 ACTTTAATC AGGGGACAG GCTCTTAAT AAAGCTGCT GCAGTGCCA GGAACAAAA 2280
 AAAAAAA

Seq ID NO: 38 DNA Sequence
 Nucleic Acid Accession #: NM_003823.2
 Coding sequence: 101..1003

75 1 11 21 31 41 51
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 GTCCGCGCT AGCGCGCTC TCCCTGCTC AGCAAGGACC ATGAGGGCG TGGAGGGSC 120
 80 AGGCCTGTG CTGCTGTGC TGGTGTGGC GCTGCTGCC CTGCTGCCG TGCCGGCTGT 180
 ACGGAGTGT GCAGAAACAC CCACCTACC CTGGCGGAG GCAGAGACAG GGGAGCGGT 240
 GGTGTGCGC CAGTGCCCC CAGGCACCT TGTGCAGCG CCGTGCCGC GAGACAGCC 300
 CACGACGTG GGGCCGTGT CACGCGCCA CTACACGAG TTCTGGAAT ACCTGAGCG 360
 CTGCGCTAC TGCAACGTC TCTCGGGGA GGGTGAAGG GAGGCAGGC CTTGCCAGC 420
 CACCCACAC CGTGCTGCC GCTGCGCAC CGGCTTCTC GCGCACGCT GTTCTGCTT 480

5 GGAGCAGCGA TCGTGTCCAC CTGGTGCCGG CGTGATTGCC CCGGGCACCC CCAGCCAGAA 540
 CACGCACTGC CAGCCGTGCC CCCCAGGCAC CTCTCAGACC AGCAGCTCCA GCTCAGAGCA 600
 GTGCCAGCCC CACCGCAACT GCACGGCCCT GGGCTTGGCC CTCAATGTGC CAGGCTCTTC 660
 CTCCCATGAC ACCCTGTGCA CCAGCTGCAC TGGCTTCCCC CTCAGCACCA GGGTACCAGG 720
 AGCTGAGGAG TGTGAGCGTG CCGTCATCGA CTTTGTGGCT TTCCAGGACA TCTCCATCAA 780
 GAGGCTGCAG CCGCTGCTGC AGGCCCTCGA GGGCCCGGAG GGCTGGGGTC CGACACCAAG 840
 GCGCGGCGCG GCGGCTGTGC AGCTGAAGCT GCGTCGGGGG CTCACGGAGC TCTTGGGGGC 900
 GCAGGACGGG GCGCTGCTGG TCGGGCTGCT GCAGGCGCTG CCGCTGGCCA GGATGCCCGG 960
 10 GCTGGAGCGG AGCGTCCGTG AGCGCTTCTT CCTGTGTCAC TGATCCTGGC CCCCCTTTAT 1020
 TTATTCTACA TCTTGTGCAC CCCACTTGCA CTGAAAGAGG CTTTTTTTAA AATAGAAGAA 1080
 ATGAGGTTTC TTAAAGCTTA TTTTATAAAA GCTTTTTCAT AAAA 1124

Seq ID NO: 39 DNA Sequence

Nucleic Acid Accession #: NM_032945.1

Coding sequence: 435..1337

15 1 11 21 31 41 51
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 20 CTGACCACTG CAAAGCCAGA GGAATTCCTC CTGCTGCACA GGTTCAGCAT GTTTGTGGGT 60
 CCACACCACA AGCAGCGCTT CTCACAGACG TGCACAGACC TGACCGGCCG GCCCTACCCG 120
 GGCATGGAGC CACCGGGACC CCAGAGGAGG AGGCTTGGCG TGCCCTCCTGT GCTTACCCAC 180
 AGGGCTCCCC AACCAGGCCC CTCACGGTCC GAGAAGACCG GGAAGACCCA GAGCAAGATC 240
 TCGTCTCTCC TTAGACAGAG GCCAGCAGGG ACTGTGGGGG CCGGCGGTGA GGTGCGAGGT 300
 25 CCAAGCCAGT CCTCAGGACC TCCCCACGGG CCTGCAGCAT CTGAGTGGGG CCTCTAGGAT 360
 GTGCCACGCC TGCCACACCG CCTCCAGGAA GCAGAGCGTC ATGCAGGTCT TCTGGCCGGA 420
 GCCCCACAAG GACCATGAGG GCGCTGGAGG GCGCAGGCC CTGCTGCTGT TGCCCTGGTGT 480
 TGGCGCTGCC TGCCCTGCTG CCGGTGCCGG CTGTACGCGG AGTGGCAGAA ACACCCACCT 540
 ACCCTTGGGG GGAAGCAGAG ACAGGGGAGC GGCTGGTGTG GCGCCAGTGC CCCCCAGGCA 600
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 30 GCACTACACG GCACTTCTGG AACTACCTGG AGCGCTGCCG CTACTGCAAC GTCTCTGGCG 720
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 GCACCGGCTT GTTCCGCGAC GCTGGTTTCT GCTTGGAGCA GGCATCGTGT CCACCTGGTG 840
 CCGGCGTGTG TGCCCGGGGC ACCCCAGGCC AGAACACGCA GTGCCAGCGG TGCCCCCAG 900
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 35 CCTTGGGCTT GGCCTCAAT GTGCCAGGCT CTTCCTCCCA TGACACCCCTG TGCAACGACT 1020
 GCACTGGCTT CCCCCTCAGC ACCAGGGTAC CAGGAGCTGA GGAGTGTGAG CGTSCCGTCA 1080
 TCGACTTTGT GCTTTTCCAG GACATCTCCA TCAAGAGGCT GCAGCGGCTG CTGCGAGGCC 1140
 TCGAGGCCCC GGAGGGCTGG GGTCCGACAC CAAGGGCGGG CCGCGCGGCC TTGCGAGTGA 1200
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 40 TGCTGCAGGC GCTGCGGTGG GCCAGGATGC CCGGGCTGGA GCGGAGCGTC CGTGAGCGCT 1320
 TCCTCCCTGT GCACTGATCC TGGCCCCCTC TTATTTATTG TACATCCTTG GCACCCCACT 1380
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 ATAAAGCTTT TCCATAAAA 1459

Seq ID NO: 40 DNA Sequence

Nucleic Acid Accession #: NM_000593

Coding sequence: 165..2591

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 50 GGCACGAGGG TGTGCGTGTG GGAGAAAATT GGGCACCAGG GCTGCTCCCG AGATTCTCAG 60
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 CCAGCGCAGG ATCAGCCTGT TCTTGGGACT TTCCGAGAGC CCGCCCTCTG TTCCCTCCCC 240
 CAGCCGCGAG TAGGGGAGGA CTGGCGGTA CCGGAGCTT CAGGCCCCAC CCGGGCGGGG 300
 55 AGAGTCCAGC ACCCGGCGGG GACCGGGACG GCGTCCGAGT GCCAATGGCT AGCTCTAGGT 360
 GTCCCGCTCC CCGCGGTGTC CGCTGCCTCC CCGGAGCTTC TCTCGCATGG CTGGGGACAG 420
 TACTGCTACT TCTGCGCCAG TGGGTGCTGC TCCGGACCGC GCTGCCCGGC ATATTCTCCC 480
 TGCTGTGTGC CACCGCGCTG CCACTGCTCC GGGTCTGGGC GGTGGGCGCT AGCCGCTGGG 540
 CCGTGTCTTG GCTGGGGGCC TGCGGGGTCC TCAGGSCAAC GGTGGCTCC AAGAGCGAAA 600
 60 ACGCAGGTGC CAGGGCTGG CTGGCTGCTT TGAAGCCATT AGCTGCCGCA CTGGGCTTGG 660
 CCTGCGCGG ACTTGCTTGG TTCCGAGAGC TGATCTCATG GGGAGCCCCC GGGTCCGCGG 720
 ATAGCACCAG GCTACTGCAC TGGGGAAGTC ACCCTACCGC CTTCGTGTGC AGTTATGCAG 780
 CGGCACTGCC CGCAGCAGCC CTGTGGCACA AACTCGGAG CTCTGGGTG CCGGCGGCTC 840
 AGGGCGGCTC TGGAAACCTT GTGCGTGGCG TTCTAGGCTG CTGGGCTCG GAGACGCGCC 900
 65 GCCTCTCGCT GTTCTGTGTC CTGGTGGTCC TCTCTCTCT TGGGAGATG GCCATTCCAT 960
 TCTTTACGGG CCGCTCACT GACTGGATTG TACAAGATGG CTCAGCCGAT ACCTTCACTC 1020
 GAAACTTAAC TCTCATGTCC ATTCTACCA TAGCCAGTGC AGTGCTGGAG TTGCTGGGTG 1080
 ACGGGATCTA TAACAACACC ATGGGCCACG TGCACAGCCA CTTCAGGGA GAGGTGTTTG 1140
 GGGCTGTCTT GCGCCAGGAG ACGGAGTTT TCCAACAGAA CCAGACAGGT AACATCATGT 1200
 70 CTCGGGTAA CAGAGGACAG TCCACCTTGA GTGATTCTCT GAGTGAGAA CTGAGCTTAT 1260
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 CCCTCACCAT GGTCACTCTG ATCACCCTGC CTCTGCTTTT CCTTCTGCCC AAGAAGGTGG 1380
 GAAAAATGTA CCAGTTGCTG GAAGTGACAG TCGGGGAATC TCTGGCAAAG TCCAGCCAGG 1440
 TGGCATTGTA GGCTCTGTGG GCCATGCTCA CAGTTGGAAG CTTTGCACAC GAGGAGGGCG 1500
 75 AAGCCAGGAA GTTTAGGAAA AAGCTGCAAG AAATAAGAC ACTCAACCAG AAGGAGGCTG 1560
 TGGCCTATGC AGTCAACTCC TGGACCACTA GTATTTTCAGG TATGCTGCTG AAGTGGGAA 1620
 TCCTCTACAT TGGTGGGCGC CTGGTGACCA GTGGGGCTGT AAGCAGTGGG AACCTTGTCA 1680
 CATTTGTCTT CTACAGATG CAGTTTCAACC AGGCTGTGGA GGTACTGCTC TCCATCTACC 1740
 CCAGAGTACA GAAGGCTGTG GGCTCCTCAG AGAAAAATAT TGAGTACCTG GACCGCACCC 1800
 80 CTCGCTGCCC ACCCAGTGGT CTGTTGACTC CTTTACACTT GGAGGGCCTT GTCCAGTTCC 1860
 AAGATGTCTC CTTTGCCTAC CCAAAACCGC CAGATGTCTT AGTGCTACAG GGGCTGACAT 1920
 TCACCCTACG CCTTGGCGAG GTGACGGCGC TGGTGGGACC CAATGGGTCT GGGAGAGGCA 1980
 CAGTGGCTGC CTGCTGCAGC AATCTGTACC AGCCCAACCG GGGACAGCTG CTGTTGGATG 2040
 GGAAGCCCTT TCCCAATAT GAGCACCGCT ACCTGCACAG GCAGGTGGCT GCAGTGGGAC 2100
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5 AGCCAACTAT GGAGGAAATC ACAGCTGCTG CAGTAAAGTC TGGGGCCCAT AGTTTCATCT 2220
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 GTACGGGACA GGCAGTGGCG TTGGCCCGAG CATTGATCCG GAAACCGTGT GTACTTATCC 2340
 TGGATGATGC CACCATGTGC CTGGATGCAA ACAGCCAGTT ACAGGTGGAG CAGCTCCTGT 2400
 10 ACCGAAAGCCC TGAGCGGTAC TCCCGCTCAG TGCTTCTCAT CACCCAGCAC CTCAGCCTGG 2460
 TGGAGCAGGC TGACCAATC CTCTTTCTGG AAGGAGGCGC TATCCGGGAG GGGGGAACCC 2520
 ACCAGCAGCT CATGGAGAAA AAGGGGTGCT ACTGGGCCAT GGTGCAGGCT CCTGCAGATG 2580
 CTCCAGAAATG AAAGCCTTCT CAGACCTGCG CACTCCATCT CCTCCCTTT TCTTCTCTCT 2640
 GTGGTGGAGA ACCACAGCTG CAGAGTAGCA GCTGCCCA GAATGAGTTA CTGAAATTT 2700
 15 GCCTTGAGTG TGTTACCTCC TTTCCAAGCT CCTCGTGATA ATGCAGACTT CCTGGAGTAC 2760
 AAACACAGGA TTTGTAATTC CTACTGTAACT GGAGTTTAGA GCCAGGGCTG ATGCTTTGGT 2820
 GTGGCCAGCA CTCTGAAACT GAGAAATGTT CAGAAATGAC GGAAGATGA TCAGCTATTT 2880
 TCAACATAAC TGAAGGCATA TGCTGGCCCA TAAACACCT GTAGGTTCTT GATATTTATA 2940
 ATAAAAATGG TGTTTTGT 2958

Seq ID NO: 41 DNA Sequence
 Nucleic Acid Accession #: NM_002423.2
 Coding sequence: 48..851

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 GAGGCATGAG TGAGCTACAG TGGGAACAGG CTCAGGACTA TCTCAAGAGA TTTTATCTCT 180
 25 ATGACTCAGA AACAAAAAT GCCAACAGTT TAGAAGCCAA ACTCAAGGAG ATGCAAAAAAT 240
 TCTTTGGCCT ACCTATAACT GGAATGTTAA ACTCCGCGCT CATAGAAATA ATGCAGAAGC 300
 CCAGATGTGG AGTGCCAGAT GTTGACAGAT ACTCACTATT TCCAAATAGC CCAAAATGGA 360
 CTTCCAAAGT GGTCACTAC AGGATCGTAT CATATACTCG AGACTTACCG CATATTACAG 420
 TGGATGATTT AGTGTCAAAG GCTTTAAACA TGTGGGGCAA AGAGATCCCG CTGCATTTC 480
 30 GGAAAGTTGT ATGGGGAATC GCTGACATCA TGATTGGCTT TGGCGAGCA GCTCATGGGG 540
 ACTCCTACCC ATTTGATGGG CCAGGAAACA GGTGGCTCA TGCTTTGGG CCTGGGACAG 600
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 GGATTAACCT CCGTATGCT GCAACTCATG AACTTGGCCA TTTCTTGGGT ATGGGACATT 720
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 35 AACTTTCCCA GGATGATATT AAAGGCATT AGAACTATA TGGAAAGAGA AGTAATTC 840
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 TGTGTACAAA TCAGAAATGA TAAGCACTGT TCCTCCACTC CATTTAGCAA TTATGTCAAC 960
 CTTTTTATT GCAGTTGGTT TTTGAATGTC TTTCACTCCT TTTATTGGTT AAACCTCCTT 1020
 ATGGTGTGAC TGTGTCTTAT TCCATCTATG AGCTTTGTCA GTGGCGGTAG ATGTCAATAA 1080
 40 ATGTTACATA CACAAATAAA TAAATGTTT ATTCATGCTG AAATTTA 1127

Seq ID NO: 42 DNA Sequence
 Nucleic Acid Accession #: NM_018674
 Coding sequence: 390..2009

45 1 11 21 31 41 51
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 ATAAGGGAAG CCACAAGGAG ACGATCGAGG AGAGAGACAA GCGGCAGCAG AGGCAGCAGC 180
 50 GGCAGAGGCA GCACAGGGC TGCGGAGCTG CTGGGAGTGG GAGTGACTCC CCCACCTCGG 240
 GCGCCCAACC TGTCCCTGTC CTCTTCCGCG TGCCTCTGAG TTTAGAAGAG CAGCCGCTGC 300
 CACCACTGCC ACTCGGAGG GCACAGGGC TGCTGGCTAG GGAGGGACAG GGCAGGGAGG 360
 CTCTGGCAG TCCGAGCAG CGGGGACAGA TGCCGATCGA GATTGTGTGC AAAATCAAAT 420
 55 TTGCTGAGGA GGATCGGAAA CCAAGGAGA AGGAGGCAGG GGATGAGCAG AGCCTCCTCG 480
 GGGCTGTTGC CCGTGGAGCA GCGCCCGGAG ACCTGGCCAC CTTTGGCAGC ACCAGCACCC 540
 TGATGAGACT GGGCCGGGCG TGTGGCCGAG GCGCCCAAGG ACTGCGCAGA ACCCTGTGGG 600
 CACTGGCCCT ACTCACTCG CTGGCTGCTC TCCTGTACCA GCGCGCTGGC CTGGCCCGGG 660
 GCTACCTGAC CCGGCTCTAC CTGGTGGCAA TGGACCCGCG TGCCCGAGCC CAGTGGCGG 720
 60 GCTTCCGGCG TGTCACTCTC TGCAATATCA ACCGCTTCCG GCATTGCGCA CTCAGCGATG 780
 CCGACATCTT CCACCTGGCC AATCTGACAG GGCTGCCCCC CAAAGACCGG GATGGGCACC 840
 GTGCGGCTGC CCGGCTGCTC CCAGAGCCTG ACATGGTAGA CATCCTCAAC CGCACTGGCC 900
 ACCAGCTCGC CGACATGCTT AAGAGCTGCA ACTTCAGTGG GCATCACTGC TCCGCCAGCA 960
 ACTTCTCTGT GGTCTATATC CGCTATGGGA AGTGTATCAC CTTCAACGCG GACCCGCGGA 1020
 65 GCTGCTGCTC CAGCCGGGCA GGGGGCATGG GCAGTGGCCT GGAGATCATG CTGGACATCC 1080
 AGCAGGAGGA GTACCTGCCC ATCTGGAGGG AGACAAATGA GACGTCGTTT GAGGCAGGTA 1140
 TTGGGGTGCA GATCCACAGC CAGGAGGAGC GCGCTACAT CCAACAGCTG GGGTTCCGGG 1200
 TGTCCCGAGG CTTCCAGACC TTTGTGCTCT GCCAGGAACA GCGGCTGACC TACCTGCCCC 1260
 AGCCCTGGGG CAACGTGCGC GCAGAGAGTG AGCTCAGGGA GCTTGAGCTT CAGGGCTACT 1320
 70 GGGCTACAG TGTGTCTGCC TGCCGGCTGC GCTGTGAAAA GGAGGCCGTG CTTAGCGCT 1380
 GCCACTGCGG GATGGTGAC ATGCCAGGCA ATGAGACCAT CTGCCACCA AATATCTACA 1440
 TCGAGTGTGC AGACCACACA CTGGACTCCC TGGGTGGGGG CCTGAGGGGC CCGTCTTCT 1500
 GCGCCACCCC CTGCAACCTG ACACGCTATG GGAAGAGAT CTCCATGGTC AGGATCCCCA 1560
 ACAGGGGCTC AGCCCGGTAC CTGGCGAGGA AGTACAACCG CAACGAGACC TACATACGGG 1620
 75 AGAACTTCTT GGTCTAGAT GTCTTCTTTG AGGCCCTGAC CTCTGAAGCC ATGGAGCAGC 1680
 GAGCAGCCTA TGGCTCTGCA GCGCTGTGAG GAGACCTCGG GGGACAGATG GGCCTGTTC 1740
 TTGGGGCCAG CATCCTCAGG TTGCTGGAGA TCCTCGACTA CATCTATGAG GTGTCTGGG 1800
 ATCGACTGAA CGGGGTATGG AGGGTCCCA AGACCCCTCC CGGCACTCC ACTGGGGGCA 1860
 TCTCCACTTT GGGGCTTCAG GAGCTGAAGG AACAGAGTCC CTGCGGAGC CTGGGCGGAG 1920
 80 CGAGGGGTGG GGGGGTCAAG AGTCTGCTCC CCAATCACC CCACCCCCAG GGTCCCCCAG 1980
 GAGGTCTCTT TGAAGATTTT GCTTGTAGG ACGGTGCTGT GACTGAAAGG ACCCAGGAGT 2040
 CTGGGACCCC TCTGGGATC CCGAGCACAT TCTCTGCTC CTGGGAGAGG CCTGGGGGCG 2100
 GTGCTCACTG GGAGGGCCAG GACTCAGTTC CTGCTCTCAT CCTCCCTGCG CTGATGTCA 2160
 GCTGCTTTGC ACAAGGTCC TTTTGTCCA CACCCCTTAT CCCCAGGCTG GTGCCCCGGG 2220
 AGGGCTGGAG ACCAGGCCAT GGGCCCTCAC GGAGAGGAAG GGAAGGAAGG AGAGGGAGGG 2280
 GGAGGATAGA GCCCATCCCA GCGGGGAGG GGGAGCCCTC GTACATTTG TAAATATTTA 2340

5 GGGAAAGCCG GGTGGGGGGA GGGGATACAG ATGTAGAAGG TGGGTAGGGC TACAGGGGTG 2400
 GGTGATTTAG GGACAGCCAG GGTCCCAGCC CCAATGTCAG CAGGATAGGG AGAGCCCCAG 2460
 GACTCAGGAG TGCTGGGCTG GTCCCTACTC CTGCCCCCTC CCAGGCCAGC CTCCTCTCTT 2520
 GGCAGGGGGA GAGGATGGCC CAGCAGGCCT GGGCCAGCTC CCAGTTCCCC CTGCACCAGC 2580
 CCCACCCCTA GAGTCCCTTC TATAGGGAGG GGGCAGGAGA CCTTCCAGAC TTCGGCTGAG 2640
 CTTGGAGGGT GGGAAAGGAG CCTTCTCAGT CCTCTCTCCC TCCAGTCTGA TTTTATAAAG 2700
 TGCTGACGAG 2710

Seq ID NO: 43 DNA Sequence
 Nucleic Acid Accession #: AK091016
 Coding sequence: 201..2291

10 1 11 21 31 41 51
 15 GATCTCAGCT CCTTTTCAGC TAGTGGGTGG AACCCAGGA GGGAAAACCT AGGGAAGCCCC 60
 AGGAGGAAAGT GAAAATACCC CATGGAGTGA AGCTTGTGTG CTACCTGGGT TCCGGGCCAG 120
 TGATCCAGCT CTGGGGGGC ATCAGCCACG GCCAGGCAGG GGGGAGCTG CCACCAAGAC 180
 TGGAGGTTCT AGAGGACTTG ATGGAGGTCA GCTCACCCTC ACCTGCCAG AGGCTCAGAA 240
 GGAAGAAAAG GCCCATGGTG CAGGGCCCTG CTGGGTGCCA GGTTTTCCAG CCTTCTCCTT 300
 CAGGAGGCAC AGCAGGGGAC CTTGGTGGCC TCTCTGACCC CTCTACCT CCAAGAAGCG 360
 20 GTTCCCTGGC CCTTGGGCGC CCCAGCTCGG ACCCTGCATG TTCCAGAGT GGGCCCAATGG 420
 AGGCTGAAGA GGATTCTCTT CCGGAGCAGC CAGAGGACTC AGCTCAGCTC CAACAGGAGA 480
 AGCCATCCCT GTATATTGCG GTGGGGGCGA CTGTTGTCCG TTCCATGCAG GAGGTACTAT 540
 GCACTCGCCT TCGGAGCTC CCAGACCCAG TGCTGAGTGA GGAGGTGGTG GAGGGCATTG 600
 25 CTGCTGGCAT TGAGGCAGCC CTCTGGGACC TGACACAAGG CACCAATGGC CGGTACAAGA 660
 CCAAGTATCG CAGCTGCTG TTCAACCTGC GGGACCCAG GAACCTGGAC TTGTTTCTCA 720
 AAGTGGTTCA TGGAGATGTC ACCCCTACG ACCTGGTGGG GATGAGCTCG ATGCAGCTGG 780
 CCCCCCAGGA GCTGGCCCGC TGGGGGACC AGGAGGAGAA AAGGGGCTG AATATCATTT 840
 AGCAGCAACA GAAGGAGCCG TGCAGACTTC CAGCTCCCAA AATGACCCAC AAGGGCGAAG 900
 TGGAGATTCA GCGGGACATG GACCAGACAC TGACCTGGGA GGATCTGGTG GGACCGCAGA 960
 30 TGTTTCATGA CTGCAGCCCA CAGGCCCTGC CCATCGCATC AGAGGACACC ACGGGGCAGC 1020
 ATGACCACCA CTTCTTAGAC CCCAACTGCC ACATCTGCAA GGACTGGGAG CCCTCGAATG 1080
 AGCTGTCTAG CTCCCTCGAA GCGGCCAAGA GCTGCGGGGA CAATATCTTC CAGAAAGCCC 1140
 TAAGCCAAAC TCCTATGCTC GCTCCAGAGA TGCCCAAAAC CAGGAGTTG TCTCCACGG 1200
 35 AACCACAGGA CAGGGTCCCT CCATCTGGGC TCATGTGCC TGCTGCACCC ACAAGGCGCC 1260
 TGCCCTGCCT GCCACCTCGG GAAGGTGTTT TGGACATGTT CTCCATCAAG CGGTTCGGGG 1320
 CCAGGGCCCA GCTGGTCTCG GGACACAGCT CTGGCTTGT CCAGGCTCTG CCCACCGTGA 1380
 TCCGCTCGGC AGGCTGCATC CCTCCAACA TTGCTGGGA CCTTCTGGCC AGCATCTGCC 1440
 CAGCCAAAGC CAAGGAGCTC TCGGTGGTCA GACTGTGCCC ACATGGGGCC CGGGACACCC 1500
 40 AGAACTGCGC CCTGCTCTAC TCATACCTCA ATGATAGGCA GCGCCACGGG CTGGCTCTG 1560
 TGGAGCACAT GGGGATGGTC CTGCTGCCCC TGCTGCGCTT CCAGCCCCTG CCCACGAGGC 1620
 TGCGCCCTTT GGGGGGCCCA GGTCTGGAGG TCACTCACTC AAGTCTGTG CTGGCTGTGC 1680
 TGCTCCCCAA GGAAGGGCTT CCAGACACAG CAGGGTCCAG CCCCTGGTGT GGGAAAGGTT 1740
 AAAAGATGGT CTCTTCAAC AGTAAGGTGG AGAAGAGATA CTATCAGCCA GATGACAGGA 1800
 45 GGCCGAATGT GCCCTGAAG GGCACCCCTC CCCAGGAGG TGCTGGCAG CAGAGCCAGG 1860
 GCAGGGGCGA TATAGCTCCA AGGGGAATCT CTGCTTGCCA GAGGGCCCCC AGAGGCCAGG 1920
 GGAGGCTCTG GCCAGAGCCT GAAAACTGGC AGCATCCTGG GCGAGGGCAG TGGCCCCCAG 1980
 AGCCAGGCTT GCGCCAGTCC CAGCATCCTT ATTCACTAGC ACCAGCTGCT CATGGCTTTG 2040
 50 CCGCTGGCCA GCATTCACG AGGACTCCTT GTCCCCACCA AGCCCTGCTC CGGCACCTCG 2100
 AATCCCTGGC GACCATGAGT CACCAGCTCC AAGCCTTACT GTGCCCCCAG ACCAAGAGCT 2160
 CCATCCCCCG CCCTCTGAGC CGTTTGTCTA GCGCCCTTGC AGCTCCAGAG CCCCTGGGCC 2220
 CAGCCCGTGA CTCTCTTTTG GGGCCTACAG ATGAAGCTGG CTCTGAGTGT CCCTTCCCTA 2280
 GAAAGGCCTG ACCCTCCTTA CCCACAGGAA CAGGGGTTTT GATGCCCTCA CTAGTGTGTA 2340
 AGCCTGTGCC AGAGAGAGGT GGGACTGCAA GGAGAGGAGT GTGAGCCCTA CCCACCTGCC 2400
 55 CTGTTTGAAC TTCTGTTTG ACAATGTTTG CTGTGATTG TTTGTTCAAT AAAGAATTG 2460
 GT 2462

Seq ID NO: 44 DNA Sequence
 Nucleic Acid Accession #: NM_005291
 Coding sequence: 75..1178

60 1 11 21 31 41 51
 65 CCGACACCCA CGGGCGGAGA TCACCTGCTG CCCCGCAGAC CCCTGTCCCT TCCTCCCGGA 60
 CCAGCAGCTA GAGGATGTCC AAAACGAGTT GGTGGGCTGG ATCCAGAAAG CCCCCAAGAG 120
 AGATGCTGAA ACTCTCAGGC TCTGACTCCA GCCAAAGCAT GAATGGCCTT GAAGTGGCTC 180
 CCCCAGGCTC GATCAACCAAC TTCTCCCTGG CCACGGCAGA GCAATGTGGC CAGGAGACGC 240
 CACTGGAGAA CATGCTGTTC GCCTCCTTCT ACCTTCTGGA TTTTATCCTG GCTTTAGTTG 300
 GCAATACCTT GGCTCTGTGG CTTTTCATCC GAGACCACAA GTCCGGGACC CCGGCCAACG 360
 70 TGTTCTGAT GCATCTGGCC GTGGCCGACT TGTGTTGGT GCTGGTCTCT CCCACCCGCC 420
 TGGTCTACCA CTCTCTGGG AACCACTGGC CATTGGGGA AATCGCATGC GGTCTCACCG 480
 GCTTCTCTT CTACCTCAAC ATGTACGCCA GCATCTACTT CCTCACCTGC ATCAGGCGCG 540
 ACCGTTTCTT GGCCATTGTG CACCCGGTCA AGTCCCTCAA GCTCCGAGG CCCCTCTACG 600
 CACACCTGGC CTGTGCCCTC CTGTGGGTGG TGGTGGCTGT GGCCATGGCC CCGCTGCTGG 660
 TGAGCCACCA GACCGTGAG ACCCAACACA CGGTGGTCTG CTTGCAGCTG TACCGGGAGA 720
 75 AGGCCCTCCA CCATGCCCTG GTGTCCCTGG CAGTGGCCTT CACCTTCCCG TTCTATACCA 780
 CGGTCACTCG CTACCTGCTG ATCATCCGCA GCCTCGGCGA GGGCCTGCTG GTGGAGAGGC 840
 GCCTCAAGAC CAAGGCAGTG GCGATGATCG CCATAGTGCT GGCCATCTTC CTGGTCTGCT 900
 TCGTGCCCTA CCACGTCAAC CGCTCCGTCT ACGTGTGCA CTACCCGAGC CATGGGGCTT 960
 80 CTTGGCCAC CCAGCGCATC CTGGCCCTGG CAAACCGCAT CACCTCTCTG CTCACCGACC 1020
 TCAACGGGGC ACTCGACCCC ATCATGTATT TCTTGTGGC TGAGAAGTTC CGCCAGCCCC 1080
 TGTGCAACTT GCTCTGTGG AAAAGGCTCA AGGGCCCCC CCCACGCTTC GAAGGGAAAA 1140
 CCAACGAGAG CTCCTGAGT GCCAAGTCAG AGCTGTGAGC GGGGGGCGCC GTCCAGGCCG 1200
 AGCGCAGAT GTTTAGGACT CAGCAGACCC AGCAAGAGGC ATCTGCCCTT TCCCCAGCCA 1260
 CCTCCCGAGC AAGCAACCTG AAATCTCAGC AGATGCCAC CATTTCTCTA GATCGCCTAG 1320
 TCTCAACCCA TAAAGAGGAA GAACGACAA AGGGATCCA TCGGCCACCC CTCTGCAGGG 1380

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GCTTGTGATG GCTACAATGG CTCCTAGACA CTCAACGACT TCATCTGTGG CAGGGAGAGA 1440
GGAGGGCCGA AGAACAAACC CTGAACAAATG GAGGCCTTTC TTTCCCGCTA GGCTCCCAGC 1500
CTGCTTCCCG CTACAGAAATG GCTCATCGGC GAGGCTCAGC AGAAAGACCC TGAAGGCAGG 1560
CTGCAAAATGA CCGAAGAGAG GGACCTGGGA GTCTGTGTGG GGACGGGGAG GGAGTCTCAA 1620
TACTCCTTTG CAGCGCAAGG TACTCTGAGT CCCCTCTGTA GTGCCTCTGC CAGACACACA 1680
CTGCCTGAGT TGAAGAGACA CAGGCCACAC ATTTTCAGGCT GGTTGCCAGC GGACGTCAAG 1740
ACTCACGGCC TGCGGGGACT CAGCACAGCT CTGGATTCTG GATCTCTCCT GCTGTAACCC 1800
CACGCACAAG CCTGCAACCC CCAGAGCTCT TTGACAGGCT CCCAGGCCCT CCAGTCTCTG 1860
ACAAGCATGT GCAGTCAAGG GAGCTCAGCT CAGGCCAGGG CTGGGCTGTG CACCTGCCTC 1920
CCACTGACCC AGACCCACTT CCTCCAGAGA GGCCTCTCTC CGCCTGAGCT ATTTCCCTTG 1980
CTAGTGTGCA GATATTTCCC TAAACATGTC TTTTGTGTAT TTGTTGTAC GGACCATAAA 2040
TATAACTGTA GCTTTAAGAC TAAAAAATAA 2070

Seq ID NO: 45 DNA Sequence
Nucleic Acid Accession #: NM_018643
Coding sequence: 48..752

1 11 21 31 41 51
| | | | |
CTACTACTAC TAAATTCGGC GCCGCTCGAC GCTGTGTCAC AGGAAGGATG AGGAAGACCA 60
GGCTCTGGGG GCTGCTGTGG ATGCTCTTTG TCTCAGAACT CCGAGCTGCA ACTAAATTAA 120
CTGAGGAAAA GTATGAACTG AAAGAGGGGC AGACCTTGGA TGTGAAATGT GACTACAGGC 180
TAGAGAAAGT TGCACAGCAG CAGAAAGCTT GGCAGATAAT AAGGGAACGA GAGATGCCCA 240
AGACCCCTGGC ATGCACAGAG AGGCCCTTCAA AGAATTCCTA TCCAGTCCAA GTGGGGAGGA 300
TCATACTAGA AGACTACCAT GATCATGGTT TACTGCGGT CCGAATGGTC AACCTTCAAG 360
TGGAAAGATT TGGACTGTAT CAGTGTGTGA TCTACCAGCC TCCCAAGGAG CCTCACATGC 420
TGTTTCATCG CATCCGCTTG GTGGTGACCA AGGGTTTTTC AGGGACCCCT GGCTCCAATG 480
AGAATTCTAT CCAGAATGTG TATAAGATTG CTCCTACCAC CACTAAGGCC TTGTGCCCATC 540
TCTATACAGC CCCACAGACT GTGACCCAAAG CTCCACCCAA GTCAACTGCC GATGTCTCCA 600
CTCTTGACTC TGAATCAAC CTTACAAATG TGACAGATAT CATCAGGTT CCGGTGTTC 660
ACATTGTGAT TCTCTGGCT GGTGGATTCC TGAGTAAGAG CCTGGTCTTC TCTGTCTCTG 720
TTGCTGTGAC GCTGAGGTCA TTTGTACCTT AGGCCCAAGA ACCACAGAGA ATGTCTCTCTG 780
ACTTCCAGCC ACATCCATCT GGCAGTTGTG CCAAGGGAGG AGGGAGGAGG TAAAAGGCAG 840
GGAGTTAATA ACATGAATTA AATCTGTAAT CACCACTAT TTCT 884

Seq ID NO: 46 DNA Sequence
Nucleic Acid Accession #: NM_003467
Coding sequence: 1..1059

1 11 21 31 41 51
| | | | |
ATGAGGGGGA TCAGTATATA CACTTCAGAT AACTACACCG AGGAAATGGG CTCAGGGGAT 60
TATGACTCCA TGAAGGAACC CTGTTTCCGT GAAGAAAATG CTAATTTCAA TAAATCTTTC 120
CTGCCACCA TCTACTCCAT CATCTTCTTA ACTGGCATTG TGGGCAATGG ATGGTTCATC 180
CTGGTCTATG GTTACAGAA GAAACTGAGA AGCATGACGG ACAAGTACAG GCTGCACCTG 240
TCAGTGGCGC ACCTCCTCTT TGTCTACAGC CTTCCTTCTT GGGCAGTTGA TGCCTGGCA 300
AACTGGTACT TTGGGAACCT CCTATGCAAG GCAGTCCATG TCATCTACAC AGTCAACCTC 360
TACAGCAGTG TCCCTCATCT GGCCTTCTAT AGTCTGGACC GCTACCTGGC CATGTGCCAC 420
GCCACCAACA GTCAGAGGCC AAGGAAGCTG TTGGCTGAAA AGGTGGTCTA TGTGGCGTC 480
TGGATCCCTG CCCTCCTGCT GACTATTCCC GACTTCATCT TTGCCAACGT CAGTGAGGCA 540
GATGACAGAT ATATCTGTGA CCGCTTCTAC CCCAATGACT TGTGGGTGGT TGTGTTCCAG 600
TTTCAGCACA TCATGGTTGG CCTTATCCTG CTGGTATTG TCATCTGTCT CTGCTATTGC 660
ATTATCATCT CCAAGCTGTC ACATCTCAAG GGGCACCAGA AGCGCAAGGC CCTCAAGACC 720
ACAGTCTGTG TCATCTGCTG TTTCTTGGCC TGTGGCTGTC CTTACTACAT TGGGATCAGC 780
ATCGACTCCT TCATCTCTCT GGAATCATC AAGCAAGGGT GTGAGTTTGA GAACACTGTG 840
CACAAGTGGT TTTCATCAC CGAGGCCCTA GCTTTCTTCC ACTGTGTGCT GAACCCCATC 900
CTCTATGCTT TCCTTGGAGC CAAATTTAAA ACCTCTGCCC AGCACGCACT CACTCTGTG 960
AGCAGAGGGT CCAGCTCAA GATCCTCTCC AAAGGAAAGC GAGGTGGACA TTCATCTGTT 1020
TCCACTGAGT CTGAGTCTTC AAGTTTTCAC TCCAGCTAA 1059

Seq ID NO: 47 DNA Sequence
Nucleic Acid Accession #: Eos sequence

1 11 21 31 41 51
| | | | |
GTGTGTAGTC GGGTATGAGA ACGATTGCAA GCAAAAGCAG CTGAGGAGG CTGTCCAAGG 60
AGTAGGCTCA GTAGCACGAA CTGCAATATC TTGAGAAAGG AAAAGTTGAG CCTTGTGCTG 120
GAAAGTGGTT TAGCATGCTG GAGCTGGTTT TCTGCTTGGT AGCCCTACAA CTTTGGCCCA 180
ACTACTTGGC CTCTGGGACT CAGATTCTCT CTCTTTAAAA TGGTGTAAAT AATAGCACCC 240
ACCTCTGTG AGGAGGATGC TGTGAGGACA AAATGAGATC ATCCACATAA GCCGTGAACC 300
CTGTTCTCTG TAAGCTCTCT GAAAGAAGTC TATGGATTAT ACTCAACCTA CACTCCAGTT 360
AAAGGAACAT CTACACAGAG AGGAAATGAA TAACATGAAG TGAAGTCTTC ATCTCCATTG 420
CCACAGTCC CCATTCTACT TGCAGAAAGG TTGCTTACAC TGAAATACAG TTTATTTTCC 480
CCTGGTGCAA AGAACAGTCG TTTCTCCAAA ACTGAAGCTG GAAATTATCT GAAATATCAG 540
GTCCTCCGGA AAAGGAGCGT GAAGCCCTCT TTGTAATTTT GCATTAGOG TGCTCTCTG 600
GCAAGCAGGA AACCTCATCA GAGAAGTCAG CCAAGGAAAG TCTTTAAATG GAAATGTGTC 660
AAACGAGGAG CAATATGATT AAAAAGTTGC TGACGGGCAT GAAATGCTTT GATGTGAAGA 720
CGGAAACTC CAAGCAGGAA GGATTTTAAAC ATTTTGAATC TGATTGACTC TGTGTTTCT 780
CAGCAGATT ATTCATGGG CTAAAAATAA TGCAGAAATG GTACTTTCAG ACCACAGCTG 840
CAGAGGGGAT CGTGTGTAAT TTCAATGAAA ATCCATTGTA ATCTTGAGGT TCAGATCTTA 900
AAAAAGCAAA GGACATGAGA GAAGTAATAT TGTGCTTGA AATTCATTG CTTATATCTA 960
AAAGAAACTC CTATTTTAA GAGAAATGTT GAATCTTTGC AACGTGGTAG ACGTCCCAC 1020
AAAACCTTCT CCTGAAATAG GAGATAAATG TTGAAAGAG GCAATGTATT GAGTATGCTG 1080
ATAGAGGTGG AGTTTCAGAG CAGGCAAGCA TACATAAGAG TCAGGATGTT TTTCAGTATT 1140
ATCTTTACAA ATGAGTTTCT TACAGTGGTC AATGACAAAC CAATTTTATT CAAAGCTTGC 1200
TTCAATAGGC AATGGTTTGA TGCCAATATG TTAGCTATT ACTTTGACCA CCGTATGCAT 1260
TAAAAGAAAG AAAAATTAAG AATACTCAAG CAGAACTCC AACTTAGATA GCACCTTCCA 1320

CAAAAAGTAA TGGAGGGATA GACTGAAGTT AAATGGGATC AGGTATGTGA TGAGATCTCA 1380
 GAAGTGTGTTG CACAATAATG CAGATACTCA TTTTAAACAG AGTCATAAGG ATTGGAACTA 1440
 ATAAAAATAA TAGAATAAAA TACCGATCAA GAATGTGTCC TCCTGCGTAT CTGGGTTTTG 1500
 AATTCTGCGT CCACAGAACT TGTGAGATAT ATGACATTAA AC 1542

Seq ID NO: 48 DNA Sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 52..1131

1 11 21 31 41 51
 | | | | |
 10 ATGCATCTCT AAGTGGTCAT CTTAAGCCTC ATCCTACATC TGGCAGATTG TGTAGCTGGT 60
 TCTGTAAAGG TTGGTGGAGA GGCAGGTCCA TCTGTACAC TACCCTGCCA CTACAGTGGG 120
 GCTGTACAT CAATGTGCTG GAATAGAGGC TCATGTTCTC TATTTCATCG CCAAAATGGC 180
 15 ATTGTCTGGA CCAATGGAAC CCAGTCAACC TATCGGAAGG ACACACGCTA TAAGCTATTG 240
 GGGGACCTTT CAAGAAGGGA TGTCTCTTTG ACCATAGAAA ATACAGCTGT GTCTGACAGT 300
 GCGGTATATT GTTGCCTGTG TGAGCACCGT GGGTGGTTCA ATGACATGAA AATCACGCTA 360
 TCATTGGAGA TTGTGCCACC CAAGGTCAAG ACTACTCCAA TTGTCAAC TGTTCACACC 420
 GTCACGACTG TTCGAACGAG CACCACTGTT CCAACGACAA CGACTGTTCC AACGACAACT 480
 20 GTTCCAACAA CAATGAGCAT TCCAACGACA ACGACTGTTT CGACGACAAAT GACTGTTTCA 540
 ACGACAAAGA GCGTTCACAC GACAACGAGC ATTCACAA CAACAAGTGT TCCAGTGACA 600
 ACAACGGTCT CTACCTTTGT TCCTCCAATG CCTTTGCCCA GGCAGAACCA TGAAACGAGTA 660
 GCCACTTCAC CATCTTCACC TCAGCCAGCA GAAACCCACC CTACGACACT GCAGGGAGCA 720
 ATAAGGAGAG AACCCACCAG CTCACCATTT TACTCTTACA CAACAGATGG GAATGACACC 780
 25 GTGACAGAGT CTTGAGATGG CCTTTGGAAT AACAAATCAA CTCACCTGTT CCTAGAACAT 840
 AGTCTACTGA CGGCAATAC CACTAAAGGA ATCTATGCTG GAGTCTGTAT TTCTGTCTTG 900
 GTGCTTCTTG CTCTTTTGGG TGTCTATCAT GCCAAAAAGT ATTTCTTCAA AAAGGAGGTT 960
 CAACAACTAA GTGTTTCATT TAGCAGCCTT CAAATTAAG CTTTGCAAAA TGCAGTTGAA 1020
 AAGGAAGTCC AAGCAGAAGA CAATATCTAC ATTGAGAATA GTCTTTATGC CACGGACTAA 1080

Seq ID NO: 49 DNA Sequence
 Nucleic Acid Accession #: NM_004932.2
 Coding sequence: 327..2699

1 11 21 31 41 51
 | | | | |
 35 ACTTCATTCA CTTGCAATC AGTGTGTGCC CACAAGAGCC AGCTCTCCCG AGCCCGTAAC 60
 CTTGCGATCC CAAGAGCTGC AGTTTCAGCC GCGACAGCAA GAACGGCAGA GCCGGCGACC 120
 GCGGCGGCGG CGGCGGCGGA GGCAGGAGCA GCCTGGGGGG GTGCGAGGGT CTCGCGGGCC 180
 GCAGGAAGGC GAGCAGAGAT ATCCTCTGAG AGCCAAGCAA AGAACATTAA GGAAGGAAGG 240
 40 AGGAATGAGG CTGGATACGG TGCAAGTAAA AAGGCACCTC CAAGAGTGGG GCACTCACTA 300
 GGCACAGACT CGACGGTGCC ATCAGCATGA GAACCTTACC CTACTCTTTG CTGCTCTTTT 360
 GGGTGGGCCA GCCCTACCCA ACTCTCTCAA CTCACATATC AAAGAGGACT AGTGGTTTCC 420
 CAGCAAGAAA AAGGGCCCTG GAGCTCTCTG GAAACAGCAA AAATGAGCTG AACCGTTCAA 480
 AAAGGAGCTG GATGTGGAAT CAGTTCTTTC TCCTGGAGGA ATACACAGGA TCCGATTATC 540
 45 AGTATGTGGG CAAGTTACAT TCAGACCAGG ATAGAGGAGA TGGATCACTT AAATATATCC 600
 TTTCAGGAGA TGGAGCAGGA GATCTCTTCA TTATTAATGA AAACACAGGC GACATACAGG 660
 CCACCAAGAG GCTGGACAGG GAAGAAAAAC CCGTTTACAT CCTTCAGCT CAAGCTATAA 720
 ACAGAAAGAC AGGGAGACCC GTGGAGCCCG AGTCTGAATT CATCATCAAG ATCCATGACA 780
 TCAATGACAA TGAACCAATA TTCACCAAGG AGGTTTACAC AGCCACTGTC CCTGAAATGT 840
 50 CTGATGTGGG TACATTGTGT GTCCAAAGTC CTGCGACGGA TGCAGATGAT CCAACATATG 900
 GGAACAGTGC TAAAGTTGTC TACAGTATTC TACAGGAGCA GCCTATTTT TCAGTTGAAT 960
 CAGAAACAGG TATTATCAAG ACAGCTTTGC TCAACATGGA TCGAGAAAAC AGGGAGCAGT 1020
 ACCAAGTGTG GATTCAAGCC AAGGATATGG GCGGCCAGAT GGGAGGATTA TCTGGGACCA 1080
 CCACCGTGAA CATCAACTG ACTGATGTCA ACGACAACCC TCCCGATTTC CCCCAGAGTA 1140
 55 CATACCACTT TAAACTCTCT GAATCTTCTC CACCGGGGAC ACCAATTGGC AGGAATCAAAG 1200
 CCAGCGACGC TGATGTGGGA GAAAAAGCTG AAATTGAGTA CAGCATCACA GACGGTGAGG 1260
 GGCTGGATAT GTTTGATGTC ATCACGAGCC AGGAAACCCA GGAAGGGATT ATAACGTGTA 1320
 AAAAGCTCTT GGACTTTGAA AAGAAGAAAG TGTATACCTT TAAAGTGGAA GCCTCCAATC 1380
 60 CTTATGTTGA GCCACGATTT CTCTACTTGG GGCCTTTCAA AGATTGAGC ACGTTAGAA 1440
 TTGTGTGGA GATGTAGAT GAGGCACCTG TCTTCAGCAA ACTGGCCTAC ATCTTACAAA 1500
 TAAGAGAAGA TGCTCAGATA AACACCACAA TAGGCTCCGT CACAGCCCAA GATCCAGATG 1560
 CTGCCAGGAA TCCTGTCAAG TACTCTGTAG ATOGACACAC AGATATGGAC AGAATATTCA 1620
 ACATTGATTC TGGAAATGGT TCGATTTTTC CATCGAAACT TCTTGACCGA GAAACACTGC 1680
 TATGGCACAA CATTACAGTG ATAGCAACAG AGATCAATAA TCCAAAGCAA AGTAGTCGAG 1740
 65 TACCTCTATA TATTAAAGTT CTAGATGTCA ATGACAACGC CCCAGAAATT GCTGAGTTCT 1800
 ATGAAACTTT TGTCTGTGAA AAAGCAAAGG CAGATCAGTT GATTGAGACC CTGCATGCTG 1860
 TTGACAAGGA TGACCTTAT AGTGGACACC AATTTTCGTT TTCCTTGGCC CCTGAAGCAG 1920
 CCAGTGGCTC AAATTTTACC ATTCAAGACA ACAAGACAA CACGGCGGGA ATCTTAACTC 1980
 70 GGAATAATGG CTATAATAGA CACGAGATGA GCACCTATCT CTTCCTGTG GTCATTTTCA 2040
 ACAACGACTA CCCAGTTCAG AGCAGCACTG GGACAGTGAC TGTCCGGGTC TGTGCATGTG 2100
 ACCACCAAGG GAACATGCAA TCCTGCCATG CCGAGGGGCT CATCCACCCC ACGGGACTGA 2160
 GCACGGGGGC TCTGTTGCCC ATCCTTCTGT GCATGTGTAT CCTACTAGTG ACAGTGGTGC 2220
 TGTGTCAGC TCTGAGGCGG CAGCGAAAAA AAGAGCCTTT GATCATTTCC AAAGAGGACA 2280
 TCAGAGATAA CATTGTCACT TACAACGACG AAGGTGGTGG AGAGGAGGAC ACCCAGGCTT 2340
 75 TTGATATCGG CACCTGAGG AATCTGTAAG CCATAGAGGA CAACAAATTA CGAAGGGACA 2400
 TTGTGCCGGA AGCCCTTTTC CTACCCGAC GGAATCCAAAC AGCTCGGAC AACACCGATG 2460
 TCAGAGATTT CATTAACCAA AGGTTAAAGG AAAATGACAC GGACCCCACT GCCCCGCCAT 2520
 ACGACTCTTT GGCCACTTAC GCCTATGAAG GCACTGGCTC CGTGGCGGAT TCCCTGAGCT 2580
 CGCTGGAGTC AGTGACCAAG GATGCAGATC AAGACTATGA TTACTTATG GACTGGGGAC 2640
 80 CTGATTCATA AAAGCTTGCA GATATGTATG GAGGAGTGGG CAGTGACAAA GACTCCTAAT 2700
 CTGTTGCCCT TTTTATTTTC CAATACGACA CTGAAATATG TGAAGTGGCT ATTTCTTTAT 2760
 ATTTATCCAC TACTCCGTGA AGGCTTCTCT GTTCTACCCG TTCCAAAAGC CAATGGCTGC 2820
 AGTCCGTGTG GATCCAATGT TAGAGACTTT TTTCTAGTAC ACTTTTATGA GCTTCCAAGG 2880
 GGCATAATTT TATTTTATAG TGCAATCCAGT TAACCAAGTC AGCCCAACAG GCAGGTGCGG 2940
 GAGGGGAGGA CAGGGAACAG TATTTCACCT TGTCTCAGG GCAGCGTGCC CGCTTCCGCT 3000

5 GTCTGTGGT TTTACTACAC TCCATGTGAG GTCAGCCAAC TGCCCTAACT GTACATTTC 3060
 CAGGCTAATG GGATAAGGA CTGTGCTTTA AAGATAAAAA TATCATCATA GTAAAAGAAA 3120
 TGAGGGCATA TCGGCTCACA AAGAGATAAA CTACATAGGG GTGTTTATTT GTGTCCACAA 3180
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 15 TTTGGATAAA CAACATTGAG ATTATGATGA AAACCTACAT ATTCCATGTT TGGGAAGACC 3900
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 25 ATATTTCTGT TTTGAAACA CACTGTGTTT TAGTTAAGTT TTAATAGGT GTATTACCCA 4500
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Seq ID NO: 50 DNA Sequence
 Nucleic Acid Accession #: Eos sequence
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Seq ID NO: 51 DNA Sequence
 Nucleic Acid Accession #: Eos sequence
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 GTGCTTGGCA CAGCTCGGA TTCTCCCTC TCGCTGCTCG AGTCAGTTTC CCTATCGGCG 300
 GCAGCGGCA AGGCGGCGCG GCGGCGGCG GCAGCGCGG TGGCGGCGT GGAACATCT 360
 CGGCAGCCAC CGCGCTTCTC CCGCTGGAG GGGGCTCCAG CTGGCTGCC CTCGCTCCTT 420

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| 5 | CCCTGCCACG | TTTCGGGTG | CCCTGCACCC | CCCACCCAGG | CTCGCTTCTC | TTGGAAGCGG | 480 |
| | GAAGGGCGCC | TTGCAGGATC | CTGCGGCCCC | TCCAACCCGA | TCTTGGGTCT | AGAGCTCCCC | 540 |
| | AGAGCGAGGC | GCTCGCCAGG | ACTCTCTGCC | CGCCAACCCCT | GACCGCCGGG | GGGTGCCCCC | 600 |
| | GGGAGCTAGC | GCCGCGGAGA | GGAAAGCGGA | AAGGGGACCA | TGCGGCGCCT | GACTCGTCGG | 660 |
| | CTGGTTCTGC | CAGTCTTCGG | GGTGCTCTGG | ATCACGGTGC | TGCTGTCTCT | CTGGGTAACC | 720 |
| | AAGAGGAAGT | TGGAGGTGCC | GACGGGACCT | GAAGTGCAGA | CCCCTAAGGT | TTGGTCTCTG | 780 |
| | TTTTTCAAGG | TGGCTGGGAT | GAGCCCTTGG | GCGCCTCAGG | TGCCCTGTATC | ACCCACTCCT | 840 |
| | CCCTACCAAA | GAGGGCATCT | TCCTACAGGA | GGACACCTTG | CTGTATGTCA | TTTCCCATGT | 900 |
| 10 | CTCTTGCAGG | AAGCTCAGTT | CCATTTCAG | ACTCAGGTCT | TTCTTCAAGT | CAGATGCACA | 960 |
| | CTGCTGGTGT | ATTGCAGGGA | CCTTCCACCC | ACTAGCATCA | TCATCACCTT | CCACAACGAG | 1020 |
| | GCCCGCTCCA | CGCTGCTCAG | GACCATCCGC | AGTGTATTAA | ACCCGACCCC | TACGCATCTG | 1080 |
| | ATCCGGGAAA | TCATATTAGT | GGATGACTTC | AGCAATGACC | CTGATGACTG | TAAACAGCTC | 1140 |
| | ATCAAAATGC | CCAAGGTGAA | ATGCTTGCGC | AATAATGAAC | GGCAAGGTCT | GGTCCGGTCT | 1200 |
| 15 | CGGATTTCGG | GCGTGCATAT | CGCCCAAGGC | ACCACTCTGA | CTTTCCTCGA | CAGCCACTGT | 1260 |
| | GAGGTGAACA | GGGACTGGCT | CCAGCCTCTG | TTGCACAGGG | TCAAAGAGGA | CTACACGCGG | 1320 |
| | GTGGTGTGCC | CTGTGATCGA | TATCATTAA | CTGGACACCT | TCACCTACAT | CGAGTCTGCC | 1380 |
| | TCGGAGCTCA | GAGGGGGGTT | TGACTGGAGC | CTCCACTTCC | AGTGGGAGCA | GCTCTCCCA | 1440 |
| | GAGCAGAAAG | CTCGGCGCCT | GGACCCACAG | GAGCCCATCA | GGACTCTCTAT | CATAGCTGGA | 1500 |
| 20 | GGCTCTTCAG | TGATCGACAA | AGCTTGGTTT | GATTACCTGG | GGAAATATGA | TATGGACATG | 1560 |
| | GACATCTGGG | GTGGGGAGAA | CTTTGAAATC | TCCTTCCGAG | TGTGGATGTG | CGGGGCGAGC | 1620 |
| | CTAGAGATCG | TCCCTGCGAG | CGAGTGGGG | CACGTCTTCC | GGAAAGAGCA | CCCCACGTTT | 1680 |
| | TTCCCTGATG | GAATATGCAA | CACGTATATA | AAGAACACCA | AGCGGACAGC | TGAAGTGTGG | 1740 |
| | ATGGATGAAT | ACAAGCAATA | CTATTACGCT | GCCCGGCCAT | TGCGCCCTGA | GAGGCCCTTC | 1800 |
| 25 | GGGAATGTTG | AGAGCAGATT | GGACCTGAGG | AAGAATCTGC | GCTGCCAGAG | CTTCAAGTGG | 1860 |
| | TACCTGGAGA | ATATCTACCC | TGAACCTCAG | ATCCCCAAGG | AGTCTCTCAT | CCAGAAGGGC | 1920 |
| | AATATCCGAC | AGAGACAGAA | GTGCCCTGAA | TCTCAAAGGC | AGAACACCA | AGAAACCCCA | 1980 |
| | AACCTAAAGT | TGAGCCCTCG | TGCCAAGGTC | AAAGGCGAAG | ATGCAAAGTC | CCAGGTATGG | 2040 |
| | GCCCTTCACT | ACACCCAGCA | GATCCTCCAG | GAGGAGCTGT | GCCTGTCTAGT | CATCACCTTG | 2100 |
| 30 | TTCCCTGGCG | CCCCAGTGGT | TCTTGTCTTT | TGCAAGAATG | GAGATGACCG | ACAGCAATGG | 2160 |
| | ACCAAAACTG | GTTCACCAT | CGAGCACATA | GCATCCCAAC | TCTGCTCTGA | TACAGATATG | 2220 |
| | TTCCGTGATG | GCACCGAGAA | CGGCAAGGAA | ATCGTGTCA | ACCCATGTGA | GTCTCTACTC | 2280 |
| | ATGAGCCAGC | ACTGGGACAT | GGTGAGCTCT | TGAGGACCCC | TGCCAGAAAG | AGCAAGGGCC | 2340 |
| | ATGGGTGGT | GCTTCCCTGG | ACCAGAACAG | ACTGGAACCT | GGGCAGCAAG | CAGCCTGCAA | 2400 |
| 35 | CCACCTCAGA | CATCCTGGAC | TGGAGGTGG | AGGCAGAGCC | CCCCAGGACA | GGAGCAACTG | 2460 |
| | TCTCAGGGAG | GACAGAGGAA | AACATCACAA | GCCAAATGGG | CTCAAAGACA | AATCCACAT | 2520 |
| | GTCTCTCAAG | CCGTTAAGTT | CCAGTCTCTG | CCAGTCATT | CTGATTGGT | ATCTGGAGAG | 2580 |
| | AGAAACCTAA | TGGGAAGTGT | TTATTGTCT | TTTCTCTACA | AAGGAAGCAG | TCTCTGGAGG | 2640 |
| | CCAGAAAGAA | AAGCCTTCTT | TTTCACTAGG | CCAGGACTAC | ATTGAGAGAT | GAAGAATGGA | 2700 |
| 40 | GGTGTGTTCC | AAAAGAAATA | AAGAGAAACT | TAGAAGTGT | CTCTGG | | 2760 |

Seq ID NO: 52 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 641..2299

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| | GGGCGCGGCT | AGCGCCCCCT | CTCAGAGCCC | CGCTCACTCC | CACCTGGGCT | CGCTCCGAGT | 180 |
| 50 | CGGCGTGTCT | GTGCGGCCCC | CCCTCCCCGC | TCACTCCCTC | CGCCCTCGTG | CTCTCCCGGG | 240 |
| | GGTGCTTGCG | ACAGGCTCGG | ATTCTCTCCT | CTCGCTGTCT | GAGTCAGTTT | CCCTATCGGC | 300 |
| | GGCAGCGGCG | CAGCGCGGCG | CGGCGGCGGC | GGCAGCGCGC | GTGGCGGCGT | GGGGAACATC | 360 |
| | TGCGGAGCCA | CCGCGCTTCT | CCGCTGGAG | CGGCGGTCCA | GCTTGGCTGC | CCTCGGTCTC | 420 |
| | TCCTTCCAC | GTTCGGGTTC | GCCCTGCACC | CCCCACCCAG | GCTCGCTTCT | CTTCGAAGCG | 480 |
| 55 | GGAAAGGCGC | CTTGCAGGAT | CCTGCGGCCC | CTCCAACCGG | ATCCTGGGTC | TAGAGCTCCC | 540 |
| | CAGAGCGAGG | CGCTCGCCAG | GACTCTCTGC | CCGCGCAACC | TGACCGCGCG | GGGGTCCCCC | 600 |
| | CGGAGCGTAG | CGCGCGGAG | AGGAAGCGGC | AAAGGGGACC | ATGCGGCGCC | TGACTCGTCG | 660 |
| | CTGGTCTCTG | CCAATCTCTG | GGGTGCTCTG | GATCACGCTG | CTGCTGTCTT | TCTGGGTAAC | 720 |
| | CAAGAGGAG | TTGGAGGTGC | CGACGGGACC | TGAAGTGCAG | ACCCCTAAGC | CTTCGGACGC | 780 |
| 60 | TGACTGGGAC | GACCTGTGGG | ACCAGTTTGA | TGAGCGGCGG | TATCTGAATG | CCAAAAAGTG | 840 |
| | CGCGTTGGT | GACGACCCCT | ATAAGCTGTA | TGCTTTCAAC | CAGCGGGAGA | GTGAGCGGAT | 900 |
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| | CACGACCTT | CCACCCACTA | GATCATCAT | CACCTTCCAC | AACGAGGCCC | GCTCCACGCT | 1020 |
| | GCTCAGGACC | ATCCGCAGTG | TATTAACCG | CACCCCTACG | CATCTGATCC | GGGAAATCAT | 1080 |
| 65 | ATTAGTGGAT | GACTTCAGCA | ATGACCTTGA | TGACTGTAAA | CAGCTCATCA | AATTGCCCAA | 1140 |
| | GGTGAATGTC | TTGCGCAATA | ATGAACGGCA | AGGTCTGGTC | CGGTCCCGGA | TTGGGGCGCG | 1200 |
| | TGACATCGCC | CAGGCGACCA | CTCTGACTTT | CCTCGACAGC | CACCTGTGAGG | TGAACAGGGA | 1260 |
| | CTGGCTCCAG | CCTCTGTGTC | ACAGGGTCAA | AGAGGACTAC | ACGCGGGTGG | TGTGCCCTGT | 1320 |
| | GATCGATATC | ATTAACCTGG | ACACCTTCAC | CTACATCGAG | TCTGCCTCGG | AGCTCAGAGG | 1380 |
| 70 | GGGGTTTGAC | TGGAGCTTCC | ACTTCCAGTG | GGAGCAGCTC | TCCCAAGAGC | AGAAGGCTCG | 1440 |
| | GCGCTGGAG | CCCACGGAGC | CCATCAGGAC | TCCTATCATA | GCTGGAGGCG | TCTTCTGTAT | 1500 |
| | CGACAAAGCT | TGGTTTGATT | ACCTGGGGAA | ATATGATATG | GACATGGACA | TCTGGGGTGG | 1560 |
| | GGAGAACTTT | GAATCTCTCT | TCCGAGTGTG | GATGTGCGGG | GGCAGCCTAG | AGATCGTCCC | 1620 |
| | CTGCAGCCGA | GTGGGGCACG | TCTTCCGAA | GAAGCACCCC | TACGTTTTCC | CTGATGGAAA | 1680 |
| 75 | TGCCAACAGC | TATATAAAGA | ACACCAAGCG | GACAGCTGAA | GTGTGGATGG | ATGAATACAA | 1740 |
| | GCAATACTAT | TACGCTGCC | GGCATTGGC | CCTGGAGAGG | CCCTTCGGGA | ATGTTGAGAG | 1800 |
| | CAGATTGGAC | CTGAGGAAGA | ATCTGGCGTG | CCAGAGCTTC | AAGTGGTACC | TGGAGAATAT | 1860 |
| | CTACCTTGAA | CTCAGCATCC | CCAAGGAGTC | CTCCATCCAG | AAGGGCAATA | TCCGACAGAG | 1920 |
| | ACAGAAAGTG | CTGGAATCTC | AAAGGCAGAA | CAACCAAGAA | ACCCCAAAAC | TAAAGTTGAG | 1980 |
| 80 | CCCTGTGGCC | AAGGTCAAAG | GCGAAGATGC | AAAGTCCCAG | GTATGGGCTC | TCACATACAC | 2040 |
| | CCAGCAGATC | CTCCAGAGG | AGCTGTGCCT | GTCAGTCATC | ACCTTGTCTC | CTGGGCGCCC | 2100 |
| | AGTGGTCTTT | GTCTTTTGCA | AGAATGGAGA | TGACCGACAG | CAATGGACCA | AAACTGGTTC | 2160 |
| | CCACATCGAG | CACATAGCAT | CCCACTCTG | CCTCGATACA | GATATGTTCC | GTGATGGCAC | 2220 |
| | CGAGAACGGC | AAGGAATCG | TCGTCAACCC | ATGTGAGTCC | TCACTCATGA | GCCAGCACTG | 2280 |
| | GGACATGGTG | AGCTCTTGAG | GACCCCTGCC | AGAAGCAGCA | AGGGCCATGG | GGTGGTGCTT | 2340 |

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10 Seq ID NO: 53 DNA Sequence
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 Coding sequence: 400..1959

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55 Seq ID NO: 54 DNA Sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 1241..2377

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Seq ID NO: 55 DNA Sequence

Nucleic Acid Accession #: NM_001218

Coding sequence: 1..1080

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CCTCTGGATC ACAGACACTG CACAGACCTT AGGGAATGGC AGGTTCAAGT TCCACTTCTT 1860
GGTGGGGATG AGAAGGGAGA GAGAGCTAGA GGGACAAAGA GAATGAGAAG ACATGGATGA 1920
TCTGGGAGAG TCTCACTTGG GAATCAGAAT TGGAAATACA TTCTGTTTAT CAAGCCATAA 1980
TGTAAGGACA GAATAATACA ATATTAAGTC CAAATCCAAC CTCCTGTGAG TGGAGCAGTT 2040
ATGTTTTATA CTCTACAGAT TTTACAAATA ATGAGGCTGT TCCTTGAAAA TGTGTTGTTG 2100
CTGTGTCCTG GAGGAGACAT GAGTTCGAG ATGACCCAAT CTGCCTTGA ATCTGGAGGA 2160
AATAGGCAGA AACAAAATGA CTGTAGAACT TATTCTCTGT AGGCCAAATT TCAATTCAGC 2220
CACTTCTGCA GGATCCCTAC TGCCAACCTG GAATGGAGAC TTTTATCTAC TTCTCTCTCT 2280
CTGAAGATGT CAAATGTTGG TTAGATCAA ATATATTCA AGCTATAAAA GCAGGAGGTT 2340
ATCTGTGAGC GGGGCTGGCA TCATGATTTT AGGGCAAGT AATAATGGAA TGCTACTAAG 2400
ATACTCCATA TTCTTCCCGG AATCACACAG ACAGTTTCTG ACAGGCGCAA CTCCTCCATT 2460
TTCTTCCCGC AGGTGAGAAC CCTGTGGAGA TGAGTCAGTG CCATGACTGA GAAGGAACCG 2520
ACCCCTAGTT GAGAGCAGCT TGCAGTTCCC CGAGAACTTT CTGATTACAA GTCTCATTTT 2580
GACAGCATGA AATGTCCTCT TGAAGCATAG CTTTTTAAAT ATCTTTTTC TTTACTCTCT 2640
CCCTCTGACT CTAAGAATTC TCTCTCTGG AATCGCTTGA ACCCAGGAGG CGGAGGTTGC 2700
AGTAAGCCAA GGTCAATGCC CTGCATCTA GCCTGGGTGA CAGAGCGAGA CTCATCTCA 2760
AAAAAAGAAA AAAAA 2775
  
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Seq ID NO: 56 DNA Sequence

Nucleic Acid Accession #: BC000278

Coding sequence: 113..1144

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CTCGCCACGG CACCCAGGCT GCGCGCACGC GGTCCCGGTG TGCAGCTGGA GAGCGAGCGG 60
CCACCGGGAG CCCCAGGAC AGCCCGCGCC CGCCCGGAG GAGCCCGGA AGATGCCCGG 120
GCGCAGCCTG CACGCGGGG CCGTGTCTCT GCTGGTGATC TTAAAGGAAC AGCCTTCCAG 180
  
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5
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CCCCGCCCA GTGAACGGTT CCAAGTGGAC TTATTTTGGT CCTGATGGGG AGAATAGCTG 240
GTCCAAGAAG TACCCGTCGT GTGGGGGCTT GCTGCAGTCC CCCATAGACC TGACACAGTGA 300
CATCCTCCAG TATGACGCCA GCCTCACGCC CCTCGAGTTC CAAGGCTACA ATCTGTCTGC 360
CAACAAGCAG TTTCTCTCTG CCAACAATGG CCATTCAAGT AAGCTGAACC TGCCCTCGGA 420
CATGCACATC CAGGCGCTCC AGTCTCGCTA CAGTGCCAAG CAGCTGCACC TGCACTGGGG 480
GAACCCGAAT GACCCGACCG GCTCTGAGCA CACCGTCAGC GACAGCACTT TCGCCGCCGA 540
GCTGCACATT GTCCATTATA ACTCAGACCT TTATCCTGAC GCCAGCACTG CCAGCAACAA 600
GTCAGAAAGC CTCGCTGTCC TGGCTGTCTT CATTTAGATG GGCTCCTTCA ATCCGTCTTA 660
TGACAAGATC TTCAGTCACC TTCAACATGT AAAGTACAAA GGCCAGGAAG CATTGCTCCC 720
GGGATTCAAC ATTGAAGAGC TGCTTCCGGA GAGGACCGCT GAATATTACC GCTACCGGGG 780
GTCCTGTACC ACACCCCTTT GCAACCCAC TGTCTCTGG ACAGTTTTCG GAAACCCCGT 840
GCAAAATTTCC CAGGAGCAGC TGCTGGCTTT GGAGACAGCC CTGTAAGTCA CACACATGGA 900
CGACCCCTTC CCCAGAGAAA TGATCAACAA CTTCGGCAG GTCCAGAAAT TCGATGAGAG 960
GCTGGTATAC ACCTCCTTCT CCCAAGGCAT CATCCTCTCA CTGGCCCTGG CTGGCATTCT 1020
TGGCATCTGT ATTTGGTGG TGGTGTCCAT TTGGCTTTTC AGAAGGAAGA GTATCAAAAA 1080
AGGTGATAAC AAGGGAGTCA TTTACAAGCC AGCCACCAAG ATGGAGACTG AGGCCCAAGC 1140
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TGCCAGGCTC CAGGATCCCT CTGCTGGGTG CCTCCTTGCC TTGGGACCAT GGCCACCCCA 1320
GAGCCATCCG ATCGATGGAT GGGATGCACT CTCAGACCAA GCAGCAGGAA TTCAAAGCTG 1380
CTTGCTGTAA CTGTGTGAGA TTGTGAAGTG GTCTGAATTC TGGAAATACA AACCAAGCCA 1440
TGCTGTGGTG CCATTAAATG TTGGAAAAACA CTTTCATCCG GGGCTTTGCC AGAGCGTGCT 1500
TTCAAGTGTC CTGGAAGAGT TGCTGCTTCT CCAAGCTTTC AGACAAGAAT GTGCACTCTC 1560
TGCTTAGGTT TTGCTGGGA AACTCAACTT CTTTCTCTG GAGACGGGGC ATCTCCCTCT 1620
GATTTCTTTC TGCTATGACA AAACCTTTAA TCTGCACCTT ACAACTCGGG GACAAATGGG 1680
GACAGGAAGG ATCAAGTTGT AAAAAAATA AAAAAAATA 1718
  
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Seq ID NO: 57 DNA Sequence
Nucleic Acid Accession #: NM_006632.1
Coding sequence: 377..1582

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GCGGCGGTGC TGGAGCACCT GACCGCCGAG ATCCTGGAGC TGGCTGGCAA CCGGCCCGGC 120
GACAAGAGAA CCCGCATCAT CCTGCGCCAC CTGTAGCTGG CCATTTCGCA CCGCGAGGAG 180
CTTAACAAGC TGCTGGGGCA AGTCACCATC GCGCAGGGCG GTGTCCTGCC CAACATTTCAG 240
GGCGTGTCTT TGCCCCAGAA GACCAAGAGC CACCACAAGG CCAAGGGTGA AAACCATTTCA 300
CTAGGAGAGG AGAAACACAA TGGCCACCAA GACAGAGTTG AGTCCACAG CAAGGGAGAG 360
CAAGAAGCCA CAGATATGCG AAGTGGATGA GACACTGATC CCCAGGAAAG GTCCAAGTTT 420
ATGTTCTGCT CGCTATGAA TAGCCCTCGT CTATACATTC TGCAATTTCA CAACGATAGC 480
ACAAAAATGC ATCATGAACA TCACCATGGT AGCCATGGTC AACAGCACA GCCCTCAATC 540
CCAGCTCAAT GATTCTCTCG AGGTGCTGCC TGTGACTCA TTTGTTGGCC TAAGTAAAGC 600
CCCAAGAGAT CTTCTGCAA AGTCTCAAT ACTTGGGGGT CAGTTTGCAG TTTGGGAAAA 660
GTGGGGCCCT CCACAAGAAC GAAGCAGACT CTGAGCATT GCTTTATCAG GAATGTTACT 720
GGGATGCTTT ACTGCCATCC TCATAGGTGG CTTCATTAGT GAAACCCCTG GGTGGCCCTT 780
TGTCTCTAT ATCTTTGGAG GTGTGGCTG TGTCTGTGC CTCTCTGGT TTGTTGTGAT 840
TTATGATGAC CCCTTTCTCT ATCCATGGAT AAGCACCTCA GAAAAAGAAT ACATCATATC 900
CTCCTTGAAA CAACAGGTGG GGTCTTCTAA GCAGCCTCTT CCCATCAAG CTATGCTCAG 960
ATCTCTACCC ATTTGGTCCA TATGTTTAGG CTGTTTCAGC CATCAATGTT TAGTTAGCAC 1020
AATGGTTGTA TACATACCAA CTTACATCAG CTCTGTGTAC CATGTTAACA TCAGAGACAA 1080
TGGACTCTTA TCTGCCCTTC CTTTATTGTT TGCTGGGTC ATAGGCATGG TGGGAGGCTA 1140
TCTGGCAGAT TTCCTCTTAA CCAAAAAGTT TAGACTCATC ACTGTGAGGA AAATTGCCAC 1200
AATTTTAGGA AGTCTCCCTC CTTAGCACT CATGTGTCT CTGCCCTACC TCAATTCCGG 1260
CTATATACA GCAACTGCCT TGCTGACGCT CTCTTGCGGA TTAAGCACAT TGTGTCACTG 1320
AGGGATTAT ATCAATGTCT TAGATATTGC TCCAAGGTAT TCCAGTTTTC TCATGGGAGC 1380
ATCAAGAGGA TTTTCGAGCA TAGCACCTGT CATGTACCC ACTGTACGG GATTTCCTCT 1440
TAGTCAGGAC CCGAGTTTGG GGTGGAGGAA TGTCTTCTTC TTGCTGTTG CCGTTAACTC 1500
GTTAGGACTA CTCTCTACCC TCATATTGG AGAAGCAGAT GTCCAAGAAT GGGCTAAAGA 1560
GAGAAAATCT ACTCGTTTAT GAAGTTATCC CACCTTGGAT GGAAAAGTCA TTAGGCACCG 1620
TATTGCATAA AATAGAAGGC TTCCGTGATG AAAATACCAG TGAAAAGATT TTTTTCCTCT 1680
GTGGCTCTTT TCAATTATGA GATCAGTTCA TTATTTTATT CAGACTTTT TTTGAGAGAA 1740
ATGTAAGATG AATAAAAAAT CAAATAAAAT GATAACTAAG AAAAAAATA AAAAA 1795
  
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Seq ID NO: 58 DNA Sequence
Nucleic Acid Accession #: NM_003058.1
Coding sequence: 145..1812

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GGGTTTGTGC TGAGCTGGCT GCAGCCGCTC TCAGCCTCGC TCCGGGCAAG TCGGGCAGCC 120
TCGGGCCCTC CTGCTGCGAG GATCATGCCC ACCACCGTGG ACGATGTCTT GGAGCATGGA 180
GGGAGATTTC ACTTTTCCCA GAAGCAAAATG TTTTCTCTCT TGGCTCTGCT CTGGCTACC 240
TTCCGGCCCA TCTACGTGGG CATGCTCTTC CTGGGCTTCA CCCTGACCA CCGCTGCCGG 300
AGCCCCGAGC TGGCCGAGCT GAGTCTGCGC TGGCGCTGGA GTCTGCAGA GAACTGAAC 360
TACACGCTGC CGGCGCCAGG ACCTGCGGGC GAAGCCTCCC CAAGACAGTG TAGGCGCTAC 420
GAGGTGGACT GGAACAGAGC CACCTTTGAC TGGCTGGACC CCCTGGCCAG CCGTGAACAC 480
AACAGAGACC GCCTGCCACT GGGGCCCTGC GGGGACGGCT GGGTGTACGA GACGCTGGC 540
TCGTCCATCG TCACCGAGTT TAACCTGGTA TGTGCCAATC CCTGATGTT GGACCTATT 600
CAGTCATCAG TGAATGTAGG ATCTTTTATT GGCTCTATGA GTATCGGCTA CATAGCAGAC 660
AGGTTTGGCC GTAAGCTCTG CCTCTAACT ACAGTCTCTA TAAATGTCTG AGCTGGAGTT 720
CTCATGGCCA TTTCCCAAC CTATACGTGG ATGTTAATTT TTGCTTAAT CCAAGGACTG 780
GTACGAGAA GAGGCTGGTT AATAGGCTAC ATCTGATTA CAGAATTTGT TGGGCGGAGA 840
TATCGGAGAA CAGTGGGGAT TTTTACCAA GTTGCTATA CAGTTGGGCT CCTGCTGCTA 900
GCTGGGGTGG CTTACGCACT TCCTCACTGG AGGTGGTTGC AGTTCACAGT TGCTCTGCC 960
  
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| | | | | | | | |
|----|--|-------------|-------------|------------|-------------|-------------|------|
| | AACTTCTTCT | TCTTGTCTA | TTACTGGTGC | ATACCTGAGT | CTCCAGGTG | GCTGATCTCC | 1020 |
| | CAGAATAAGA | ATGCTGAAGC | CATGAGAATC | ATTAAGCACA | TCGCAAGAA | AAATGGAAAA | 1080 |
| | TCTCTACCCG | CCTCCCTTCA | GCGCCTGAGA | CTTGAAGAGG | AAACTGGCAA | GAAATTGAAC | 1140 |
| 5 | CCTTCATTTT | TTGACTTGGT | CAGAACTCCT | CAGATAAGGA | AACATACTAT | GATATTGATG | 1200 |
| | TACAACCTGGT | TCACGAGCTC | TGTGCTCTAC | CAGGGCCTCA | TCATGCACAT | GGGCCTTGCA | 1260 |
| | GGTGACAATA | TCTACCTGGA | TTTCTTCTAC | TCTGCCCTGG | TTGAATTCCT | AGCTGCCTTC | 1320 |
| | ATGATCATCC | TCACCATCGA | CGCATCGGA | GCGCGTTACC | CTTGGGCTGC | ATCAAAATATG | 1380 |
| | GTTCGAGGGG | CAGCCTGTCT | GGCCTCAGTT | TTTATACCTG | GTGATCTACA | ATGGCTAAAA | 1440 |
| 10 | ATTATTATCT | CATGCTTGGG | AAGAATGGGG | ATCACAATGG | CCTATGAGAT | AGTCTGCCTG | 1500 |
| | GTCAATGCTG | AGCTGTACCC | CACATTCAAT | AGGAATCTTG | GCGTCCACAT | CTGTTCCTCA | 1560 |
| | ATGTGTGACA | TTGGTGGCAT | CATCACGCCA | TTCTGGTCT | ACCGCTCAC | TAAACATCTGG | 1620 |
| | CTTGAGCTCC | CGCTGATGGT | TTTCGGCGTA | CTTGCTTGG | TTGCTGGAGG | TCTGGTGCTG | 1680 |
| | TTGCTTCCAG | AACTAAAGG | GAAAGCTTGG | CCTGAGACCA | TCGAGGAAGC | CGAAAATATG | 1740 |
| | CAAGACCAA | GAAAAATATA | AGAAAAGATG | ATTTACCTCC | AAGTTCAGAA | ACTAGACATT | 1800 |
| 15 | CCATTGAATC | AAGAAAGAGG | ACCGTTGCTG | CTGTGATGAC | CTAGCTTTGA | TGGCAGCAAG | 1860 |
| | ACCAAAAGTA | GAAATCCCTG | CATCATCTAC | AAAGCCCAT | CAACTCAACC | AAACTTACCC | 1920 |
| | CTGAGCCCTA | TCAACCTAGG | TCTACAGCCA | GTGGAGTCTA | TTGTACACTG | TGAAAAATA | 1980 |
| | CCCATGGGAC | CAGATCTCTG | CAAAATCTTC | CAGCTCACTT | TAITCTCAGC | ATTCCTAGGA | 2040 |
| 20 | CATTGGACAT | TGGTTTTCTG | GAGGGTTTTT | TTTCCGATCT | TTGTATTTTT | TTAAATTTGA | 2100 |
| | TTCTTTTCTT | TGCAATGCTA | GCAACCAGAA | TACATAGGGG | AACTGTGGGC | TAGGCAANA | 2160 |
| | AAATAGAAAA | ATGTGAAAA | ACAGTAAAGT | TGGGAGAGGA | GCATCTATTT | TCTTAAAGAA | 2220 |
| | ATAAACACCC | NAAAACAAA | AAAAAATAAA | AAAAAATA | | | 2257 |
| 25 | Seq ID NO: 59 DNA Sequence | | | | | | |
| | Nucleic Acid Accession #: Eos sequence | | | | | | |
| | Coding sequence: 227..2311 | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
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| 30 | GTGAGGGGCG | TGTTGGCCCC | GCACAGATTG | AGCCGAGTTG | TGCCCCCGCT | GGGAGAAGTG | 60 |
| | ACCCCTCTCG | GCCTGATCAG | AACACTGAGG | CTCAGAGAAG | TTAACTACTC | CAAAAGTCATA | 120 |
| | TAGCCAGTAT | TTTCTGGAGC | TGTAATTCAA | ATCAGATGTG | TTCAATACTT | TCTACTACCC | 180 |
| | CATTGCTGTC | TTTATGAAAA | GAAATTTTCA | TTCAATATAG | GTGACTATGC | AGCCTGCAAT | 240 |
| | TCAAGTATGG | TTTGAGGAAG | ATCTGCCTCT | AAGTCTCTCG | AGTCTCTGTA | CTCCAGACA | 300 |
| 35 | CGGACCAAGG | TTGCTTAATG | TTTGTCACTA | CGATGAGTGG | ATAGCTGTGA | GGCATGAAGC | 360 |
| | CACTTTGTGG | CCCATGCAAG | AAGATCTGTC | AATCTGGTTA | TCTGGTTTAT | TAGGTATTAA | 420 |
| | AGTTAAGGCA | GAAAAATTAT | TGGAAAGACT | TGATAATGGA | GTACTATTAT | GTCAACTGAT | 480 |
| | TGATGTTCTT | CAAAACATGG | TGAAAACATG | CAACTCTGAA | GAATCAGGGA | ATTTTCCAAT | 540 |
| | GAGAAAAGTG | CCCTGTAAGA | AAGATGCTGC | ATCAGGTTCA | TTCTTTGCTC | GGGACAATAC | 600 |
| 40 | CGCAAACTTC | CTTCACTGGT | GTAGGGACAT | TGGGGTTGAT | GAAACTTACC | TCTTTGAATC | 660 |
| | TGAAGGTTTA | GTTTTGACCA | AAGATCCAAG | ACAGGTGTAT | CTTTGTCTTC | TTGAAATTGG | 720 |
| | TCGAATTGTG | TCAAGATACG | GGGTTGAGCC | ACCAGTGTTA | GTAAAACTGT | AGAAAGAAAT | 780 |
| | TGAGTTAGAA | GAGACTTTGC | TTAATACTTC | TGGGCTGAA | GATTCATCA | GCATTCAAA | 840 |
| | ATCATGCTGT | CGGCATGAAG | AGCTACATGA | AGCTGTTAAA | CATATTGCTG | AGGACCTTCC | 900 |
| 45 | TTGTAGTTGT | TCTCATCGAT | TTTCTATTGA | GTATTATTCT | GAAGGACGGT | ACCGACTAGG | 960 |
| | GGATAAATA | CTCTTTATAA | GAATGCTTCA | TGAAAAACAT | GTGATGGTTC | CGGTTGGTGG | 1020 |
| | AGGCTGGGAT | ACTCTTCAAG | GATTTTGGCT | TAAATATGAC | CCCTGTGCAA | TATTACAGTT | 1080 |
| | TGCCACATTA | GAACAAAAAA | TTTTAGCATT | TCAAAAAGGA | GTTCCTAATG | AAAGTGATCC | 1140 |
| | TGATTTCGCT | GCCAGAACAC | CTCAGCTTCC | TGAAATGAAT | CCTTTGTGAG | CAGTTAACT | 1200 |
| 50 | GTTCAGAAAA | CAAAATTCAA | AACCCAGCGT | GCCAGTTAGT | ATTCCAAAAA | GCAAGGAAAA | 1260 |
| | ACAGGGAGCT | CCACAGGCTG | CATTGGTGCC | AGCATCTTCA | CTGAAAGGAG | GTAACTCTGG | 1320 |
| | CTCTATTTGA | GTCCGTTCTA | AATTGCCAAA | TTCTCCAGCA | GCATCTTCTC | ATCCCAAGCT | 1380 |
| | CAAGTCTTCA | AAAGGCATAA | CGAAGAAACC | GCAGGCTCCT | TCAAAACAATG | CATCATCTTC | 1440 |
| 55 | ACTTGCTTCA | TTAAATCCAG | TAGGTAAAAA | CACCTTCTCA | CCAGCTTTAC | CAAGAACTGC | 1500 |
| | ACCTTGATTA | TCTGAGTCA | CGAGAAAAATG | TATTTTATCC | CCCAATACCC | CCAGGCCCAA | 1560 |
| | GGTTATTCCA | GCCAGAAATT | CAGCAGATCT | GCCCGAGTCC | ACACTTTTGC | CAATAAAGTG | 1620 |
| | TTACGAAAAA | ACTCAACCTA | AGTATTGAAA | ACATAATCAT | ATTTCTTCCA | GAGATAATGC | 1680 |
| | AGTATCTCAC | TTAGCTGCAC | ATTCAAATTC | ATCCTCAAAA | TGTCCTCAAGC | TGCCTAAAGC | 1740 |
| | AAATATACCT | GTAAGACCTA | AACCTTCTTT | CCAGTCTCTT | GCAAAAATGA | CAAAAACCCAG | 1800 |
| 60 | TTCCAAAACC | ATAGCCACGG | GTCTAGGAAC | ACAGTCTCAA | CCATCCGATG | GAGCCCCACA | 1860 |
| | AGCAAGGCCA | GTCCAGCAGC | AGAACTTAA | ATCGGCTTGT | AATTTAAATC | AGCCAGTTTC | 1920 |
| | TGTGTCTTCA | GTTCCTCTGT | TAAAAGCCAC | ACAGAAATCA | AAAGATAAGA | ATATAGTTTC | 1980 |
| | AGCTACCAAA | AAGCAGCCTC | AGAATAAAAG | TGCATTTCAG | AAGACAGSAC | CCAGCTCCTT | 2040 |
| | GAAAGTCTCT | GGCCGTACCC | CACGTGCCAT | CGTGAGCCTA | CCCCAGTCTT | CTACCAAAAC | 2100 |
| 65 | ACAAACTGCA | CCGAAGTCA | CACAGACTGT | CGCTAAGAGC | CAGCATTTCA | CTAAAGGGCC | 2160 |
| | TCCAGAAAGT | GGCAAAACCC | CAGCTTCAAT | CAGGAAACCA | CCCTCATCTG | TAAAGGATGC | 2220 |
| | AGATAGTGG | GATAAAAAAC | CTACTGCAAA | GAAAAAGGAA | GATGATGACC | ATTATTTTGT | 2280 |
| | CATGACTGGA | AGTAAGAAAC | CTAGAAAAATA | AATACATACT | CATTATAAAA | AAAGAGAAAA | 2340 |
| | GGAAAGATGA | ATGTGTTAGC | TTACATCTTT | AAAAGTTTCT | CCTATTTTGT | TCTGTCTAAA | 2400 |
| 70 | TAGGTGCAGA | CACATAAGGAT | AGTGAGGATG | GAGGCTGGGA | TGAGGAAAGG | GTTTATCAGA | 2460 |
| | ATTACATAT | CTGAATTCAC | TGGAAAGAGC | CCTTCTGAAG | CAACAGTTTG | TAAATCACT | 2520 |
| | GCAAGGTTTT | TATTAATAAT | AGACATGTAT | ATGATTTTCA | GTCTATAGCA | TCTTTGTTAA | 2580 |
| | CATCTGCCTT | TGCGAGGAAA | TGTAAGAGTT | ATTTAACACT | ACAAGAAATT | TAACAATAGT | 2640 |
| | TGCTCTATT | TTGAATATGT | ATTAATAATG | GAGTTTCAAT | ACCTGTCTAT | ATCAACGGTG | 2700 |
| 75 | GTGCTCTTAC | TATTAGTTAA | TTGCATTTTG | GTAAAAAATA | AAAAAGCAAC | AGTTTGGCAC | 2760 |
| | TTGTCTTACA | AAAGGCACCT | AATTTAATTT | TCTGATCAGG | ATTGCTGTAT | CCAACAGTGC | 2820 |
| | TAAGTCATGG | CTGCTGCTGA | CTAGCTTGGC | ATTATTTCTG | GTTAGGTAGA | ATTCTTATTA | 2880 |
| | TTTATTTTTT | TAAGCTTTTC | AAATTGGAAG | GAACCTGATT | TTTATGTGG | CTTATATTTA | 2940 |
| | CATTGGTAAT | ATTTTGTCA | CAATATTTTT | GGTTAAAAAA | AATCCAACAA | ATTAACCTAC | 3000 |
| 80 | TGAAATATA | ACAAATTTTG | TAAACAATTT | TTTATATTAT | CTATAAAAC | GTAGACACCT | 3060 |
| | TATGTTTTC | ATGTTGTGCA | ATGTGACAGG | GGAAGCTGAT | TTAGTAGCTT | TAGCATATT | 3120 |
| | AAAAATAATT | TTTTATAATG | TAATTTCTCT | TGAGTGCAGA | CCTGACATTT | TACATTAATA | 3180 |
| | TAAATGTAAA | CATCAGAATT | ATGTTTAAAC | AACTTTAAAA | TAAAGATGAT | GTTAAAAATA | 3240 |
| | TTTTAGAGTT | ATGCTATGGA | AAAATTCTAT | CATGAAATTA | TTTTTCTCTA | GATAGCACAA | 3300 |
| | TACCAATTTT | AATTAATTTT | TTCCAATTAG | GTTACTTTTC | TTAATAAAG | TTATGCTGCC | 3360 |

| | | | | | | | |
|----|-------------|-------------|-------------|------------|------------|-------------|------|
| | TTCAAGTTTTC | CAATGGCAAG | TAGACAGGAT | ATGTTCAAGG | TTTTCTGCAC | TGTAGGCACA | 3420 |
| | GTCTCTCAAG | CATATCTCTGA | TCATGTAATG | ACTGCATAAA | CTCCATCAAC | CTAAGGTGAT | 3480 |
| | ACCTGTAAAT | AATTTATTTT | TAAAGGATGG | TGACTTTAAA | AATTATTAAT | GAACCTTGAG | 3540 |
| | AAGTTTAAAG | AGTGCTTTTA | AAACTTCACA | GTATTGCCAA | TTATCTTAGG | TTATTCAGTA | 3600 |
| 5 | TTCAAGTTTG | TGTTTCTCTG | TTTTAAACTA | AAATGTGTTT | TCTGAAGAAA | AAATAATAG | 3660 |
| | TTTACACAAA | TGTACAATCA | TAGAATAAGC | ATTTTAAGCT | GGCGACTAGT | GTTCTATAGA | 3720 |
| | TTACAAAGCA | AGAAAACCTT | CTATGAAGAT | AAATGACCTT | TTGCCTGAAG | AGTACAGATA | 3780 |
| | AAATCAAAGA | TGTGTGCAAG | CTAGTTTTTG | GAAGAAGTGA | TGCTTCTCTT | CTTTAAAGAG | 3840 |
| | ACAGTCACCA | AATACTTGTT | TTAACTCGAC | TATTGACTTG | GGCATTGAGA | GAGATGATAT | 3900 |
| 10 | ATACATCTTT | GGAAAGTGAA | GTCAATGTTC | AAGAGGTGAT | AGAAGCTTTA | CTTTTTAGTG | 3960 |
| | ATCAGAAATA | TTTAGTGAT | CTTTTCAGAC | AGGAAGAATT | TTATCATCAA | GTATTCCTT | 4020 |
| | ATAAAACCAA | GTAAACACTT | TTTATCAGTA | ACTTTTAGAA | CTTAAAGAA | AGCAAAAAGT | 4080 |
| | AAATGGAATT | GTAGGCAATT | TATGAATCCT | AGTAGATTTT | ACAATATGTA | ATTTATGTTG | 4140 |
| | TTTACAGTAT | ATAAACACTA | AGTTTGTGT | TAAATGTGAT | CAGGAATAAA | AGTATCCCAC | 4200 |
| 15 | AGGCATCTGA | CACAAATTC | AGAAATAGCC | AAAGAATTGT | TTATTTGAGG | CCAGGCAATC | 4260 |
| | CCAGCATTTT | GGGAAGCCAA | GTGGGCGAGA | TCACGAAGTC | AGGAGTTTGA | AATCAGCCTG | 4320 |
| | ACCAACATGG | TGAAACCTCT | TCTCTACTAA | AAATACAAAA | TTAGCCGGGC | ATGGTGGCAC | 4380 |
| | ATGCCTATAA | TCTCAGCTAC | TCAGGAGGCT | GAGGCAGGAG | GATCGCTTGA | ACCCGGGAGG | 4440 |
| | CAGAGGTGTC | AGTGAGCCAA | GATTGGGCCA | CTGCACTCCA | GCCCTGGCAA | CAGAGTGAGA | 4500 |
| 20 | CTCTGTCTCA | AAAAAAGAAA | AAAAAAGAAA | AGGTTTATTT | GAATAATTGG | | 4560 |
| | AAGTCAGTTT | ATACATTACT | ATTTTTCAGC | AGTAGGGAAT | TTCTCCAATT | ACATTTCATG | 4620 |
| | TGAATGAATT | TTTATTTATA | TATAGCTTAC | CCTTCCAAAA | TAAAGTGT | TTTTAATGT | 4680 |
| | TGTTTTGT | TGTTTTGT | TTTTCTTTT | TTGAGACGGA | GTTTCACTCT | TGTTGCCAG | 4740 |
| | ACTGGAGTGC | AGTGCCACAA | TCTCAGCTCA | TTGCAACCTC | TGCTTCTGG | GTTCAAGTGA | 4800 |
| 25 | TTCTGCTGCC | TCAGCTCCT | GAGTGGTTGG | GATTACAGGC | ATCCACCACC | AGGCCAGCT | 4860 |
| | AATTTTTTTG | TATTTTCAGT | AGAGATGGGG | GTTTCAACAT | GTGCGCCAGG | CTGATCTCAA | 4920 |
| | ACTCCTGACC | TCAGGTGATC | CACCTGCCTC | AGCCTCCCAA | AGCGCTGGGA | TTACAGGCAT | 4980 |
| | GAGCCATCAC | ACCCAGCGAA | AAGTTTGT | TGAATAAACA | ATATCCGAAA | GACAATTAGT | 5040 |
| | TTCTTCAGAT | GTATTTTGAA | ATTCTCTAA | AGAGCTAGTG | TTTCTATTCA | TTTTACAAT | 5100 |
| 30 | TTAAAAACAG | CTCTTAACAT | TGCTGAAGTT | GGGAGAAGCT | TCCATCTCTT | CTTAATAACA | 5160 |
| | GTGCAAGATT | TTGTAATTC | TTTTTTGTGT | TTAATGTTTA | ATAAAACGAG | TATTAAGCTT | 5220 |
| | AAATTACTGA | AGTACCTGGG | AGAAAGTAATG | ATGTGACTT | TCAAAAAAAT | GGAAAAATGCT | 5280 |
| | TTTATTTTAT | TTTCTATAAT | TTGTTAACAT | GATATGTAAA | ATTAACCTTC | GGAGCACAAT | 5340 |
| | GAAATGCCGA | TTATTTTAC | CTTGTTTGGG | CTTAAAGTAG | GTATTTAAGG | TTTATGTGTT | 5400 |
| 35 | CAAAATGCCT | TGGTAAATTG | GATGACCTCT | AACCTTACTG | TCCATATGGA | GTTTGTCAAT | 5460 |
| | CTTTATGGAT | AAGAGAACTT | AAGGAAAAAT | TACTGTTTTT | CTTCAGTCTT | TTTATATCTA | 5520 |
| | TCTGATTTAA | AATCTGTTAC | TTTATTAAAA | GGCTTCAACA | ACAGGTTGTT | AGGATGTAGT | 5580 |
| | CTTACATCCA | GGTTACATA | ATAACCCCAT | TTGAATCCAA | ATTGTGTAT | ATTTTCTTAT | 5640 |
| 40 | GCCAGCAGTA | TTGTATCCA | ATTTTAACTT | AGGTTTGT | TCTTGAG | | 5687 |

Seq ID NO: 60 DNA Sequence

Nucleic Acid Accession #: Eos sequence

| | | | | | | | |
|----|-------------|------------|------------|------------|-------------|------------|-----|
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| 45 | | | | | | | |
| | TTTTTTTTT | TTTTTTTAA | TCACAACACC | TCTGAATATG | TTTAATGACA | GAGCAATTAG | 60 |
| | AAACAAAGT | TTAATTTTAT | ACATCATAGA | ATTACTATTT | AGAAACAAAT | AGGACATGTT | 120 |
| | AGAAAGTAAGA | AAAAATAAAA | CACTTTGTG | AAGTTATATA | CCTATTTGGA | TTTTTTTAAA | 180 |
| | AGCATTACCC | AATAGGCTAT | AGAACGATGC | CAACACATAA | TGCCAGGTTG | CAAGGCATGG | 240 |
| | AGAATGGGAG | AATGTGACAT | GACTGTCTAA | TGGGTATAAA | GCTCCCTTTT | GAAGTGAAAA | 300 |
| 50 | AATTACTTTG | GATCTAGATA | GTAGTGGTAC | TGGCAAAATG | GCTAAACGCC | AATGAATAAT | 360 |
| | GCACTATAAA | TGGTTTAATT | GTATAATTTT | GTGGTGTAAT | ATTCCTATAT | CAATTATTCT | 420 |
| | TTAAATAAAC | AAGTGCTGCA | CCAGATTGGA | CCAAGAGACC | ATAGTTTGTG | AGCCCTTGTT | 480 |
| | TTATGCTACA | AATTTAATTC | CCATATGCTT | GAAATAGTAA | ATGCTGTCTAT | TTAATTCATT | 540 |
| | TACATTAGAA | ACATGGGATG | TTTTGAAACT | ATAATATGTT | ATGCAATTAT | ATGAACACTA | 600 |
| 55 | AAATTATTAC | TGTGGAATTT | TTTTATTGTT | AGTAACGGGA | GTATGCAATT | TTATTTTGCT | 660 |
| | GTACACA | | | | | | 667 |

Seq ID NO: 61 DNA Sequence

Nucleic Acid Accession #: Eos sequence

| | | | | | | | |
|----|------------|------------|------------|------------|------------|------------|-----|
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| 60 | | | | | | | |
| | GACCTAAGAA | CTTATCAAA | AACTCAGCAG | TATGAGAATA | GATCAATACA | TAGAGGGTTT | 60 |
| | CCTTTAAGTC | TTGTAGAAAC | TCATTACTCT | CCAGTCTCTT | TTTCCACTTA | TAGTAGAGAG | 120 |
| | AATCAGACTT | CGCGATATCC | AGTTAACTAT | CAATACCTTT | AAAAAATGTG | AACAAGCAGT | 180 |
| 65 | CCATCTGAAT | AATTATACCA | AATGTCAAGG | CTTTTAAAG | TGCTTAACTT | TAAAGGTOCT | 240 |
| | TTGCAGTTGT | TCAGACCTAG | ATTCTCAGTT | CAGTTAGCAC | AGAGAGAGAC | AAGGAAAAAA | 300 |
| | TGAGGAACAC | TTTCTCACG | CATAAATATT | CACTGGTTTT | TGAATACTA | TTGATTCTTT | 360 |
| | GGATAAGAAA | ATAGGTCAAC | TTTATAGCTT | TTTGTCTCGA | AATTGATTG | CGCCACAGA | 420 |
| | CAGTGGCTTG | GTGCTATATA | TCCAGCCTA | CATGGGAGGC | TGAGTGGGGA | GATCGCTTGA | 480 |
| 70 | GCCCAAAAAG | TCAGAGGTGC | AGTGAGCTGT | GATTGTGCCA | CTGTATCCCA | ACCTCAT | 537 |

Seq ID NO: 62 DNA Sequence

Nucleic Acid Accession #: Eos sequence

| | | | | | | | |
|----|------------|------------|------------|------------|------------|-------------|-----|
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| 75 | | | | | | | |
| | TTTTTTTTT | TTTTAATTTT | AATAAGTTAA | ATTTTAAATA | ATTGATTAT | TTATACTCCA | 60 |
| | AAGGATACAA | CATGCAAAAT | GTCTACCCAC | TCCAGCTACC | ATCAGTTTCA | CATTTATAAC | 120 |
| | TACTATCAAT | ATGTTTTTCA | TGTAAGACAG | CCATCACCTA | AAGGAATACT | TTTAAACAG | 180 |
| | GTTGTACAAT | AAAAACAGTT | GGACCAATAT | AAAAGAAATA | TAAATAAAGG | TGTTTTATTT | 240 |
| 80 | AAATGTAAAT | ACACAGATAC | TTCCATTAAA | TCTAAACAAA | CTTTAAAAAG | AGGAGCAAAAT | 300 |
| | AATGAGTAAT | GCCATAGAAC | ATTAGAAGAA | CACAGTTAAC | GAATGGAAAC | TTGTAAACAG | 360 |
| | ATACACACAC | ACGCATGCAT | ATATATATGT | ATCATATATA | TCAACTAAAA | GACATTTTCT | 420 |
| | TAGAGCATAT | TGAATTGTTA | ATAATTATTT | GAAGTGACAT | GTGGTGGGAC | ATAAATCAAG | 480 |
| | ACTCAGTAAA | TTTGAAGAAG | TTCAATATCA | TAAAGAATAT | ATGATCCAGC | CTTAGTAGAA | 540 |

GTAAGGGAAA TTTAAAAAAT GTAACATAAA TATCTTTAAT TTTGGAAATT AAGAAAATAC 600
 ACTTCAAAAA AATTTAAAGT CCTGCCCTCAG CCTCCCCAGT AGCTGGGATT ACAAGCATGC 660
 ACCACCATGT CCAAGCCAATT TTGTAATTAT AGTAGAGACA GG 702

5

Seq ID NO: 63 DNA Sequence

Nucleic Acid Accession #: AK025967

| | 1 | 11 | 21 | 31 | 41 | 51 | |
|----|------------|------------|------------|-------------|------------|-------------|------|
| 10 | ACAACAGGAA | CACATATAGC | TGGAATGCAG | ATGGGATCTG | TGCTACTTAC | GCTAGCCATG | 60 |
| | GGATGATTAG | AACAAGATAA | GAGACATGAG | GAAGACTTCT | TCAAGGAGGT | GCTCAAGCCA | 120 |
| | TGTTTTGGAA | AAGAGAACTC | AAGGTCTGGC | AGGGAGAAAG | GAGCAAGGTC | CTCTTCTCCC | 180 |
| | TGAAGGCTGT | CACAGTTCTT | GTGCAGAGAG | AGAGGGCACT | GCAGCACCCA | GGCGCTGACT | 240 |
| | GCCTTTTGTC | AGTCTCAATT | GCAGGCCCCC | AGCTGGAGAA | CCCAGGAGGA | AGAGGAAAAA | 300 |
| 15 | AGTTTTTTCC | TCCTCTACAC | TCCCATGCA | TGACTAAAGA | GTAGGAGGAG | TCAGCAAGGC | 360 |
| | AGACATATAT | AGTACCCAGG | AGGTGGACAA | ACAACCTGCT | TGGTGGAAAC | TCGTCTCTTT | 420 |
| | CTGGACTTAT | CCTGGTGGCA | CTGAGACTGT | GCAGATTTAG | ATCTACAATC | CACCTGGAAT | 480 |
| | TGATTTTTGT | ATATGGAGTG | AGGTCCCAAC | CTTACAGGGA | AAGCATCACC | CGAAAGTGAG | 540 |
| | AATGCCTAGA | GGCAGGAATC | ATGGAGGCTT | CCTTAAACGT | CTGTCTGCAA | CAGCAGGTGC | 600 |
| 20 | TAGAGATGAC | ACTGCAGAGT | AGAGAACAAA | GGAATCTTAG | TAATTGTTCA | ATCCAAATCTC | 660 |
| | CACACTTTAA | AGATGAAGAA | ACTGGTATTG | AGAAAAATAC | ACAGCTTATC | CAAGGTTGCA | 720 |
| | CTGCTGGTGT | GTAGCTGAGA | TGAATTTAGA | ACCCACATCT | GATGACTACA | CCATATTGCT | 780 |
| | CCCAGTTTTT | CTGTCTGTTT | CACATGTAAA | AGTCTGACTC | TTCACTTCTC | CTTTGAGTAT | 840 |
| | ATAGACTTTT | AACATTTTGT | TATGTCAAGA | TGGACTTTTC | CTCATACCCA | GCCCCTGCTT | 900 |
| 25 | TTTCTCTCTC | CTCTCAACCT | TGCAGGATCT | TTAACAAGAT | TTAAAAGGAG | TTTTTTGTTT | 960 |
| | TGTTTTGATG | TATCTAATAA | AAGTCAAGGG | AGGGAGAGGG | CCAGTATAAG | CAAGAGTACA | 1020 |
| | GTTTCTTAGT | TGTAGATGTC | GGTAGTCTGA | GGAATCAGAA | ACACACAAAG | GTTTGGAGAA | 1080 |
| | CTGGTACATG | CTCCACGGTG | GGAAGCCAGG | ACTCTTGGTA | GGATCTTGAG | GACAAGGCCAA | 1140 |
| | AGGACAATAA | AGGACCGAGG | GGATCCTAGA | GGTGGAAATCA | AGGAAGAGAA | ACTAGAGAGA | 1200 |
| 30 | GAAAAAGGAA | CTGGCTATCC | ATCCATGATG | GATCCTGTGT | GGACTGATGG | GTGGCTTGGC | 1260 |
| | ATCATCCTTT | AGTAGACTTC | ATGTGGTTGA | ATAATTGGCC | AATGGAAGGA | ATTTCTTTTT | 1320 |
| | TGGTAACAGA | CTCTGTGTGT | ACAGTTATGG | GTCTTAATTT | ATAATAAAG | GTTACATTGA | 1380 |
| | AAATTGAAAA | AAAAAAA | | | | | 1398 |

35

Seq ID NO: 64 DNA Sequence

Nucleic Acid Accession #: Eos sequence

| | 1 | 11 | 21 | 31 | 41 | 51 | |
|----|-------------|------------|------------|------------|-------------|------------|------|
| 40 | GGCAGGAGGA | GAGAAACTCC | ATCTCAAAAA | CAAAACAACA | CAAAACAAAA | AAAGAGAGAG | 60 |
| | AATCAAAAGT | TGTTCCCTGT | CTCTCTCTCT | CCACATGTGA | GCACACAAAG | AGGTCAAGTG | 120 |
| | AACACACAAT | GAGAAGGAGG | CTGCCCTGCA | GTTAAGAGAA | GAGGCCCTCAG | CATGAAACCT | 180 |
| | GCCTTACTGG | CACCTTGGTC | TTGAACCTCC | CAGCCTCTAA | AACCTGTGAG | AATAAGTTTC | 240 |
| | TGTTGTTCAA | GCCACCCAGT | CTATGGTATT | CTGTATGGCA | GCCAGAAATTA | AGACACCAGT | 300 |
| | GAAGCAAGAT | AATCAGTAAC | TGGATACTTA | ACTGTGTGGT | ATAAAACATA | GGGGCTTTAG | 360 |
| 45 | TAGAGAAGAA | AATTGGACTT | TGTTGGGGAC | ATCCTTACTA | CTTCTGCTCA | TGTATCATGC | 420 |
| | TTTAGCTTGT | TTCTGTCTTT | GGAGGAGGCT | GCAATTTTTT | AAAATACCCC | CAAAAGTACA | 480 |
| | AAGACTAATG | TTATAGCCCC | TGTGTTCTCA | TTATCCAGGC | TTAATAAATG | TTGGCCATTT | 540 |
| | TCCACTTTTT | TTTCATATAT | AAGTTTCTAC | AAAATGACAA | CACCTTAGAT | AAAGCTGAAG | 600 |
| | TTCATGTTTC | ATTCTGCATC | CCTTCCCCCA | AGGGCTTCTT | TTGCTCAATA | TGGGACTCAT | 660 |
| 50 | GAGAGTCATC | GGTGTGTGTG | GAGGCAGCTG | TTTGTGATT | TTCTGGACCA | AATAATGTTT | 720 |
| | CACCGTGTGA | CTGGACATAC | CTTAGTCTAT | CCATTCTACC | ACTGATGAGC | ATGTAAGCTG | 780 |
| | TTACTATTTT | TAACATTAAC | AAATTATCTT | GCTAACACAT | TTTTGTGCAT | GTCTTTTGGT | 840 |
| | GACCAAATGG | ACTCATTTCT | CTCAGGTATG | TATCTCAGAG | TGAAACTGTT | TTATCACAGT | 900 |
| | GTATGCTTTA | TATTTAGTGC | TTTCCAATTC | CTGATTAAGA | AATCTTTGCC | TGCTCCTAAG | 960 |
| 55 | GATGTAAAG | TATGCTCTTA | TGGCTGGCT | CAGTGGCTCA | TGCTGTAAAT | CCAGCAATTT | 1020 |
| | TGGGAGGCCA | AGGTGGGAGG | ATTGCTTGAG | GCCAGGAGTT | CAAGACCAGC | CTGGGCAACA | 1080 |
| | TACTGAGACC | CTCATCTCTA | CAAAAAAATA | AAATTTGTTT | AATTAGCTGA | GCTTGGTGGT | 1140 |
| | ATGCACCTAT | AGTCCCTAGC | ACTCAGGAGG | CTGAGGCAGG | AGGATCGCTT | GAGCCAGGGA | 1200 |
| | ATTGAGAGAT | GCAGTAAGCT | ATGATCATGC | CAGTGTATTA | CAGCCTGGGT | GATAGGGTGA | 1260 |
| 60 | GACCCGTGCT | CTAAAGAGAT | ACATCTATTA | AAAATAATAT | TATTTTATTT | TATTTTATTT | 1320 |
| | TATTTTATTA | TTATACTTTA | AGTTTATGGG | TACATGTGCA | CATTGTGCAG | GTTAGTTACA | 1380 |
| | TATGTATACA | TGTGCCATGC | TGGTGCATCG | CACCCACTAA | CTCGTCATCT | AGCATTAGGT | 1440 |
| | ATATCTCCCA | GTGCTATCCC | TCCCCCTCCC | CCCGACCCCA | CAACAGTCCC | CAGAGTGTGA | 1500 |
| 65 | TGTTCCCTTT | CCTGTGTCCA | TGTGATCTCA | TTGTTCAATT | CCCACCTATG | AGTGAGAATA | 1560 |
| | TGCGGTGTTT | GGTTTTTTGT | TCTTGCATA | GTTTACTGAG | AATGATGATT | TCCAATTICA | 1620 |
| | TCCATGTCCC | TACAAAGGAC | ATGAACCTAT | CATTTTTTAT | GGCTGCATAG | TAAAAATACA | 1680 |
| | TTTTAAAAAA | TAATAAATTA | TTCTCTTATG | TTATTGTCTA | GAATCTTCAT | TATTTTACCT | 1740 |
| | TTTCAATTTA | GATCTACAAT | CCACCTGGAA | TTGATTTTTG | TATATGGAGT | GAGGTCCAC | 1800 |
| | ACTTACAGGG | TAAGTATCAC | CCGAAAGTGA | GAATGCCTAG | AGGCAGGAAT | CATGGAGGCT | 1860 |
| 70 | TCCTTAACCG | TCTGTCTGCA | ACAGCAGGTG | CTAGAGATGA | CATGTCAGAG | TAGAGAACAA | 1920 |
| | AGGAATCTTA | GTAATTGTTT | AATCCAATCT | CCACACTTTA | AAGATGAAGA | AACGTGTATT | 1980 |
| | GAGAAAAATA | CACAGCTTAT | CCAAGGTTGC | ACTGCTGGTT | GGTAGCTGAG | ATGAATTTAG | 2040 |
| | AACCCACATC | TGATGACTAC | ACCATATTGC | TCCAGTTTTC | CCTGTCTGTT | CCACATGTAA | 2100 |
| | AAGTCTGACT | CTTCACCTCT | CCTTTGAGTA | TATAGACTTT | TAACATTTT | GTATGTCAAG | 2160 |
| 75 | ATGGACTTTT | CCTCATACCC | AGCCCCGTCC | TTTTCTCCTC | CCTTCATACC | TTGAGGATC | 2220 |
| | TTTAAACAGAA | TTTAAAGGGA | GTTTTTGT | TTGTTTTGAT | GTATCTAATA | AAAGTCAAGG | 2280 |
| | GAGGGAGAGG | GCCAGTATAA | GCAAGAGTAC | AGTTTCTTAG | TTTGTAGATG | CGGTAGTCTG | 2340 |
| | AGGAATCCTA | AACACACAAA | GGTTTGGAGA | ACTGCTACAT | GCTCCAGGTT | GGGAAGCCAG | 2400 |
| | GACTCTTGTT | AGGATCTTGA | GGACAAGGCA | AAGGACAATA | AGAGAGCGAG | GGGATCCTAG | 2460 |
| 80 | AGGTGGAATC | AAGGAAGAGA | AACTAGAGAG | AGAAAAAGGA | ACTGGCTATC | CATCCATGAT | 2520 |
| | GGATCCTGTG | TGGACTGATG | GGTGGCTTGG | CATCATCCTT | TAGTAGACTT | CATGTGGTTG | 2580 |
| | AATAAATGGC | CAATGGAAGG | AATTTCTTTT | TTGGTAACAG | ACTCTGTGTG | TACAGTTATG | 2640 |
| | GGTCTTAATT | TATAATAAAA | GGTTACATTG | AAAAATTGAA | AAAAAAAATA | AAAAAAAATA | 2700 |
| | GCATTATAAG | TGTACTTCTA | GCCTTACTTC | GTCCGGGTAA | TTGATCTCTG | CTCTTGTCTG | 2760 |
| | CTG | | | | | | 2763 |

Seq ID NO: 65 DNA Sequence
Nucleic Acid Accession #: Eos sequence
Coding sequence: 1..1863

| | | | | | | | |
|----|------------|-------------|------------|------------|-------------|------------|------|
| 5 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| | ATGAGTAAGA | GCAAAATGCTC | CGTGGGACTC | ATGTCTTCGG | TGGTGGCCCC | GGCTAAGGAG | 60 |
| | CCCAATGCCG | TGGGCCCGAA | GGAGGTGGAG | CTCATCTTGG | TCAAGGAGCA | GAACGGAGTG | 120 |
| 10 | CAGCTCACCA | GCTCCACCCT | CACCAACCCT | CGGCAGAGCC | CCGTGGAGGC | CCAGGATCGG | 180 |
| | GAGACCTGGG | GCAAGAAGAT | CGACTTTCTC | CTGTCCGTCA | TTGGCTTTGC | TGTGGACCTG | 240 |
| | GCCAACTGCT | GGCGGTTCCC | CTACCTGTGC | TACAAAAATG | GTGGCGGTGC | CTTCTGGTTC | 300 |
| | CCCTACCTGC | TCTTCTGGT | CATTGCTGGG | ATGCCACTTT | TCTACATGGA | GCTGGCCCTC | 360 |
| | GGCCAGTTCA | ACAGGGAAGG | GGCCGCTGGT | GTCTGGAAGA | TCTGCCCAT | ACTGAAAGGT | 420 |
| 15 | GTGGGCTTCA | CGGTATCCT | CATCTCACTG | TATGTGCGCT | TCTTCTACAA | CGTCATCATC | 480 |
| | GCCTGGGCGC | TGCATATCT | CTTCTCTCTC | TTACCCAGG | AGCTCCCTG | GATCCACTGC | 540 |
| | AACAACCTCT | GGAAACAGCC | CAACTGTCTG | GATGCCATC | CTGGTGACTC | CAGTGGAGAC | 600 |
| | AGCTCGGGCC | TCAACAGCAC | TTTGGGACC | ACACCTGCTG | CCGAGTACTT | TGAACGTGGC | 660 |
| | GTGCTGCACC | TCCACCAGAG | CCATGGCATC | GACGACCTGG | GGCTCCGCG | GTGGCAGCTC | 720 |
| | ACAGCCTGCC | TGGTGCTGGT | CATCGTGCTG | CTCTACTTCA | GCCTCTGGAA | GGGCGTGAAG | 780 |
| 20 | ACCTCAGGGA | AGGTGGTATG | GATCAGAGCC | ACCATGCCAT | ACGTGGTCTC | CACTGCCCTG | 840 |
| | CTCCTGCGTG | GGGTCACTCT | CCCTGGAGCC | ATAGACGGCA | TCAGAGCATA | CCTGAGCGTT | 900 |
| | GACTTCTACT | GGCTCTGCGA | GGCGTCTGTT | TGGATTGACG | CGGCCACCCA | GGTGTGCTTC | 960 |
| | TCCCTGGGCG | TGGGTTCTGG | GGTGCTGATC | GCCTTCTCCA | GCTCAACAA | GTTCAACAA | 1020 |
| 25 | AACTGTCTCA | GGGAGCGGAT | TGTCAACACC | TCCATCAACT | CCCTGACGAG | CTTCTCTCTC | 1080 |
| | GGCTTCTGTC | TCTTCTCTCT | CCTGGGGTAC | ATGGCAGAGA | AGCACAGTGT | GCCCCATCGG | 1140 |
| | GACGTGGGCA | AGGACGGGCC | AGGGCTGATC | TTTATCATCT | ACCCGGAAGC | CATCGGCAAC | 1200 |
| | CTCCCTCTGT | CCTCAGCGCTG | GGCCGTGGTC | TTCTTCTATC | TGCTGTCTAC | CTGGGTATC | 1260 |
| | GACAGCGCCA | TGGGTGGTAT | GGAGTCAGTG | ATCACCGGGC | TCATCGATGA | GTTCCAGCTG | 1320 |
| 30 | CTGCACAGAC | ACCGTGAGCT | CTTCACGCTC | TTTATCTGTC | TGGCGACCTT | CCTCTGTCTC | 1380 |
| | CTGTTCTGCG | TCAACCAACG | TGGCATCTAC | GTCTTCAAGC | TCCTGGACCA | TTTTGCAGCC | 1440 |
| | GGCAGCTCCA | TCTCTTTTGG | AGTGCTCATC | GAAGCCATCG | GAGTGGCCCTG | GTTCTATGTT | 1500 |
| | GTTGGGCAGT | TCAGGAGCGA | CATCCAGCAG | ATGACCGGGC | AGCGGCCAG | CCGTACTGG | 1560 |
| | CGGCTGTGCT | GGAAGCTGGT | CAGCCCTGCT | TTTCTCTGTT | TGCTGTGCTG | GGTCAAGATT | 1620 |
| 35 | GTGACCTTCA | GACCCGCCCA | CTACGGAGCC | TACATCTTCC | CCGACTGGGC | CAACGCGCTG | 1680 |
| | GGCTGGGTCA | TGCCACATC | CTCCATGGCC | ATGGTGCCCA | TCTATGCGGC | CTACAAGTTT | 1740 |
| | TGCAGCCTGC | CTGGGTCTTT | TCGAGAGAAA | CTGGCCTAAG | CCATTGCAAC | CGAGAAGGAC | 1800 |
| | CGTGAGCTGG | TGGACAGAGG | GGAGGTGGGC | CAGTTCAGGC | TCCGCCACTG | GCTCAAGGTG | 1860 |
| | TAG | | | | | | 1863 |

Seq ID NO: 66 DNA Sequence
Nucleic Acid Accession #: NM_022073.1
Coding sequence: 327..1046

| | | | | | | | |
|----|------------|-------------|------------|------------|------------|------------|------|
| 45 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| | GAGTCTGGCC | GCAGTCGCGG | CAGTGGTGCC | TTCCCATCCC | CAAAAGGCGC | CCTCCGACTC | 60 |
| | CTTGGCGCGC | ACTGTGCGCC | GGGCCAGTCC | GGAAACGGGT | CGTGGAGCTC | CGCACCACTC | 120 |
| | CGCGTGGTTC | CCGAAGGCAG | ATCCCTTCTC | CCGAGAGTTG | CGAGAAACTT | TCCCTTGTCC | 180 |
| | CCGACGCTGC | AGCGGCTCGG | GTACCGTGCG | AGCCGCAAGT | TTCTGAACCC | CGGGCCACGC | 240 |
| 50 | TCGCCGCGCC | TGGGCTTTCG | GCTCGTGTAG | ATCGTTCCCT | CTCTGGTTGC | ACGCTGGGGA | 300 |
| | TCCCGGACCT | CGATTCTGCG | GGCGAGATGC | CCCTGGGACA | CATCATGAGG | CTGGACCTGG | 360 |
| | AGAAAAATGC | CCTGGAGTAC | ATCGTGCCCT | GTCTGCACGA | GGTGGGCTTC | TGCTACCTGG | 420 |
| | ACAACTTCTT | GGCGAGGTGG | GTGGGCGACT | GGTCTCTGGA | GGCGTCAAG | CAGCTGCACT | 480 |
| | GCACCGGGGC | CCTGCGGGAC | GGCCAGCTGG | CGGGGCGCGG | CGCCGCGCTC | TCCAAGCGAC | 540 |
| 55 | ACCTGCGGGG | CGACAGATGC | ACGTGGATCG | GGGGCAACGA | GGAGGGCTGC | GAGGCCATCA | 600 |
| | GCTTCTCTCT | GTCCCTCATC | GACAGGCTGG | TCTCTACTG | CGGGAGCCCG | CTGGGCAAA | 660 |
| | ACTACGTCAA | GGAGAGGTCT | AAGGCAATGG | TGGCTTGCTA | TCCGGGAAAT | GGAACAGGTT | 720 |
| | ATGTTGCGCA | CGTGGACAA | CCCAACGGTG | ATGGTGGCTG | CATCACCTGC | ATCTACTATC | 780 |
| | TGAACAAGAA | TGGGATGCC | AAGCTACATG | GTGGGATCCT | CGCGATATTT | CCAGAGGGGA | 840 |
| 60 | AATCATTAT | AGCAGATGTG | GAGCCCATTT | TTGACAGACT | CCTGTTCTTC | TGGTCAGATC | 900 |
| | GTAGGAACCC | ACACGAAGTG | CAGCCCTCTT | ACGCAACCCG | ATATGCTATG | ACTGTCTGGT | 960 |
| | ACTTTGATGC | TGAAGAAAGG | GCAGAAGCCA | AAAAGAAATT | CAGGAATTTA | ACTAGGAAAA | 1020 |
| | CTGAATCTGC | CCTCACTGAA | GACTGACCGT | GCTCTGAAAT | CTGCTGGCCT | TGTTCAATTT | 1080 |
| | AGTAACGGTT | CCTGAATTTT | CTTAAATCTT | TTGAGATCCA | AAGATGGCCT | CTTCAGTGAC | 1140 |
| | AACAATCTCC | CTGCTACTTC | TTGATCCTTT | CACATCCCTG | TCTTGTGTGT | GGTACTTCTA | 1200 |
| 65 | GTTTTCTTGC | CAAGACTGTG | TTGATCTTCA | GATACTCTCT | TTGCCAGATG | AAGTTATTTG | 1260 |
| | CTAACTCCAG | AAATTTCTGC | AGACATCTTA | CTCGGCCAGC | GGTTTACCTG | ATAGATTCCG | 1320 |
| | TAATACTATC | AAGAGAAGAG | CCTAGGAGCA | CAGCGAGGGA | ATGAACCTTA | CTTGCACTTT | 1380 |
| | ATGTATACTT | CCTGATTTGA | AAGGAGGAGG | TTTGAAGAAG | AAAAAATGGA | GCTGGTAGAT | 1440 |
| 70 | GCCACAGAGA | GGCATCACGG | AAGCCTTAAC | AGCAGGAAAC | AGAGAAATTT | GTGTCATCTG | 1500 |
| | AACAATTTCC | AGATGTTCTT | AATCCAGGGC | TGTTGGGGTT | TCTGGAGAA | TATCACAACC | 1560 |
| | TAATGACATT | AATACCTCTA | GAAAGGGCTG | CTGTATAGT | GAACAATTTA | TAAGTGTCCC | 1620 |
| | ATGGGGCAGA | CACCTCTTTT | TTCCAGTCC | TGCAACCTGG | ATTTTCTGCC | TCAGCTCCAT | 1680 |
| | TTTGCTGAAA | ATAATGACTT | TCTGAATAAA | GATGGCAACA | CAATTTTTC | TCCATTTTCA | 1740 |
| | GTTCTTACCT | GGGAACCTAA | TTCCCCAGAA | GCTAAAAAAC | TAGACATTAG | TTGTTTGGT | 1800 |
| 75 | TGCTTTGTG | GAATGGAATT | TAAATTTAAA | TGAAAGGAAA | AATATATCCC | TGGTAGTTTT | 1860 |
| | GTGTTAAACA | CTGATAACTG | TGGAAGAGGC | TAGGTCTACT | GATATACAAT | AAACATGTGT | 1920 |
| | GCATCTTGAA | CAATTGAGA | GGGGAGGTGG | AGTTGGAAAT | GTGGGTGTTT | CTGTTTTTTT | 1980 |
| | TTTTTTTTTT | TTTTTTTTTT | AGTTTTCTTT | TTTAATGAGC | TCACCCCTTA | ACACAAAAAA | 2040 |
| 80 | AGCAGGGTGA | TGTATTTTAA | AAAAGGAAGT | GGAATAAAAA | AAATCTCAAA | GCTATTTGAG | 2100 |
| | TTCTGTCTG | TCCCTAGCAG | TCTTTCTTCA | GCTCACTTGG | CTCTCTAGAT | CCACTGTGGT | 2160 |
| | TGGCAGTATG | ACCAGAAATCA | TGGAACCTGC | TAGAATCTGT | GAAGCTTCTA | CTCCTGCACT | 2220 |
| | AAGCACAGAT | CGCACTGCCT | CAATAACTTG | GTATTGAGCA | CGTATTTTGC | AAAAGCTACT | 2280 |
| | TTTCTAGTT | TTTCTAGTTA | CTTTTCTAGT | TTAAAAATCC | CTTTAATTTT | TTGCTTGAAG | 2340 |
| | ATCCCATGAA | CATTAAAGAG | CCAGAAATAT | TTTCTTTTGT | TATGTACGGA | TATATATATA | 2400 |

5
TATATAGTCT TCCAAGATAG AAGTTTACTT TTTCTCTTTC TGGTTTGGGA AAATTTCCAG 2460
ATAAGACATG TCACCATTA TTTCTCAACGA CTGCTCTATT TTGTTGTACG GTAATAGTTA 2520
TCACCTTCTA AATTACTATG TAATTTACTC ACTTATTATG TTTATTGTCT TGTATCCTTT 2580
CTCTGGAGTG TAAGCACAAT GAAGACAGGA ATTTTGTATA TTTTAAACCA ATGCAACATA 2640
CTCTCAGCAC CTAAATAGT GCCGGGAACA TAGTAAGGGC TCAGTAAATA CTGTGTGAAT 2700
AAACTCAGTC TCCTACATTA GCATTCTAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 2760
AAAAAAAAAG 2770

10 Seq ID NO: 67 DNA Sequence
Nucleic Acid Accession #: NM_139314.1
Coding sequence: 196..1416

| | | | | | | |
|----|-------------|------------|------------|-------------|------------|-----------------|
| 1 | 11 | 21 | 31 | 41 | 51 | |
| 15 | ATAAAAACCG | TCCTCGGGCG | CGGCGGGGAG | AAGCCGAGCT | GAGCGGATCC | TCACACGACT 60 |
| | GTGATCCGAT | TCTTTCCAGC | GGCTTCTGCA | ACCAAGCGGG | TCTTACCCCC | GGTCTCTCCG 120 |
| | GTCTCCAGTC | CTCGCACCTG | GAACCCCAAC | GTCCCGGAGA | GTCCCGGAAT | CCCGCTCCCC 180 |
| | AGGCTACCTA | AGAGGATGAG | CGGTGCTCCG | ACGGCCGGGG | CAGCCCTGAT | GCTCTGCGCC 240 |
| | GCCACCGCCG | TGCTACTGAG | CGCTCAGGGC | GGACCCGTGC | AGTCCAAGTC | GCCCGGCTTT 300 |
| 20 | GGTCTCTGGG | ACGAGATGAA | TGTCTTGGCG | CACGACTCC | TGCAGCTCGG | CCAGGGGCTG 360 |
| | CGCGAACAGC | CGGAGCGCAC | CCGCAGTCAG | CTGAGCGCGC | TGGAGCGGCG | CCTGAGCGCG 420 |
| | TGCGGGTCCG | CCTGTGAGGG | AACCGAGGGG | TCCACCGACC | TCCCGTTAGC | CCCTGAGAGC 480 |
| | CGGGTGGACC | CTGAGGTCTT | TCACAGCCTG | CAGACACAAC | TCAAGGCTCA | GAACAGCAGG 540 |
| | ATCCAGCAAC | TCTTCCACAA | GGTGGCCGAG | CAGCAGCGGC | ACCTGGAGAA | GCAGCACCTG 600 |
| 25 | CGAATTGAGC | ATCTGCAAG | CCAGTTTGGC | CTCCTGGACC | ACAAGCACCT | AGACCATGAG 660 |
| | GTGGCCAAGC | CTGCCCAGAG | AAAGAGGCTG | CCGAGATGG | CCCAGCCAGT | TGACCCCGGT 720 |
| | CACAAATGTCA | GCCGCTGCA | CCGCTGCCCG | AGGGATTGCC | AGGAGCTGTT | CCAGGTTGGG 780 |
| | GAGAGGCAGA | GTGGACTATT | TGAAATCCAG | CCTCAGGGGT | CTCCGCCATT | TTTGGTGAAC 840 |
| | TGCAAGATGA | CCTCAGATGG | AGGCTGGACA | GTAATTGAGA | GGCGCCACGA | TGGCTCAGTG 900 |
| 30 | GACTTCAACC | GGCCCTGGGA | AGCCTACAAG | GCGGGGTTTG | GGGATCCCCA | CGCGAGTTTC 960 |
| | TGGCTGGGTC | TGGAGAAGGT | GCATAGCATC | ACGGGGGACC | GCAACAGCCG | CCTGGCCGTG 1020 |
| | CAGCTGGGGC | ACTGGGATGG | CAACGCCGAG | TTGCTGCAGT | TCTCCGTGCA | CCTGGGTGGC 1080 |
| | GAGGACACGG | CCTATAGCCT | GCAGCTCACT | GCACCCGTGG | CCGGCCAGCT | GGCGCCACCC 1140 |
| | ACCGTCCAC | CCAGCGGCTT | CTCGTACCC | TTCTCCACTT | GGGACCAGGA | TCACGACCTC 1200 |
| 35 | CGCAGGGACA | AGAACTGCGC | CAAGAGCCTC | TCTGGAGGCT | GGTGGTTTGG | CACCTGCAGC 1260 |
| | CATTCCAACC | TCAACGGCCA | GTACTTCCGC | TCCATCCCAAC | AGCAGCGGCA | GAAGCTTAAG 1320 |
| | AAGGGAATCT | TCTGGAAGAC | CTGGCGGGGC | CGCTACTACC | CGCTGCAGGC | CACCACCATG 1380 |
| | TTGATCCAGC | CCATGGCAGC | AGAGGCGAGC | TCCTAGCGTC | CTGGCTGGGC | CTGGTCCCAG 1440 |
| | GCCACGAAA | GACGGTGACT | CTTGGCTCTG | CCCGAGGATG | TGGCGTTTCC | CTGCCTGGGC 1500 |
| 40 | AGGGGCTCCA | AGGAGGGGCC | ATCTGGAAC | TTGTGGACAG | AGAAGAAGAC | CACGACTGGA 1560 |
| | GAAGCCCCCT | TTCTGAGTGC | AGGGGGGCTG | CATGCGTTGC | CTCCTGAGAT | CGAGGCTGCA 1620 |
| | GGATATGCTC | AGCTCTAGA | GGCGTGGACC | AAGGGGCATG | GAGCTTCACT | CCTTGCTGGC 1680 |
| | CAGGAGTTTG | GGGACTCAGA | GGGACCACTT | GGGGCCAGCC | AGACTGGCCT | CAATGGCGGA 1740 |
| | CTCAGTCACA | TTGACTGACG | GGGACAGGG | CTTGTGTGGG | TCGAGAGCGC | CCTCATGGTG 1800 |
| 45 | CTGGTGCTGT | TGTGTGTAGG | TCCCTGGGG | ACACAAGCAG | GGGCCAATGG | TATCTGGGCG 1860 |
| | GAGTCCACAG | AGTTCTTGGA | ATAAAGCAA | CCTCAGAACA | CTTAAAAAAA | AAAAAAA 1920 |
| | AAAAAAA | AAAAAAA | AAAAAAA | AAAAAAA | AAAAAAA | 1967 |

50 Seq ID NO: 68 DNA Sequence
Nucleic Acid Accession #: NM_016109.2
Coding sequence: 196..1416

| | | | | | | |
|----|-------------|------------|------------|-------------|------------|-----------------|
| 1 | 11 | 21 | 31 | 41 | 51 | |
| 55 | ATAAAAACCG | TCCTCGGGCG | CGGCGGGGAG | AAGCCGAGCT | GAGCGGATCC | TCACACGACT 60 |
| | GTGATCCGAT | TCTTTCCAGC | GGCTTCTGCA | ACCAAGCGGG | TCTTACCCCC | GGTCTCTCCG 120 |
| | GTCTCCAGTC | CTCGCACCTG | GAACCCCAAC | GTCCCGGAGA | GTCCCGGAAT | CCCGCTCCCC 180 |
| | AGGCTACCTA | AGAGGATGAG | CGGTGCTCCG | ACGGCCGGGG | CAGCCCTGAT | GCTCTGCGCC 240 |
| | GCCACCGCCG | TGCTACTGAG | CGCTCAGGGC | GGACCCGTGC | AGTCCAAGTC | GCCCGGCTTT 300 |
| 60 | GGTCTCTGGG | ACGAGATGAA | TGTCTTGGCG | CACGACTCC | TGCAGCTCGG | CCAGGGGCTG 360 |
| | CGCGAACAGC | CGGAGCGCAC | CCGCAGTCAG | CTGAGCGCGC | TGGAGCGGCG | CCTGAGCGCG 420 |
| | TGCGGGTCCG | CCTGTGAGGG | AACCGAGGGG | TCCACCGACC | TCCCGTTAGC | CCCTGAGAGC 480 |
| | CGGGTGGACC | CTGAGGTCTT | TCACAGCCTG | CAGACACAAC | TCAAGGCTCA | GAACAGCAGG 540 |
| | ATCCAGCAAC | TCTTCCACAA | GGTGGCCGAG | CAGCAGCGGC | ACCTGGAGAA | GCAGCACCTG 600 |
| | CGAATTGAGC | ATCTGCAAG | CCAGTTTGGC | CTCCTGGACC | ACAAGCACCT | AGACCATGAG 660 |
| 65 | GTGGCCAAGC | CTGCCCAGAG | AAAGAGGCTG | CCCGAGATGG | CCCAGCCAGT | TGACCCGGCT 720 |
| | CACAAATGTCA | GCCGCTGCA | CCGCTGCCCG | AGGGATTGCC | AGGAGCTGTT | CCAGGTTGGG 780 |
| | GAGAGGCAGA | GTGGACTATT | TGAAATCCAG | CCTCAGGGGT | CTCCGCCATT | TTTGGTGAAC 840 |
| | TGCAAGATGA | CCTCAGATGG | AGGCTGGACA | GTAATTGAGA | GGCGCCACGA | TGGCTCAGTG 900 |
| | GACTTCAACC | GGCCCTGGGA | AGCCTACAAG | GCGGGGTTTG | GGGATCCCCA | CGCGAGTTTC 960 |
| 70 | TGGCTGGGTC | TGGAGAAGGT | GCATAGCATC | ACGGGGGACC | GCAACAGCCG | CCTGGCCGTG 1020 |
| | CAGCTGGGGC | ACTGGATGG | CAACGCCGAG | TTGCTGCAGT | TCTCCGTGCA | CCTGGGTGGC 1080 |
| | GAGGACACGG | CCTATAGCCT | GCAGCTCACT | GCACCCGTGG | CCGGCCAGCT | GGCGCCACCC 1140 |
| | ACCGTCCAC | CCAGCGGCTT | CTCGTACCC | TTCTCCACTT | GGGACCAGGA | TCACGACCTC 1200 |
| | CGCAGGGACA | AGAACTGCGC | CAAGAGCCTC | TCTGGAGGCT | GGTGGTTTGG | CACCTGCAGC 1260 |
| 75 | CATTCCAACC | TCAACGGCCA | GTACTTCCGC | TCCATCCCAAC | AGCAGCGGCA | GAAGCTTAAG 1320 |
| | AAGGGAATCT | TCTGGAAGAC | CTGGCGGGGC | CGCTACTACC | CGCTGCAGGC | CACCACCATG 1380 |
| | TTGATCCAGC | CCATGGCAGC | AGAGGCGAGC | TCCTAGCGTC | CTGGCTGGGC | CTGGTCCCAG 1440 |
| | GCCACGAAA | GACGGTGACT | CTTGGCTCTG | CCCGAGGATG | TGGCCAAGAC | CACGACTGGA 1500 |
| | GAAGCCCCCT | TTCTGAGTGC | AGGGGGGCTG | CATGCGTTGC | CTCCTGAGAT | CGAGGCTGCA 1560 |
| 80 | GGATATGCTC | AGACTCTAGA | GGCGTGGACC | AAGGGGCATG | GAGCTTCACT | CCTTGCTGGC 1620 |
| | CAGGGAGTTG | GGGACTCAGA | GGGACCACTT | GGGGCCAGCC | AGACTGGCCT | CAATGGCGGA 1680 |
| | CTCAGTCACA | TTGACTGACG | GGGACAGGG | CTTGTGTGGG | TCGAGAGCGC | CCTCATGGTG 1740 |
| | CTGGTGCTGT | TGTGTGTAGG | TCCCTGGGG | ACACAAGCAG | GCGCCAATGG | TATCTGGGCG 1800 |
| | GAGTCCACAG | AGTTCTTGGA | ATAAAGCAA | CCTCAGAACA | CTT | 1843 |

Seq ID NO: 69 DNA Sequence
Nucleic Acid Accession #: NM_001216.1
Coding sequence: 43..1422

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5 1 11 21 31 41 51
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GCCCGTACAC ACCGTGTGCT GGGACACCCC ACAGTCAGCC GCATGGCTCC CCTGTGCCCC 60
AGCCCCCTGGC TCCCTCTGTT GATCCCGGCC CCTGCTCCAG GCCTCACTGT GCAACTGCTG 120
CTGTCACTGC TGCTTCTGAT GCCTGTCCAT CCCCAGAGGT TGCCCCGGAT GCAGGAGGAT 180
TCCCCCTTGG GAGGAGGCTC TTCTGGGGAA GATGACCCAC TGGGCGAGGA GGATCTGCCC 240
10 AGTGAAGAGG ATTACCCAG AGAGGAGGAT CCACCCGGAG AGGAGGATCT ACCTGGAGAG 300
GAGGATCTAC CTGGAGAGGA GGATCTACCT GAAGTTAAGC CTAAATCAGA AGAAGAGGGC 360
TCCCTGAAGT TAGAGGATCT ACCTACTGTT GAGGCTCCTG GAGATCTCA AGAACCCAG 420
AATAATCCCC ACAGGACAA AGAAGGGGAT GACCAGAGTC ATTGGCGCTA TGGAGGCGAC 480
CGCCCTGGC CCGGCTGTC CCCAGCCTGC GCGGGCCGCT TCCAGTCCCC GGTGGATATC 540
15 CGCCCCCAGC TCGCCGCTT CTGCCCGGCC CTGGGCCCCC TGGAACTCCT GGGCTTCCAG 600
CTCCCGCCGC TCCCAGAACT GCGCTGCGC AACAAATGGCC ACAGTGTGCA ACTGACCCTG 660
CCTCTGCGGC TAGAGATGGC TCTGGGTCCC GGGCGGGAGT ACOGGGCTCT GCAGCTGCAT 720
CTGCACTGGG GGGCTGCAGG TCGTCCGGGC TCGGAGCACA CTGTGGAAAG CCACGTTTC 780
20 CTGCGGAGA TCACCTGAGT ACCGCTTTG CAGAGTTGA CGAGGCTTTG AGAGGCTTTG 840
GGGCGCCCGG GAGGCTGGC CGTGTGGCC GCCTTTCTGG AGGAGGGCCC GGAAGAAAAC 900
AGTGCTATG AGCAGTTGCT GTCTCGCTTG GAAGAAATCG CTGAGGAAGG CTCAGAGACT 960
CAGGTCCAG GACTGGACAT ATCTGCATC CTGCCCTCTG ACTTCAGCG CTACTTCAA 1020
TATGAGGGGT CTCTGACTAC ACCGCCCTGT GCCAGGGTG TCATCTGGAG TGTGTTTAA 1080
25 CAGACAGTGA TGCTGAGTGC TAAGCAGCTC CACACCCCTC CTGACACCTC GTGGGACCT 1140
GGTGACTCTC GCCTACAGCT GAACTTCCGA GCGACGAGC CTTTGAATGG GCGAGTGATT 1200
GAGGCTCCT TCCCTGCTGG AGTGGACAGC AGTCTCGGG CTGCTGAGCC AGTCCAGCTG 1260
AATTCTTGCC TGGCTGCTGG TGACATCCTA GCCCTGGTTT TTGGCTCCTT TTTTGTCTGC 1320
ACCAAGCTGC CGTCTCTGT GCAGATGAGA AGGCAGCACA GAAGGGGAAC CAAAGGGGGT 1380
GTGAGCTACT GGTAGCCAGA CTGAGCCGAG ACTGGAGCCT AGAGGCTGGA TCTTGGAGAA 1440
30 TGTGAGAAGC CAGCCAGAGG CATCTGAGG GAGCCGGTA ACTGTCTGT CCTGCTCATT 1500
ATGCCACTTC CTTTAACTG CCAAGAAATT TTTTAAATA AATATTTATA AT 1552
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Seq ID NO: 70 DNA Sequence
Nucleic Acid Accession #: NM_003039.1
Coding sequence: 107..1612

```
35 1 11 21 31 41 51
| | | | |
CTTCTCTCTC CATTCACTGC ACGCGTACT TTGGCTAAAA GGAGGTGAGC GGCACCTCTC 60
CCTTCCAGAG CAAGCATGGA GCAACAGGAT CAGAGCATGA AGGAAGGGAG GCTGACGCTT 120
40 GTGCTTGCCC TGGCAACCTT GATAGCTGCC TTGGGTCTAT CCTTCCAGTA TGGGTACAAC 180
GTGGCTGCTG TCAACTCCCC AGCACTGCTC ATGCAACAAT TTTACAATGA GACTTACTAT 240
GGTAGGACCG GTGAATTCTT GGAAGACTTC CCCTTGACGT TGCTGTGGTC TGTAAACGCTG 300
TCCATGTTTC CATTGGAGG GTTTATCGGA TCCCTCCTGG TCGGCCCTTT GGTGAATAAA 360
45 TTTGGCAGAA AAGGGGCTT GCTGTTCAAC AACATATTTT CTATCGTGCC TGCATCTTA 420
ATGGGATGCA GCAGAGTCGC CACATCATT GAGCTTATCA TTATTTCCAG ACTTTTGGTG 480
GGAATATGTG CAGGTGTATC TTCAAACGTG GTCCCATAGT ACTTAGGGGA GCTGGCCCTT 540
AAAAACCTGC GGGGGGCTCT CGGGGTGGTG CCCCAGCTCT TCATCACTGT TGGCATCCTT 600
GTGGCCAGAA TCTTTGGTCT TCGGAATCTC CTTGCAAAAG TAGATGGCTG GCCGATCCTG 660
50 TGGGGCTGA CCGGGGCTCC CGGGGCGCTG CAGCTCCTTC TGCTGCCCTT CTTCCCGAG 720
AGCCCCAGGT ACCTGCTGAT TCAGAAGAAA GACGAAGCGG CCGCCAAGAA AGCCCTACAG 780
ACGTGCGCG GCTGGGACTC TGTGGACAGG GAGGTGGCCG AGATCCGGGA GGAGGATGAG 840
GCAGAGAAGG CCGCGGCTT CATCTCGTG CTGAAGCTGT TCGGATGCG CTGCTGCGC 900
TGGCAGCTGC TGTCCATCAT CGTCTCATG GCGGCCAGC AGCTGTGGG CGTCAACGCT 960
55 ATCTACTACT ACGCGACCA GATCTACCTG AGCGCGGGG TGCGGAGGA GCAGTGCAG 1020
TAGGTGACG CCGGCACCGG GCGCGTGAAC GTGGTATGTA CCTTCTGCGC CGTGTTCGTG 1080
GTGGAGCTCC TGGGTGGAG GCTGCTGCTG CTGCTGGGCT TCTCCATCTG CCTCATAGCC 1140
TGCTGCGTGC TCACTGCAGC TCTGGCACTG CAGGACACAG TGTCTGGAT GCCATACATC 1200
AGCATGCTCT GTGTCTCTC CTACGTCTA GGACATGCCC TCGGGCCAG TCCCATACCC 1260
60 GCGCTGCTCA TCACTGAGT CTTCTGCGC TCCTCTGCGC CATCTGCTT CATGGTGGG 1320
GGCAGTGTG ACTGGCTCTC CAACTTCACC GTGGGCTTGA TCTTCCGCTT CATCCAGGAG 1380
GGCTCGGCC CGTACAGCTT CATGTCTTC GCGTGATCT GCCTCCTCAC CACCATCTAC 1440
ATCTTCTTGA TTGTCCCGGA GACCAAGGCC AAGACGTTCA TAGAGATCAA CCAGATTTTC 1500
ACCAAGATGA ATAAGGTGTC TGAAGTGTAC CCGGAAAAGG AGGAACGTAA AGAGCTTCCA 1560
65 CTTGTCACTT CCGAACAGTG ACTCTGAGA GGAAGCCAGT GGAGCTGGTC TGGCAGGGG 1620
TTCCCACTTT GGCTTATTTT TCTGACTTCT AGCTGTCTGT GAATATCCAG AAATAAAACA 1680
ACTCTGATGT GGAATGAGT CCTCATCTCC AGCCTCCCA CCCCAGTGGG AACTGTGCAA 1740
AGGGCTGCCT TGCTGTCTT GAAGCTGGG TGCTCTCTC CATGTTGGCC TGTCAACAGA 1800
CCGAGTCAA TTAACAGCT GGTCTCCAC TTTGCTGGT CAGCCTTCGT GTGGCTCCTG 1860
70 GTAAAGTGGC TCCACCTGA TGGGTCAACC TTTGTGTGGC TCCTGGTAAC ATAACAACA 1920
CAGTTACTAT AGTGGTGA GAAGGAAT CAAATTTTGC CAGAGAAACT AACTCGGTGG 1980
CCCCAACAGG TCTTCCGGG CCATGGGCAT TTGTTTAGAG CCAAAATCAT CCTCTTACCA 2040
GATCCTTTTC CAGAAATACC TGTCTAGGAA GGTGTGATGT CAGAAACAAT GACATCCAGA 2100
AAGCTGAGGA ACAGGTTCTC GTGGAGACAC TGAGTCAGAA TTCTTCTATC AAATTTTTC 2160
75 GTTAGTGGAA AATGGAATTG CTTCTGTGTA GTCAATAAAA TGAACCTGAT CACTTTTC 2218
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Seq ID NO: 71 DNA Sequence
Nucleic Acid Accession #: NM_001252.1
Coding sequence: 138..719

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80 1 11 21 31 41 51
| | | | |
GGCTGGTCCC CTGACAGGTT GAAGCAAGTA GACGCCCAGG AGCCCCGGGA GGGGCTGCA 60
GTTTCTCTCC TTCTTCTCG GCAGCGCTCC GCGCCCCCAT CGCCCTCCT GCGCTAGCGG 120
AGGTGATCGC CGCGCGGATG CCGGAGGAGG GTTCGGGCTG CTGGTGCGG CGCAGGCCCT 180
ATGGGTGCGT CCTGCGGGCT GCTTTGGTCC CATTGGTTCG GGGCTTGGTG ATCTGCCTCG 240
```

5 TGGTGTGCAT CCAGCGCTTC GCACAGGCTC AGCAGCAGCT GCCGCTCGAG TCACTTGGGT 300
 GGGACGTAGC TGAGCTGCAG CTGAATCACA CAGGACCTCA GCAGGACCCC AGGCTATACT 360
 GGCAGGGGGG CCAGCACTG GGCCTCTCTT TCCTGCATGG ACCAGAGCTG GACAAAGGGC 420
 AGCTACGTAT CCATCGTGAT GGCATCTACA TGGTACACAT CCAGGTGACG CTGGCCATCT 480
 GCTCTCCAC GAGCGCTCC AGGCACACC CCACCACCTT GGCCGTGGGA ATCTGCTCTC 540
 CCGCTCCCG TAGCATCAGC CTGCTGCGTC TCAGCTTCCA CCAAGTTGT ACCATTGCCT 600
 CCCAGCGCCT GAGCGCCCTG GCCGAGGGG ACACACTCTG CACCAACCTC ACTGGGACAC 660
 TTTTGCCTTC CCGAAACACT GATGACACCT TCTTTGGAGT GCAGTGGGTG CGCCCTGAC 720
 10 CACTGTCTGT GATTAGGGTT TTTTAAATTT TATTTTATTT TATTTAAGTT CAAGAGAAAA 780
 AGTGTACACA CAGGGCCAC CCGGGTGTG GGTGGGAGTG TGGTGGGGG TAGTGGTGGC 840
 AGGACAAGAG AAGGCATTGA GCTTTTCTT TCATTTCTT ATTAATAA 888

Seq ID NO: 72 DNA Sequence

Nucleic Acid Accession #: NM_018092.2

Coding sequence: 13..618

15 1 11 21 31 41 51
 | | | | |
 AGCAGGTTTC GAATGCTCTT TACTTCCTTT GTGGAGCAAA AGAAAAAAGC AGGAGTATTT 60
 20 GAACAAATCA CTAAGACTCA TGAACAATT ATTGGCATT CTTAGGGAT TGTCTTGGTC 120
 CTCTCATTAT TTCTATTTT AGTACAAGTG AAACAGCCTC GAAAAAAGGT CATGGCTTGC 180
 AAAACCGCTT TTAATAAAAC CGGGTTCCAA GAAGTGTGTG ATCCTCTCTCA TTATGAACTG 240
 TTTTCACTAA GGGACAAGA GATTTCGTCA GACCTGGCAG ACTGTGCGGA AGAATTGGAC 300
 AACTACCAGA GGATGGGGG CTCTCCACC GCCTCCCGCT GCATCCACGA CCACCACTGT 360
 25 GGGTCCGAGG CTCCAGCGT CAAACAAAGC AGGACCAACC TCAGTTCCTT GGAGCTTCTT 420
 CTCCGAATG ACTTTGCACA ACCACAGCCA ATGAAAAAT TAAATAGCAC CTTCAAGAAA 480
 AGTAGTTACA CTTTCAACA GGGACATGAG TGCCCTGAGC AGGCCCTGGA AGACCGAGTA 540
 ATGGAGGAGA TTCCCTGTGA AATTATATGC AGGGGGCGAG AAGATTCTGC ACAAGCATCC 600
 ATATCCATTG ACTTCTAAT TTCTGTAAT GGTGATGTGA ATTCTTAGGG TGTGTAGTA 660
 CGCAGCTCC AGGGCACCAT ACTGTTTCCA GCAGCCAACC CTTTCTCC CTTCAACTA 720
 30 CGAAGACCTT GATTTACCGT TAACCTATTG TATGGTGATG TTTTATTCT CTCAGGCAGT 780
 CTATATATGT TAAACCAAT AAGGAACCTA CTCTATTGAG TGGAAACAAT AATCATCTCT 840
 ATTGCTTGGT GTCAATTATA GGAAGCACTG CCAGTTAAAG AGCATTAGAA GAGGTGGTTG 900
 GATGGAGCCA GGCTCAGGCT GCCTCTCGT TTTAGCAACA AGAAGACTGC TCTTGACTGA 960
 35 TAACAGCTCT GTCAATATTT TGATGCCACA ATAACTTGA TTTTCTTTA CATTCCTTTT 1020
 ATTTTCTCTT TCTCTAAAT TAAITTTGTT TATAAGCCTA TCGTTTACC ATTTCATTTT 1080
 CTTACATAAG TACAAGTGGT TAATGTACCA CATACTTCAG TATAGGCATT TGTCTTGAG 1140
 TGTGTCAAAA TACAGCTAGT TACTGTGCCA ATTAAGACCC AGTTGTATTT CACCCATCTG 1200
 TTTCTTCTG GCTAATCTCT GTACTTCTGC CTTTAAATTA CTGGGCCCTT ATTCCTTATT 1260
 40 TTCTGTGAGA AATAATAGAT GATATGATT ATTACCTTTC AATTATATTT TTCTCAGTTA 1320
 TACTAGAAAA TTTCAATAT CTGGGATATA TGTACCATTG TCAGCTATGA CTAATAATTT 1380
 GAAAAAGATA AAAATTTCTA GCAAGCCTTT GAAGTTTACC AAGTATAGTC ACATTCAGTG 1440
 ACAGCCCATT CATTCAGTA AAGAATCATT TCATTCACTT TGGGAGAGGC CTATAATTAC 1500
 45 ATTTATTGTC AATGTTTCTC TTGCTAGAT TGTACATAG CTCCCTCTCT GTTGGTTTGT 1560
 CTTACAGCAT ATGTAAACCA AGGTTAGATG CCAGTTAAAA TTCTTTAGAA ATTGGATGAG 1620
 CCTTGAGATT GCTTCTTAAC TGGGACATGA CATTTTCTA GCTCTTATCA AGAATAACAA 1680
 CTTCCACTTT TTTTAAACT GCACTTTGA CTTTCTTAT GGTATAAAAA CAATAATTTA 1740
 TAAACATAAA AGCTCATTGT GTTTTTTGA CTTTGTATG TATTTGATAC TGTACAACT 1800
 50 TTATTAATC AAGATGAAAG ACCTACAGGA CAGATTCCCT TCAGTGTTC CATTAGTGGC 1860
 TTTGATGCA AATATGCTGT GTTGGACCTG GACCTATAA CTTATTGTAA AGACCTTGGA 1920
 AATGTGGACA TAAGCTCTTT CTTTCTTTT GTTACTGTAT TTAGTTTGTG ATAAATTTT 1980
 CACTGTGTGA TATTTATGCT CTAATCACT ACACAAATCC CATATTAAAA TATACATTGT 2040
 ACCTGACCTT TTAATCATGT TATTTATGCC ACCAAGGTTG TGGATCTTAA GGTATGTATG 2100
 GAAAGGAATC TTAATCATCA ATTGTAAAGT ATACAGACAT GCCATTAAAA AGAGGTAAAT 2160
 55 TCTTGTTCCT TATATTGTGT TAGTAAATTC TCAATGAAAT AAGTTGAAGT TTCCTGGAT 2220
 TTTCAATACT TTTAAATATT ACATATATGT GTTTCTCAG ATTAGTGAAG ATTGTGACCT 2280
 TAAATTTAAT ACACATATAC TGCCCTCAG 2308

Seq ID NO: 73 DNA Sequence

Nucleic Acid Accession #: Eos sequence

60 1 11 21 31 41 51
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 GCTGAATGTT TTTTCACTT TCCTGAGAGA TGCAATGTT CATTCACTCA TCTCATTATA 60
 CAACACAGTA CATAAATGTA GCTTCAGAGC GTATTAAGTG CTTTATACA CAAGTGCTGG 120
 65 CTGTGTGGAC CAGGTGGTAG CTCAATTAGG CCCCATAATC ATTAAGGGCA GGGTCTGACT 180
 CTTAGGCTTC TTAATATTGT GTTGGTGCA TGGTCAAGAG CTGGACCCAC ATGTTGCATA 240
 GCAGCAGGGC TGATATGTTT AAAGACGCTG GGCTTTTCT GCTCTGGGGC CCTTCCCGG 300
 GGGTCCCGGT GAGTCCCTCC CCAGGTGGGT CTGCCCCAC CCGTGTGGGC GGGATTAGCT 360
 CCCAGAGGCT GGCAGGGCCC CACCTGGGGG AGGCTTGAGG GCAGGGCCCC AAGCTGAGA 420
 70 TTCAGGCTTG GGGGAACAGA GCAGGAAGA GACCCGATAC CGAAAGTGAG CCGGCAGGC 480
 ACCTAGTCAC ATGGGTAATG GGCAGGGGTC GGTCACTGGC TTTGGCTCCA GGGCCAGAGC 540
 AGTCTGACTT AGTGTGAGC TCCAAGCATG GAACACTGGA GTTGGTTTAT TTTGACCAGC 600
 AAGCCTCTAA ATGGGTGCTT TGATTACCCA CCGCAAGGAG AGGGCAGTTG CCTTTTATG 660
 ACATGTTAAT TCCAGCCAGG TGAGTCACCA GGTAGCTCTC ATCCTCTGTC CAGGCTCCCC 720
 75 TGCCGTGCGG TTTGGCATTG TCAGATAATG TGATCATTCA TTGAAGTGAC ATTTGAGTTC 780
 CAAACAGTTT TTCTCTTTA ACCATTTTAC CTTCAAGAGT GATTCTCCTT TGTGTGGCAT 840
 TGTCAAGGAA TGTGATGATC CATTCAATG ACTTTTGAGT TCCAAATAGT GTTCTACTT 900
 TAACCTCCTA AATGAAAAA AAAAAAAAAA AAA 933

Seq ID NO: 74 DNA Sequence

Nucleic Acid Accession #: Eos sequence

80 1 11 21 31 41 51
 | | | | |
 TTTTCTTTT TCAATTAGGA AGTTAAAGTA GAAACACTAT TTGGAACCTA AAAGTCATT 60
 GAATGGATCA TCACATTCCC TGACAATGCC AAACAAAGGA GAATCACTCC TGAGGTGAA 120

| | | | | | | | |
|----|--|-------------|-------------|-------------|-------------|-------------|------|
| | ATGGTTAAAG | GAGAAAACTG | GTTTGGAACT | CAAAATGTCAC | TTCAATGAAT | GATCACATTA | 180 |
| | TCTGACAATG | CCAAAACGAC | AGGCAGGGGA | GCCTGGCAGG | AGGATGAGAG | CTACCTGGTG | 240 |
| | ACTCACCTGG | CTGGAATTA | CATGTCTATA | AAAGGCAACT | GCCTCTCTCT | TGCGGTGGGT | 300 |
| 5 | AATCAAGGCA | CCCAATTTAGA | GGCTTGCTGG | TCAAAATGAA | CCAACTCCAG | TGTTCCATGC | 360 |
| | TTGGAGCTCA | ACACTAAGTC | AGACTGCTCT | GGCCTGGAG | CCAAAGCCAG | TGACCGACCC | 420 |
| | CTGCCCATTA | CCCATGTGAC | TAGGTGCCCTG | CCCCGCTCAC | TTTCGGTACC | GGGTCTCTTT | 480 |
| | CCTGCTCTGT | TCGCCCAAGC | CTGAATCTCA | GCCTTGGGGC | CCTGCCCTCA | AGCCTCCCCC | 540 |
| | AGGTGGGGCC | TGGCCAGCCT | C | | | | 561 |
| 10 | Seq ID NO: 75 DNA Sequence | | | | | | |
| | Nucleic Acid Accession #: Eos sequence | | | | | | |
| | Coding sequence: 1..459 | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| 15 | ATCATTGCGC | CCACGATTAA | TAATGCCAGC | ATGACTTCCC | CAATTGACAA | TGCTGGACTT | 60 |
| | GCAGCAGATG | ACTTCAAAT | GAATGCATCC | TTGCAGACAC | AGATCTCCAC | GGATGCTGAA | 120 |
| | CGAGTTAGCT | CGGCCAAGAG | TGAGATAATG | GAGCTGAAAC | AAGTCTCTCA | GTCCCTCCAG | 180 |
| | CATGAATGCG | AGTCTGTCTT | GGCCATGCAA | AGCTCCCCAG | AAGGAACCCCT | GGCTGACACA | 240 |
| | GAAGCTGGCT | ACGTGGCTCA | CCTGTACAGAA | ATTAAGATGT | ATATCAGCAT | CCTGGAGGAG | 300 |
| 20 | CAGATCTGCC | AGATCCGGGG | CGAGACTGAA | TACCAGAACA | CAGAGTATGC | ACAACTGCGAG | 360 |
| | GACATCAAGA | CAGCCCTGGA | GGTGGAGATC | GAGACCTACC | ACCGCCTGCT | CGGTGGAGAG | 420 |
| | GGAGGTTCTG | AGGCCAGAGA | AGCTGAATCT | AAAGGATGAT | TCTCTGTGGA | CTCCAAAGGA | 480 |
| | ATAACCAACA | CAGCTCAATC | GAGGGGAAGA | GTCGCTTTT | AAAATTTCAC | TAAAGCAGA | 540 |
| | GGAACCGGCG | TGTTGACGGA | TAATGACCAA | CTAATTTCAT | CTCAACACTG | TTTCTGATGT | 600 |
| 25 | AAAATTCAAG | AGTAAGATGC | AGGCAGCTGA | GTCTGTCCC | CAGGATGTAA | ATGATGACAC | 660 |
| | CTAACAAAGG | CGTGTCTGAG | CAGTGCACAA | AACTTGCAGC | CACAGAGCTG | CAGCTACTCC | 720 |
| | TGTAATCCTT | TCTCAGATTG | TTTTGTCTTA | TTGGTTCGGT | TTTGTCTTTA | AATTGCAAAA | 780 |
| | TGTGTTTTCC | TTCTTAATCA | TTCTGTGTGG | ATAAACTTTT | TGCTGTGTGC | AAATCAA | 837 |
| 30 | Seq ID NO: 76 DNA Sequence | | | | | | |
| | Nucleic Acid Accession #: NM_003265.2 | | | | | | |
| | Coding sequence: 102..2816 | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| 35 | CACCTTCGAG | AGTGCCTGCT | ATTTGCCACA | CACCTCCCTG | ATGAAATGTC | TGGATTGGA | 60 |
| | CTAAAGAAAA | AAGGAAGGC | TAGCAGTCAT | CCACAGAAAT | CATGAGACAG | ACTTTGCCCT | 120 |
| | GTATCTACTT | TTGGGGGGGC | CTTTGCCCT | TTGGGATGCT | GTGTGCATCC | TCCACCACCA | 180 |
| | AGTGCACTGT | TAGCCATGAA | GTGTCTGACT | GCAGCCACCT | GAAGTTGACT | CAGGTACCCG | 240 |
| 40 | ATGATCTACC | CACAAACATA | ACAGTGTGGA | ACCTTACCCA | TAATCAACTC | AGAAGATTAC | 300 |
| | CAGCCGCCAA | CTTCACAAGG | TATAGCCAGC | TAATAGCTT | GGATGTAGGA | TTTAACACCA | 360 |
| | TCTCAAACT | GGAGCCAGAA | TTGTGCCAGA | AACTTCCCAT | GTTAAAAGTT | TGAAACCTCC | 420 |
| | AGCAAAATGA | GCTATCTCAA | CTTTCTGATA | AAACCTTTGC | CTTCTGCAGC | AATTGACTG | 480 |
| | AACTCCATCT | CATGTCCAAC | TCAATCCAGA | AAATTAATAA | TAATCCCTTT | GTCAAGCAGA | 540 |
| 45 | AGAATTTAAT | CACATTAGAT | CTGTCTCATA | ATGGCTTGTC | ATCTACAAA | TTAGGAATCT | 600 |
| | AGGTTGAGCT | GGAAATCTCT | CAAGAGCTTC | TATTATCAAA | CAATAAAATT | CAAGCGCTAA | 660 |
| | AAAGTGAAGA | ACTGGATATC | TTTGCCAAAT | CATCTTTAAA | AAAATTAGAG | TTGTCATCGA | 720 |
| | ATCAAAATTA | AGAGTTTCTC | CCAGGGTGT | TTACGCAAT | TGGAAGATTA | TTTGGCCTCT | 780 |
| | TTCTGAACAA | TGTCAGCTG | GGTCCCAGCC | TTACAGAGAA | GCTATGTTG | GAATTAGCAA | 840 |
| 50 | ACACAAGCAT | TCGGAATCTG | TCTCTGAGTA | ACAGCCAGCT | GTCCACCACC | AGCAATACAA | 900 |
| | CTTTCTTGGG | ACTAAAGTGG | ACAAATCTCA | CTATGCTCGA | TCTTCTCTAC | AACAATCTAA | 960 |
| | ATGTGGTGGG | TAAAGATCTC | TTTGCTTGGC | TTCCACAAC | AGAATATTTC | TTCTAGAGT | 1020 |
| | ATAAATATAT | ACAGCATTTG | TTTTCTCACT | CTTTGCACGG | GCTTTTCAAT | GTGAGGTACC | 1080 |
| | TGAATTTGAA | ACGGTCTTTT | ACTAAACAAA | GTATTTCCCT | TGCTCACTC | CCCAAGATTG | 1140 |
| 55 | ATGATTTTTT | TTTTAGTGG | CTAAAAATG | TGGAGCACCT | TAACATGGAA | GATAATGATA | 1200 |
| | TTCCAGGCA | AAAAAGCAAT | ATGTTACAG | GATTGATAAA | CCTGAAATAC | TTAAGCTAT | 1260 |
| | CCAACTCCTT | TACAAGTTTG | CGAACTTTGA | CAAAATGAAAC | ATTTGATCA | CTTGCTCATT | 1320 |
| | CTCCCTTACA | CATACTCAAC | CTAACCAAGA | ATAAAATCTC | AAAAATAGAG | AGTGATGCTT | 1380 |
| | TCTCTGGTT | GGGCCACCTA | GAAGTACTTG | ACCTGGGCTT | TAATGAAATT | GGGCAAGAAC | 1440 |
| 60 | TCACAGGCCA | GGAAATGAGA | GGTCTAGAAA | ATATTTTCGA | AATCTATCTT | TCCTACAACA | 1500 |
| | AGTACCTGCA | GCTGACTAGG | AACTCCTTTG | CCTTGGTCCC | AAGCCTTCAA | CGACTGATGC | 1560 |
| | TCCGAAGGGT | GGCCCTTAAA | AATGTGGATA | GCTCTCCTTC | ACCATTCCAG | CCTCTTCGTA | 1620 |
| | ACTTGACCAT | TCTGGATCTA | AGCAACAACA | ACATAGCCAA | CATAAATGAT | GACATGTTGG | 1680 |
| | AGGGTCTTGA | GAACACTAGAA | ATTCTCGATT | TGCAGCATAA | CAACTTAGCA | CGGCTCTGGA | 1740 |
| 65 | AACACGCCAA | CCCTGGTGGT | CCCATTATT | TCCTAAAGGG | TCTGTCTCAC | CTCCACATCC | 1800 |
| | TTAACTTGGG | GTCCAAACGG | TTTGACGAGA | TCCAGTTGA | GGTCTTCAAG | GATTTATTGT | 1860 |
| | AACTAAAGAT | CATCGATTGA | GGATTGAATA | ATTTAAACAC | ACTTCCAGCA | TCGTCTTTTA | 1920 |
| | ATAATCAGGT | GTCTCTAAAG | TCATTGAACC | TTCAGAAGAA | TCTCATAACA | TCGGTTGAGA | 1980 |
| | AGAAGGTTTT | CGGCCACGCT | TTAGGAACC | TGACTGAGTT | AGATATGCGC | TTTAATCCCT | 2040 |
| 70 | TTGATTGCAC | GTGTGAAAGT | ATTGCCTGGT | TGTTAATTG | GATTAAACGAG | ACCCATACCA | 2100 |
| | ACATCCCTGA | GCTGTCAAGC | CACTACCTTT | GCAACACTCC | ACCTCACTAT | CATGGGTTCC | 2160 |
| | CAGTGAGACT | TTTTGATACA | TCATCTTGCA | AAGACAGTGC | CCCTTTTGAA | CTCTTTTICA | 2220 |
| | TGATCAATAC | CAGTATCTCT | TGATTTTTTA | TCTTTATTGT | ACTTCTCATC | CACCTTGAGG | 2280 |
| | GCTGGAGGAT | ATCTTTTTAT | TGGAATGTTT | CAGTACATCG | AGTTCCTGGT | TTCAAGAAA | 2340 |
| 75 | TAGACAGACA | GACGAACAG | TTTGAATATG | CAGCATATAT | AATCATGCC | TATAAGATA | 2400 |
| | AGGATTGGGT | GTGGGAACAT | TTCTCTTCAA | TGGAAAAGGA | AGACCAATCT | CTCAAAATTT | 2460 |
| | GTCTGGGAAG | AAGGACCTTT | GAGGCGGGTG | TTTTTGAAT | AGAAGCAATT | GTTAACAGCA | 2520 |
| | TCAAAAGAG | CAGAAAATTT | ATTTTGTGTA | TAACACACCA | TCTATTAAAA | GACCATTAT | 2580 |
| | GCAAAAGATT | CAAGGTACAT | CATGCAGTTC | AACAAGCTAT | TGAACAAAAT | CTGATTCCA | 2640 |
| 80 | TTATATTGGT | TTTCTTTGAG | GAGATTCCAG | ATTATAAAT | GAACCATGCA | CTCTGTTTGC | 2700 |
| | GAAGAGGAAT | GTTTAAATCT | CACTGCATCT | TGAACCTGGC | AGTTCAAGAA | GAACGGATAG | 2760 |
| | GTGCCTTTTG | TCAATAATG | CAAGTAGCAC | TTGGATCCAA | AAACTCTGTA | CATTAAATTT | 2820 |
| | ATTTAAATAT | TCAATTAGCA | AAGGAGAAAC | TTTCTCAATT | TAAAAAGTTC | TATGGCAAA | 2880 |
| | TTAAGTTTTT | CATAAAGGTG | TTATAATTG | TTTATTCATA | TTTGTAAATG | ATTATATTCT | 2940 |
| | ATCACAATTA | CATCTCTTCT | AGGAAAATGT | GTCTCCTTAT | TTTCAAGCCTA | TTTTTGACAA | 3000 |

TTGACTTAAT TTTACCCAAA ATAAACATA TAAGCACGTA AAAAAAAAAA AAAAAAA 3057

Seq ID NO: 77 DNA Sequence

Nucleic Acid Accession #: Eos sequence

| | | | | | | | |
|----|------------|------------|------------|------------|------------|------------|-----|
| 5 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| | ATCAAGGAGG | ACAGATTTTA | TATGCTTAAG | ACTGGAGGGA | GAGAGACCAG | TTAGAAAGAC | 60 |
| | TCTGGCTATA | ATCCAAGCAA | GCCATACTAT | GGGCTGGTTT | GGTGGAGGTA | GAGGAATGTC | 120 |
| 10 | CAGATTGGAG | AAACAGGAAG | TTAAAAATGG | GCAGGGCTTG | CTGACTGTTT | GAAACTAGGG | 180 |
| | GGTGTGAAGG | GAGGCAGCAC | TCTAGGATAA | ACACCAGACT | TGCCGATTGT | TTGGGAATAT | 240 |
| | CCAATTTCTG | TGTAGAAGAC | AGGAAAAACA | TAAACTCAAA | AGAAAGTGTG | CACATAGATA | 300 |
| | ACTAAATTAG | TCATCTGTAG | ATAGTACAAC | ATATTCTGTG | GTACAGAGAT | CAAAAGGGAC | 360 |
| | AGAAAGACCA | AGGAGGCACT | AAATATTCAC | GGTACCCCTA | ATACGTGAGA | CATGAGGCAC | 420 |
| 15 | TCAGGATGCA | GGAGGTTTCA | ATTTGACAGG | ATGGATGCAC | ACTGCATGAC | CCACAGTTCA | 480 |
| | GCTGGTGTGA | TCATTCCACC | CAACTTCCCC | CCTCTCCCGT | GTGTTGACCC | ACCCAGCAC | 540 |
| | CTGCCTCCTG | CTTCTCAGAA | TGTGTTTTAC | ATTTATTTAA | TAAACGATGT | TATTTGAGCA | 600 |
| | TTTA | | | | | | 604 |

Seq ID NO: 78 DNA Sequence

Nucleic Acid Accession #: Eos sequence

| | | | | | | | |
|----|------------|------------|------------|------------|------------|-------------|-----|
| 20 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| | TTTTTTTTTT | TTTTTTTTTA | AATGCTCAAA | TAACATCGTT | TATTAAATAA | ATGTAAACAA | 60 |
| | CATTCTGAGA | AGCAGGAGGC | AGGTGCTGGG | GTGGGTCAAC | ACACGGGAGA | GGGGCAAGT | 120 |
| 25 | TGGGTGGAAT | GATCGATCAC | ACCAGCTGAA | CTGTGGGTCA | TGCAGTGTGC | ATCCATCTCTG | 180 |
| | TCAAATTCGA | ACCTCTCTGA | TCCTGAGTGC | CTCATGTCTC | ACGTATTTAG | GGTACCGTGA | 240 |
| | ATATTAGTGC | CCTCTCTGGT | CTTCTGTGCC | CTTTGTGATC | CTGTACACAC | GAATACGTTG | 300 |
| | TACTATCTAC | AGATGACTAA | TTAGTTATC | TGTGTGAAC | ACTTCTTTTG | AGTTTATTGT | 360 |
| 30 | TTTCTGTCT | TCTACAGCAG | AATTGGATAT | TCCCAAAACA | TCTGCAAGTC | TGGTGTTTAT | 420 |
| | CCTAGAGTGC | TGCCCTCCCT | CACACCCCT | AGTTTCAAA | AGTCAGCAAG | CCCTGCCCAT | 480 |
| | TTTTAACTTC | CTGGTTTCTC | AATCTGGACA | TTCTCTTACC | TCCCAAAACA | CAGCCCATAG | 540 |
| | TATGGCTTGC | TTGGATTATA | GCCAGAGTCT | TTCTAACTGG | TCTCTCTCCC | TCCAGTCTTA | 600 |
| | AGCTTAAAT | CGTCTCCTTG | ATT | | | | 623 |

Seq ID NO: 79 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: 315..1416

| | | | | | | | |
|----|-------------|-------------|-------------|------------|------------|------------|------|
| 35 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| 40 | CTTCAGATAG | ATTATATCTG | GAGTGAAGAA | TCCTGCCACC | TATGTATCTG | GCATAGTATT | 60 |
| | CTGTGTAGTG | GGATGAGCAG | AGAACAAAAA | CAAAATAATC | CAGTGAGAAA | AGCCCGTAAA | 120 |
| | TAAACTTTCA | GACCCAGAGAT | CTATTCTCTA | GCTTATTTTA | AGCTCAACTT | AAAGGAAGA | 180 |
| | ACTGTTCTCT | GATTCTTTTC | GCCTCAATA | CACCTAATGA | TTTAACTCCA | CCCTCCTTCA | 240 |
| 45 | AAAGAAACAG | CATTTCCTAC | TTTTATAC TG | TCTATATGAT | TGATTTGAC | AGCTCATCTG | 300 |
| | GCCAGAAAGAG | CTGAGACATC | CGTTCCCTCA | CAAGAAACTC | TCCCGGGTGC | GAACAAGATG | 360 |
| | GATTATCAAG | TGTCAGATCC | AATCTATGAC | ATCAATTATT | ATACATCGGA | GCCTGCCCAA | 420 |
| | AAAAATCAATG | TGAAGCAAA | CGCAGCCCGC | CTCCTGCGCT | CGCTCTACTC | ACTGGTGTTC | 480 |
| | ATCTTTGGTT | TTGTGGGCAA | CATGCTGGTC | ATCCTCATCC | TGATAAACTG | CAAAAGGCTG | 540 |
| 50 | AAGAGCATGA | CTGACATCTA | CCTGCTCAAC | CTGGCCATCT | CTGACCTGTT | TTTCTTCTTT | 600 |
| | ACTGTCCCTT | TCCTGGGTCA | CTATGCTGCC | GCCTCAGTGG | ACTTTGGAAA | TACAATGTGT | 660 |
| | CAACTCTTGA | TGCTGAGTCA | TTTTATAGGC | TTCTTCTCTG | GAATCTTCTT | CATCATCTCT | 720 |
| | CTGACAAATCG | ATAGGTACCT | GGCTGTGCTC | CATGCTGTGT | TTGCTTTAAA | AGCCAGGACG | 780 |
| | GTCACTTCTG | GGGTGGTGAC | AAGTGTGATC | ACTTGGGTGG | TGGCTGTGTT | TGCTCTCTCT | 840 |
| 55 | CCAGGAATCA | TCTTTACCAG | ATCTCAAAAA | GAAGGTCTTC | ATTACACCTG | CAGCTCTCAT | 900 |
| | TTTCCATACA | GTCAGATACA | ATTCTGGAAG | AATTTCAGAA | CATTAAAGAT | AGTCATCTTG | 960 |
| | GGGCTGGTCC | TGCCGCTGCT | TGTCATGGTC | ATCTGCTACT | CGGGAATCCT | AAAACTCTG | 1020 |
| | CTTCGGTGTG | GAAATGAGAA | GAAGAGGCAC | AGGGCTGTGA | GGCTTATCTT | CACCATCATG | 1080 |
| | ATTGTTTATT | TTCTCTTCTG | GGCTCCCTAC | AACATTGTCC | TTCTCTTGAA | CACCTTCCAG | 1140 |
| 60 | GAATCTTTTG | GCCTGAATAA | TTGCAGTAGC | TCTAACAGGT | TGGACCAAGC | TATGCAGGTG | 1200 |
| | ACAGAGACTC | TTGGGATGAC | GCACTGTGTC | ATCAACCCCA | TCATCTATGC | CTTTGTCCGG | 1260 |
| | GAGAAGTTCA | GAAACTACCT | CTTAGTCTTC | TTCCAAAAGC | ACATTGCCAA | ACGCTTCTGC | 1320 |
| | AAATGCTGTT | CTATTTTCCA | GCAAGAGGCT | CCCGAGCCAG | CAAGCTCAGT | TTACACCCGA | 1380 |
| | TCCACTGGGG | AGCAGGAAAT | ATCTGTGGGC | TTGTGACACG | GACTCAAGTG | GGCTGGTGAC | 1440 |
| 65 | CCAGTCAGAG | TTGTGCACAT | GGCTTAGTTT | TCATACACAG | CCTGGGCTGG | GGGTGGGGTG | 1500 |
| | GGAGAGGTCT | TTTTTAAAGG | GAAGTTACTG | TTATAGAGGG | TCTAAGATTG | ATCCATTTAT | 1560 |
| | TTGGCATCTG | TTTAAAGTAG | ATTAGATCTT | TTAAGCCCAT | CAATTATAGA | AAGCCAAATC | 1620 |
| | AAAAATATGT | GATGAAAAAT | AGCAACCTTT | TTATCTCCCC | TTCAATGCA | TCAAGTTATT | 1680 |
| | GACAAACTCT | CCCTTCACTC | CGAAAGTTCC | TTATGTATAT | TTAAAGGAAA | GCCTCAGAGA | 1740 |
| 70 | ATTGCTGATT | CTTGAGTTTA | GTGATCTGAA | CAGAAATACC | AAAAATTATT | CAGAAATGTA | 1800 |
| | CAACTTTTTA | CCTAGTACAA | GGCAACATAT | AGGTTGTAAA | TGTGTTTAAA | ACAGGTCTTT | 1860 |
| | GTCTTGCTAT | GGGGAGAAAA | GACATGAATA | TGATTAGTAA | AGAAATGACA | CTTTTCATGT | 1920 |
| | GTGATTTCCC | CTCCAAGSTA | TGTTTAATAA | GTTCCTACTG | CTTAGAACCA | GGCGAGAGAC | 1980 |
| | TTGTGGGCTG | GGAGAGCTGG | GGAAGCTTCT | TAAATGAGAA | GGAATTTGAG | TTGGATCATC | 2040 |
| 75 | TATTGCTGGC | AAAGACAGAA | GCCTCACTGC | AAGCACTGCA | TGGGCAAGCT | TGGCTGTAGA | 2100 |
| | AGGAGACAGA | GCTGTTTGGG | AAGACATGGG | GAGGAAGGAC | AAGGCTAGAT | CATGAAGAAC | 2160 |
| | CTTGACGGCA | TGAGTCCCTC | TAAGTCATGA | GCTGAGCAGG | GAGATCCTGG | TTGGTGTTCG | 2220 |
| | AGAAAGTTTA | CTCTGTGGCC | AAAGGAGGGT | CAGGAAGGAT | GAGCATTTAG | GGCAAGGAGA | 2280 |
| | CCACCAACAG | CCCTCAGTGC | AGGGTGAGGA | TGGCCTCTGC | TAAGCTCAAG | GCCTGAGGAT | 2340 |
| 80 | GGGAAGGAGG | GAGGTATTGG | TAAGGATGGG | AAGGAGGGAG | GTATTCGTGC | AGCATATGAG | 2400 |
| | GATGCAGAGT | CAGCAGAACT | GGGGTGGATT | TGGTTTGGAA | GTGAGGGTCA | GAGAGGAGTC | 2460 |
| | AGAGAGAAAT | CCTAGTCTTC | AAGCAGATTG | GAGAAACCTC | TGAAAGACAA | TCAAGCACAG | 2520 |
| | AAGGAGGAGG | AGGAGGTTTA | GGTCAAGAAG | AAGATGGATT | GGGTGAAAGC | TGAGGGTCTG | 2580 |
| | GTTTGACAGG | CTTGAACACA | GTCTCACCCA | GACTCCAGGC | TGCTTTTCA | GTAATGCTTC | 2640 |
| | TGACTTCATA | GATTTCCTTC | CCATCCACGC | TGAAATACTG | AGGGGTCTCC | AGGAGGAGAC | 2700 |

5 TAGATTTATG AATACACGAG GTATGAGGTC TAGGAACATA CTTGAGCTCA CACATGAGAT 2760
 CTAGGTGAGG ATTGATTACC TAGTAGTCAT TTCATGGGTT GTTGGGAGGA TTCTATGAGG 2820
 CAACACAGG CAGCATTAG CACATACTAC ACATTCAATA AGCATCAAAC TCTTAGTTAC 2880
 TCATTAGGG ATAGCACTGA GCAAAGCATT GAGCAAAGGG GTCCCATAGA GGTGAGGGAA 2940
 GCCTGAAAA CTAAGATGCT GCCTGCCAG TGCACACAAG TGATAGTATC ATTTTCTGCA 3000
 TTAAACCGTC AATAGGCAAA GGGGGGAAGS GACATATTCA TTTGAAAATA AGCTGCCCTT 3060
 AGCCTTAAAA CCCACAAAAG TACAATTAC CAGCCTCCGT ATTTGAGACT GAATGGGGGT 3120
 GGGGGGGCG CCTTAGGTAC TTATTCCAGA TGCCTTCTCC AGACAAACCA GAAGCAACAG 3180
 AAAAAATCGT CTCTCCCTCC CTTTGAATG AATATACCCC TTAGTGTTTG GGTATATTCA 3240
 10 TTTCAAAGGG AGAGAGAGAG GTTTTTTTCT GTTCTTCTC ATATGATTGT GCACATACTT 3300
 GAGACTGTTT TGAATTTGGG GGATGGCTAA AACCATCATA GTACAGGTAA GGTGAGGGAA 3360
 TAGTAAGTGG TGAGAACTAC TCAGGGAATG AAGGTGTCAG AATAATAAGA GGTGCTACTG 3420
 ACTTCTCAG CCTCTGAATA TGAACGGTGA GCATTGTGGC TGTACGACAG AAGCAACGAA 3480
 15 GGGAAATGGT TTTCTTTTG CTCTTAAGTT GTGGAGAGTG CAACAGTAGC ATAGGACCCT 3540
 ACCCTCTGG CCAAGTCAAA GACATTCTGA CATCTTAGTA TTTGATATT CTTATGTATG 3600
 TGAAGTTAC AAATTGCTG AAAGAAAATA TGCATCTAAT AAAAAACACC TTCTA 3655

Seq ID NO: 80 DNA Sequence

Nucleic Acid Accession #: Eos sequence

20 1 11 21 31 41 51
 | | | | |
 GCCCTGAAG TTAGCGGAAG GGAACGGGCA TGTTTTGGAA AGGCCCGCGG GGAATTCCTT 60
 CAGAAACAGG GGAAGCTCC CTGCTGGGCC AGGCCCCCTT CGTGTGCTTG AGGAGGATGG 120
 25 GAGCCCGGCC TCGGTTTGT ATCCTAATTA AGTGGAAAAT TAAGAAAATA ATAGAATAGC 180
 GTAAGTACTA ATAGTAAAT TATAGTAAGA GAAATAACAA TAGCTAGAAT GGAATGAATT 240
 GCTGTATTAA CCAAGGCTAG AAGAAATTTT AGCCCTCCGA AAGTTAAAGC GAGGGAAGAG 300
 AGAGACCCCT TCATATTGTT TATACTCAG TACCTGTTTT TTTTTTTTTT TTTAAAAAAA 360
 AGGAAGTGAA ATCAAGACA GGCAGCCGAG CGCCAGGCCG AAAACTGGAC CTGGGCCTGC 420
 30 CTGGCCTAAA CCTAGTAGTT AAAAAACAAC TCATGACTTA GAAACCGATG TTATTCATAG 480
 ATTCCAGACA TTCTATAGAA GAACATTGTG AAACCTCCCTG CCCTGTTCTG TTTCTCTCTG 540
 ACCATCGGTG CATGCAGCCC CTGTCACTGA CCCCTTGCTT GCTCAAATCA ATCAGGACCC 600
 TTTCTATGTA AATTTTAGTG TTGTGAGCTC TTAAGAGCGA CAGAAATGCT GCACTCGGGG 660
 AGCTCGGATT TTAAGCAGT AGCTTGCCAA TGCTCCGAGC TGAATAAAGC CCTTCTCTCT 720
 35 ACAGCTCCGT GTCTGAGAGG TTTTGTCTGT GCCTTGCTCT GCTACAGTCC TTGGTTCCTT 780
 GACCAGGAAG CGAGGTGACT GACAAGCCCT GTGGAGCGTC CCTGCAGAGG ACTCCGCGCA 840
 GCCTGAGTGA CGCAATCCAA AGAGCGCTCC CGGGTAGGAA ATGGCCCGCG TGGAAATGCC 900
 TGCCAGAGCA GGCATAGCA GGCTCCGAG AAGGATTAACT ACTGGCTGAA CACCGGGAAG 960
 GAACTGGCAC TGAAGTCCA GACATCTGAA GCTTGTCAAG ACTAGTCTTT GGAACCTTGC 1020
 40 CCACTCCATG TGAGTGAAG CATGGCCTGA TCACCCACCG TGTGCCTGTA TTGACATCTT 1080
 TGTCTCTGTT TTGACTTGGC TTGACTTGGT AAGACTAGTC TTTGGAACTT GCCCACTCC 1140
 AGCTGAGTGG AAGCGTGGCC TGATCAACCA CGGTGTGCTT GTATTGGCAC TTTTGTCTGT 1200
 GTTTTGACTT GGCTTGACTT GGTAAAGACTA GTCTTTGGAA CTTGCCCCAC TCCATCTGAG 1260
 TGGAAACGTG GCCTGATCAC CCACAGCATG CTTGCTATGG CACTCTTGTG CTGGTTTGA 1320
 45 CTTGACTTGA ATTGCTGGAT ACTTTGGTTT TGGTTTTGAC TTGGCTTGAA TTTTGTGTA 1380
 CTGGGATTTT GAATTTGCTG ATTTTGGTTT GGTATAAAGC GTAAAGTGTG GTGTGCCCTC 1440
 TTTACCTGTT CTTTGTCTTG TGGTATGTGT GGTGTGAGCG TGGTATTTTG TCTGGAAAAA 1500
 AAAAAAAAAA 1510

Seq ID NO: 81 DNA Sequence

Nucleic Acid Accession #: Eos sequence

50 1 11 21 31 41 51
 | | | | |
 CGCTGCCGGG CCGGGGCTGG GCCGGAGCGG CGCGCGCTCG ATGCCGGCCC GGGGCTGGGC 60
 CGGAGACTGG CGCCCGCCCC GAAGCGACTT TCGGTCCCGG ACCCGCTCCG CCTGACCCCT 120
 55 ATGATGAAGA GGGCGTCCAC TGGAGTTCTT GCTGTGACAC TCTTTGACAA GTTCAACTTC 180
 ACGGGAGCCA GAGTCCCATG GTTCGACGCC ATTCATGAAG AATTTCCCGG GGAGCTGGAG 240
 TCCTCCATCT CTTTCCGAGC CAATCTCTTC AAACCACTG AAGAAAAAGT GCTTAGGTAG 300
 AGGTTGAGCA TCCTAATCCT GAAATCTGAA ATGCTCCAGA ATCTGAACCT TCTTGAGCAC 360
 60 CAACCTGACA CTTAAAGGAA GTGCTCATTG GAGGATCTGT GACAATTAAT AAAAACTTCC 420
 CCAAAATAAAA AGGACATGAA AAGAACTCA CGCTATCGCC CAGGCTGGAG TGCAGTGGCG 480
 CGATCTCCGC TCACTGCAAG CTCGGCTCCG CGGGTTCGCG CCATCTCTCT GCCTCAGCCT 540
 CCGGAGAGTA GCTGGGACTG CAGGCGCCCG CCACCAAGCC CAGCTAATTT TTTGTATTTT 600
 TAGTGGAGAC GGGGTTTCAC CGTGTGGGCC AGAATGTTT CGATCTCTC ACCTCGCGAT 660
 65 CCATCCGCTC CAGCTCCCA AAGTGTGGG ATTACAGCG TGAGCCACCG TGCTGGCCCC 720
 TCATGTGTCT TAAAAAGAGG GGTGACTCTG ATGTGGGGTC ATGCTTGAAA CTGAGAGGAC 780
 GAGGTCCCGG ACCCTCCATT GCAGCCAGCT CTCTCTGGAA CTAACAGAGT GAGAATCGC 840
 TCATTACCAA GGGGAGGACA CCAAGCCATT CATGGGGGAC CCACCCCAT GACCCAAACA 900
 ACCCCGACCA CGCCCACTC CAACCTTAA GCAGTCCATC TCCAGAACTC TTTTCATCCT 960
 70 GCAGATCTGA AACTCTAGCC CACAAAACAC CAATCCACT CCCCAGCCAC TGGTGCCAC 1020
 CGTGTCTTCT GTCTCTGAAT TTGACTCCTC TAGGGACCTC CCATAAGTGG AATCATACAA 1080
 TATTTGTCTT TTTGTGCTTG GCTTATTICA CTGAGCGTAA TGTCTCTAG GTTCACTGT 1140
 GTTGTAGCAA ACGTCAGACT TTCCCTCCTT TTGAAGGCTG AGTAATATTG TGTGTGTGG 1200
 ATGGAGCAGC CATTTGTTAT CCACTCACCT GTTGACGCT GCCTGGGTGC TTTCCACCTT 1260
 75 TCGGCTGTG TGAATGTGTC TGCTCTGAAC AGGGGTGAAG ACGTATCTGG GCGTCTGCTT 1320
 TCAGTTCTTT TGGGTGTATA CCAGAAAGTG GGCTTGCTGG GTCACGTGGT AAATCCTGTG 1380
 GTTGATTTTT TGAGGAGCGA CCATACTGTT TCGGTGGGGA CATCTGTGAG GTTTGAGAA 1440
 GCACCTGCTG GCATGAGAG CTGCTTGGG GAACACAGGT GCTCCTGCCG GAGTCTCTAC 1500
 80 GCTCTGCTCA GCTTGAGAA GGGCCCTGG TAAGGCCAGC CAGCCGGAGG ACCACCCCGC 1560
 AGACCAACAG CCCAGGCGCT GGCACCGAGG GGGAGGCCCC GATCAGCAGG TGAAGCGGAC 1620
 ACCCTGATGA CACTGTAGT TTCACCTTCA CTCTGGTCA CTGTTACTGT ACCCGGGGCG 1680
 AGCTCCGCGC TGAGCCCTAT GACCCCAACC GCGGCAGCCT CTGGTAAGGC CTGGGTATGG 1740
 GGCACATGGA GAGGGCCCAT TCCAGAGGCT CCTAAGTCAA AAGAGATTCC ACAAGTCAA 1800
 ATCCTGATCC TGATCAAGCA CAGGCTTCA CAGTGACATT TCACTGTGAC CTGGCCCGAG 1860
 AGACAGAGAC CACTGTCTG CAGTGTCCCT GGGAGGGAGG TTCTGGGTCT GCCACAGGAC 1920

| | | | | | | | |
|----|-------------|-------------|-------------|------------|-------------|------------|------|
| | ACCAACACCT | GGAAACATTGC | ACACCCCTTGS | CCTGGCCCTT | TCCCAGCGTT | TCTGTCAGAA | 1980 |
| | ATGCCCCCTC | CCAAGCATAC | ACCCCATCTT | GTGCCCCGAG | GGACTCGATT | CTCTCCCCAC | 2040 |
| | ACACCCGACC | CGAGGCTGTC | ATGGGTAGTG | CCTGCTGCTG | GCCCCAGGGT | TAGGGCTGCT | 2100 |
| 5 | CAGCCAGTCC | TGCTTGAAAA | GGATGAATGT | CCCACAAGCA | GCTTTGGGGC | CTGCTTGGTG | 2160 |
| | GGAGCAGCCC | GAGGATCCGC | CCTTGGTCTC | CCTGCCATT | CCCACCTCCC | TGGCTCTGGG | 2220 |
| | GTCCCTCATGT | TACGCTGGTT | CTCAGTGACT | GGGTGATTGA | CMNNNNNNNN | NNNNNNNNNN | 2280 |
| | NNNNNNNGGT | GTCTTTTGCT | GGACATTAA | GCCATTCCCT | GTGTTTCTGC | CATTAGCTAT | 2340 |
| | TATGGGCTGT | AACATCTTTG | CACCTGTGCC | TTCTTTCTTT | TTAAATTTCT | GAAGTCTCTA | 2400 |
| 10 | TTTGACCCAA | AGGTGACACA | TCTCCCTGTG | TGCCCTGTCA | GTGATGAAAC | CTGCTCTGGG | 2460 |
| | GATGAAGATG | CCGTGGGGCC | CACAGATCCA | AGCTCTCGGA | GTGTGATTCT | GTCTCCCTTA | 2520 |
| | GAAACACATC | CATGGCATGT | CCTCAGGGCA | TTTGTGCATG | GGATTAAGCA | AATGTTTCCT | 2580 |
| | AATCATGTTT | GTCCCTGTGC | TCTGGCTTCT | TGACCTCAGG | CTGCCCTCACT | GGCCCATCAT | 2640 |
| | TAATACGTGC | ATGGTGAGCG | CACCTGTGTA | CAGCGAGGGG | GCTCCACTTC | CGAGCCCCCT | 2700 |
| 15 | GGAGAGGCC | GTCCCTGTGG | AGTTCACCCT | GCTGGAGATG | GAGAAGCGAA | CCAAGCTGTG | 2760 |
| | CTGTGTGTTT | TGGAACCAAT | CCCTGGCGTA | AATGTGATGC | CGGGAGTTCT | GCATCTTCAT | 2820 |
| | GTGAGGCGT | TGCCAAGACA | CAGAGAACCC | GCAGGGTTGT | TGGCTCAGCG | CGAGATCGTC | 2880 |
| | CCACGGGGAC | AGTCTCTTGT | GGTCTGTGTC | TCCCCCTTCA | GCCCCCTGTG | GGGCAGTTAG | 2940 |
| | CCTCCTGCTC | TGCTTCTGTG | GGTGATCAG | AGCCCCCACA | GATGCCCA | CGCAGACGG | 3000 |
| 20 | CACAGGCGT | CACGTGGA | CACAGACATG | CGCACACGCA | GGCCACACA | CAGACGCACA | 3060 |
| | CAGAGCTGCA | CGTGGAGACA | CGTGGGCACA | CGCAGGCCCA | CACGACAGCC | CACACACAGG | 3120 |
| | TGCACGCGGA | CTGCACTGT | GAGACACAGA | TGTGTGACA | TGCAGGCCCA | CACACAGGTG | 3180 |
| | AGCGTGGACC | TGTGTGAACA | GATGCGCGCA | GACCTGCACG | TGGAGACACA | GACATGCAGG | 3240 |
| | CGCACAAAGA | GATCCCTCAA | GGCTGACACC | CAGGAAGGGG | CCTCTCACTT | GTGGGACTCC | 3300 |
| 25 | CGAGATGCAG | TGGCCAAAC | TAGTGTAGTG | CCCAGTTTAC | TGCTGGATAA | GACAGAGGCC | 3360 |
| | TGTTCTGGTC | ACACATGGGA | GGCAGAACC | AGAGACTGGG | CCCAGGAGCC | CTTCTGCTGA | 3420 |
| | CAGTGGGAAC | TCCAGCTAC | GTGTGGGGGT | CCCCATACCA | GACAAAGGTC | CTGACCTTTA | 3480 |
| | GTCTTGCCCG | AGAGGCCGAC | ACAGCCACAG | TTTGGGGTCT | GGCTTTACCC | ACAAGAGGCC | 3540 |
| | ACACCTTGCC | ACAGCACTGT | TTATCTGGCC | TGTTTCAGAA | GCACCGTCAG | AGTGGCGAAG | 3600 |
| 30 | GCAGGAGGTG | GTGCACGAGA | GTCTACGTTT | TAGCATCCAT | TCAAGTGAGG | GAAAGCGGTT | 3660 |
| | TGCTACTTAG | AAAAATGCAA | AATTAATGAT | TCTCACCCAC | ACATGAGACT | TGGGATTCAC | 3720 |
| | CCATGTATGA | GACACTGGAT | TCAGAGCCAT | GCTGTGGCTC | TCACTCTGCT | GGAGCCAGTA | 3780 |
| | GTGTTTGTGC | TTTGGTTTGT | TTTTTTTAGC | TACATGGTTT | ATGTGAGGTG | CGGACTTACT | 3840 |
| | TGAGTTGCTC | TGTCTTACA | GGGAGCTTGC | TTTTTCTCTG | CTGGTTTGTG | TTCACTTTTG | 3900 |
| 35 | CTGTCTCTGT | TTAGAAGAAA | ACATTAGAAC | TGGGGTGTGG | TGGAAGGATG | GGAGCACAAT | 3960 |
| | CTGGGAGGGG | AAGACCTGCT | CTCTCTCCAC | ATACCAGGAG | GGAGTGGCAG | GAAGGGGAGA | 4020 |
| | CAGTGTGCGG | GACTCAGGGA | GTCAAGAGCG | TGAGCACCCC | CAGGCTTCAA | TCTGCTGAAC | 4080 |
| | GTGTGTGATC | TGGGGGCGCC | CGTGACGAG | GAACACTCTC | CCCATCACAA | TTCTCTGGG | 4140 |
| | CACAGTGGAG | AGCCATGAGT | GGGGCTGTCT | CTGGGGCGTG | CGCTATGGTG | AGTGAGCCCA | 4200 |
| 40 | CGCCAGGAGC | CAGTTCAGCC | CAGCCTCATT | CTTCTCTCTG | TTCTTTGCTT | TCGAAGTTCT | 4260 |
| | AGTTCATAAG | CAACACGAC | AGTACCTGGA | ATGTAAGAGG | CGCTTGGCTT | ATAAAGAGAG | 4320 |
| | GAAGAAAGGA | GACCTTTTCA | CCACGAGGGA | CGTCAGGCC | AGCTCTCTGT | CCGGGCATT | 4380 |
| | CATCTTTTTC | CCGGCAATTA | GCTTCAGCTC | TAATGACCTG | CTGTCTGCTT | TATGTTGCAC | 4440 |
| | CTATGATTTC | CAGATTGTAA | AGTTTGTGGC | AAATGTATTA | ACGTTTACAT | CCCATTTACA | 4500 |
| 45 | GATTAGCAAA | CTAAGGATCT | GAGAGGTTAT | GTGATTTTCC | CAGTCTGGCG | GAGGGCAGGG | 4560 |
| | CCCTGTGAGA | AGCCGAGACA | CACCTCGTAA | CAGCTTGTTA | TTTGGGGCTT | CCCATCAGTG | 4620 |
| | AGGCAGAGGT | CATAATGGGG | CCCTGGCTTC | TGGGCAATTC | CCATAAACA | TTGTGCCACC | 4680 |
| | TGAAGATGGA | AGTGTGAGAG | GAAGGCGAGA | TGTTATTCTT | GAAAGCATCT | ACCCTCAGAA | 4740 |
| | AGAGACAGAG | GAGTGATCG | CAGCTGTGTG | AAACCGGGGT | GGTGGTGGTT | CCAGCAGCGG | 4800 |
| 50 | GGCACGTGGT | GGACGCAAGA | CGGCCCGGTT | TGAGTTTTCG | TGCTAGGTGA | CACGTAGAAC | 4860 |
| | TGGAACCTCA | GAGGGTGCTC | CTTGGGGGCC | CTGATGAGAG | AGACACAGAA | GGGAAGGGAG | 4920 |
| | ACTGTTTCCA | TGCTCTGTCC | TCTGCGGCAG | CGAGCCTGCT | GCTCTTGACG | CTGGGTGGCT | 4980 |
| | GTTCGGTGCA | GGGGGCGGTT | GAGGAACACG | GTGGGGAGCA | GCCTGCGAGG | GGCCCGGGCT | 5040 |
| | TTCACTACTC | ACTATACCTG | CTGTTTGGTT | TGGCCAGGAT | GGCCTGGGAG | TCCCAGGGGC | 5100 |
| 55 | CGGGCAAAAG | CTGCCCCCAA | CAGACATGGG | CGGAGGGAAC | CGTCTCACCC | CTGCCCTTTC | 5160 |
| | TCCTCTCTCT | ACGCACTGTC | AGTGGGACGG | GAGGGTGGTC | TGCCCGGGGC | TTCAAGCTCC | 5220 |
| | TGTCAGGAA | CCGGACCCAT | GTCTACGCC | AGTGACGCCA | CACGGCCAGC | TTGAGGTTGC | 5280 |
| | TCATGGAAGT | CTCCAGGTGT | GAGATGGGCA | TCTTCTTGTT | GCCACTATGC | CGCTGAGGCC | 5340 |
| | TACCCCAAA | CCTGCCCTTC | CTCAAACTAA | ATCTTCCATT | CTAAGCACTT | TGAAGGAAGC | 5400 |
| 60 | AAATCAACCA | ATTAACAAAA | TATATCCAG | GAAAAAATA | AAAAAATAA | AAAAAATAA | 5460 |
| | AAA | | | | | | 5463 |

Seq ID NO: 82 DNA Sequence

Nucleic Acid Accession #: Eos sequence

Coding sequence: ..651

| | | | | | | | |
|----|------------|-------------|------------|------------|------------|-------------|------|
| 65 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| | CCACAGGGGC | CCCCAGGGCC | ACCAGGGATC | CCTGGAGCCA | AGGGCGAGCT | TGGATTGCCC | 60 |
| | GGTGCCCCAG | GAAATCGATGG | AGAGAAAGGC | CCCAAAGGAC | AGAAAGGAGA | CCCAGGAGAG | 120 |
| 70 | CCTGGGCGAG | CAGGACTCAA | AGGGGAAGCA | GGCGAGATGG | GCTTGTCCGG | CCTCCCGGGC | 180 |
| | GCTGACGGCC | TCAAGGGGGA | GAAGGGGGAG | TCGGCATCTG | ACAGCCTACA | GGAGAGCCTG | 240 |
| | GCTCAGCTCA | TAGTGGAGCC | AGGGCCCCCT | GGCCCCCTTG | GCCCCCAGG | CCGATGGGGC | 300 |
| | CTCCAGGGAA | TCCAGGGTCC | CAAGGGCTTG | GATGGAGCAA | ACGGAGAGAA | GGGTGGGTGG | 360 |
| | GGTGAGAGAG | GCCCCAGCGG | CTGGCTGGG | CAAGTTGGCC | CACCGGGCCT | TATTTGGGCTG | 420 |
| 75 | CCAGGAACCA | AAGGAGAGAA | GGGCAGACCC | GGGAGGCCAG | GACTAGATGG | TTTCCCTGGA | 480 |
| | CCCCAGGAG | AGAAAGGTGA | TCGGAGCGAG | CGTGAGAGAG | AGGGAGAACG | AGGGGTCCCC | 540 |
| | GGCCGGAAG | GAGTGAAGGG | CCAGAAAGGC | GAGCCGGGAC | CACAGGCCT | GGACAGCCG | 600 |
| | TGTCCCGTGG | GCCCCGACGG | GCTGCCTGTG | CCTGGCTGCT | GGCATAAGTG | ACCCACAGGC | 660 |
| | CCAGCTCACA | CCTGTACAGA | TCGGTGGGA | CATTTTAAAT | TTTTGTAAAA | ACAAACAGT | 720 |
| 80 | AAATATTTGA | TCTTTTTC | TGGAATGCGC | TACCTGTGGC | CTTTTAACAT | TCAGAGTAT | 780 |
| | GGCCACCCAG | CCCCAAAGCC | ACGGGATGTT | GAAGCTGCCG | GAAAGTGGAC | AGGCCAGACC | 840 |
| | AGGGAGATGT | GTACCTGAGG | GGCACCTTTG | GGCCTGGGCT | TTCCACAGAA | GAGAGTGAAG | 900 |
| | GTAGAAGCAC | CTGGCTCGGG | CAAGGCTAGA | AAGATGCTAC | GTGGGGCTTT | CAGTCACTGC | 960 |
| | ATCAGCAGAG | AGACTCTCAG | CTGTGGTACT | GCCCTGTAAG | AACCTGCCCC | CGCAAACTC | 1020 |
| | TGGAGTCCCT | GGGACACACC | CTATCCAAGA | AGACCCAGGG | GTGGAAACAG | GCGTCTGTT | 1080 |

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GCTCCTGGCC TCATCAGCCT CCAAACTCAA CCACAACCAAG CTGCCTCTGC AGTTGGACAA 1140
GACTTGGCCC CCGGACAAGA CTGCCCCAGC ACTTGGCGCT GGGCCCGGGG AGCAGTGAGT 1200
GGAAATCCCC CAGCAGGGTC TAGCTCTACC ACATTCAAGG GGCCTCAGGA GGCCAGCCTG 1260
CCATGAGAGC ACATGTCTCT TGGCCAGGAG TAGTGGCTGA GCTCTGTGAT CGCTGTGATG 1320
TGGACCCAGC TCCAGGGGAG AGAGTGTGCA GGATGGAGGG GCCCAGCCTG GACTGACTGC 1380
TACTTCTGT CTCTGTTTCC ATTATCACCC AGAGAGGGAC AAGATAGGAC ATGGCCTGGA 1440
CCAGGGAGGC AGGCCTCCCA CTCAGAGTCT GGGTCTCACT GGGCCCAAGT CTCCCACCCA 1500
GAACTCTGGC CAAAAATGGC TCTCTAGGTG GGCTGTGCAG GCAAAAGCAA GCTCAGGGCT 1560
GGTTCACAGC TGGCCTGAGC AGGGGGCCTG CCACCAGACC CACCCACGCT CTGACGAGAG 1620
GCTTTTCCAC CTCAGCAAG TGTTCACAGC AACCAAGCTCC ATCCTGGCTG CTGCGCTTCC 1680
ATTTCCGTGT AGATGGAGAT CACTGTGTGT AATAAACCAAC AAGTCCGTGT C 1731

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Seq ID NO: 83 DNA Sequence

Nucleic Acid Accession #: Eos sequence

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1 11 21 31 41 51
| | | | |
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GTGCCCCAGG AATCGATGGA GAGAAAGGCC CCAAAGGACA GAAAGGAGAC CCAGGAGAGC 120
CTGGGCCAGC AGGACTCAAA GGGGAAGCAG GCGAGATGGG CTTGTCCGGC CTCCCGGGCG 180
CTGACGCGCT CAAGGGGGAG AAGGGGGAGT CGGCATCTGA CAGCCTACAG GAGAGCCTGG 240
CTCAGCTCAT AGTGGAGCCA GGGCCCCCTG GCCCCCTTGG CCCCCCAGGC CCGATGGGCC 300
TCCAGGGAAT CCAGGGTCCC AAGGGCTTGG ATGGAGCAA GGGAGAGAAG GGTGCGTCGG 360
GTGAGAGAGG CCCCAGCGGC CTGCCTGGGC CAGTTGGCCC ACCGGGCTT ATTGGGCTGC 420
CAGGAACCAA AGGAGAGAAG GGCAGACCCG GGGAGCCAGG ACTAGATGTT TTCCCTGGAC 480
CCCGAGGAGA GAAAGGTGAT CGGAGCGAGC GTGGAGAGAA GGGAGAACGA GGGGTCCCGC 540
GCCGGAAGG AGTGAAGGGC CAGAAGGGGC AGCCGGGACC ACCAGGCTG GACCAAGCGT 600
GTCCCGTGGT CCCCAGGGGC CTGCCTGTGC CTGGCTGCTG GCATAAGTGA CCCACAGGCC 660
CAGCTCACAC CTGTACAGAT CCGTGTGGAC ATTTTAAATT TTTGAAAAA CAAAACAGTA 720
ATATATTGAT CTTTTTTCAT GGAATGCGCT ACCTGTGGCC TTTTAACTT CAAGAGTATG 780
CCCAACCCAG CCAAGAGCCA CCGCATGTG AAGCTGCCGG AAAGTGGACA GGCCAGACCA 840
GGGAGATGTG TACCTGAGGG GCACCTCTGG GCCTGGGCTT TCCAGGAAG GAGATGAAGG 900
TAGAAGCACT TGGCTCGGGC AAGGCTAGAA AGATGCTACG TTGGGCTTTC AGTCACCTGA 960
TCAGCAGAGA GACTCTCAGC TGTGGTACTG CCCTGTAAGA ACCTGCTCCC GCAAACTCT 1020
GGAGTCCCTG GGACACACCC TATCCAAGAA GACCCAGGGG TGAACACGCG GCTGCTGTTG 1080
CTCCTGGGCT CATCAGCCTC CAAACTCAAC CACAACCAAG TGCTCTGCA GTTGGACAA 1140
ACTTGGCCCC CGGACAAGAC TCGCCAGCA CTGTGGGCTG GGGCCGGGGA GCAGTGAGTG 1200
GAAATCCCCC ACGAGGGTCT AGCTCTACCA CATTAGGAG GCCTCAGGAG GCCAGCCTGC 1260
CATGAGAGCA CATGTCTCTT GGCAGGAGT AGTGGCTGAG CTCTGTGATC GCTGTGATGT 1320
GGACCCAGCT CCAGGGAGCA GAGTGTGGGG GATGGAGGGG CCCAGCCTGG ACTGACTGCT 1380
ACTTCTGCTC TCTGTTTCCA TTATCACCCA GAGAGGGACA AGATAGGACA TGGCCTGGAC 1440
CAGGAGGACA GGCTCCAC TCAGAGTCTG GGTCTCACTG GCCCCAAGTC TCCACCCAG 1500
AACTCTGGCC AAAAAATGCT CTCTAGGTGG GCTGTGCAG CAAAGCAAAG CTCAGGGCTG 1560
GTTCCACAGT GGCCTGAGCA GGGGGCCTGC CACCAGACCC ACCCAGCTC TGACGAGAGG 1620
CTTTTCCACC TCACGCAAGT GTTCCACGCA ACCAGCTCCA TCCTGGCTGC TTGCCTTCCA 1680
TTTCCGTGTA GATGGAGATC ACTGTGTGTA AATAAACCAA AGTGCGTGAA AAAAAAAA 1740
AAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AG 1782

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Seq ID NO: 84 DNA Sequence

Nucleic Acid Accession #: Eos sequence

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60

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1 11 21 31 41 51
| | | | |
TCCTGAAGT GGCTGCTATC CAGGATGACT GTGTTGCTGC AGTCTTTGAG TGGTTGGAGC 60
GCTGTAATGT CTATGTTAAT AGCTGGGAAA TCGCAGTAGC AGCAACCAGA CCACTCCAAT 120
GGAACAATCC AAGTTGGGGT AAGTTTGATT GAGCAAAAAA GTCATGCTGA CTGTGTGATG 180
AAGAGGCAGA ACTGGTAAAC GTGACAGGCC CTGCAGTCAG CAGCTGTGGA TTTTATGTGC 240
AGGGCAGACT GATCTGGAAA ATGGGAAGAG CTGACTGCCA ATAACACCTT GGGGGGAGGT 300
TTGTTCACTG CATCTCCCTA CTCTTGTAT ACCTCTGATG ACATGCAGAA GCTTAGGAAA 360
TAAACACAC TGTAAATC ACAGGGTGCA AGTAAGTACA TGTGGATGCC AGTGTAGAGA 420
GAAGCGAAG CTAGTTTCCA TTGCAAGAA CCAACAGAG TAACAGGGCT TTGTCCAATG 480
TCTCCAGTCC ATGGTTCCCT GGTGTTCTTA GAGTCTATT AAAAAAAA AAAAAAAA 539

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Seq ID NO: 85 DNA Sequence

Nucleic Acid Accession #: NM_004861.1

Coding sequence: 204..1475

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70
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80

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1 11 21 31 41 51
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CCGAGGGTCT CACTGTGTCA TCCAGAGCTG GAGTGCAGCG GCACAGTCAT GGCTCACTGG 120
AACTCAGGCT CAAGCAATCC TCCCGCTCA GCCTTCCAAG TAACTAGGAC TACAGGCATG 180
TGCCACCAAG CTTGGTGTCT GAGATGCTGC CACCGCAGAA GAAGCCCTGG GAGTCCAATG 240
CTAAGGGGCT GGTGCTGGGC GCGCTCTTCA CTAGTTTCTT GCTGCTGGTG TACTCTATG 300
CCGTGCCCCC GCTGCATGCC GGCCTGGCCT CCACGACCCC GGAGGCCGCA GCGTCTGCT 360
CTCCACCTGC ACTCGAGCCA GAGGCAGTGA TCCGGGCCAA CGGCTCGGGG GGGGAGTGCC 420
AGCCGGGGG CAACATCGTG TTCTTGAAGA CGCAAGAGC GGCCAGCAGC ACCCTGCTCA 480
ACATCTCTGT CCGCTTGGGC CAGAAGCACC GGCTCAAGTT CGCTTCTCTT AACGGCCGCA 540
ATGACTTCGA CTACCCGACC TTCTTGGCCC GCAGCCTGGT GCAGGACTAT CGGCCCGGGG 600
CCTGTTCAA CATCATCTGC AACCACATGC GCTTCCAATA CGACGAGTG CGCGCCTGG 660
TGCGACCAA CGCATCTTC ATCACGGTGC TCCGGGACCC CGCCCGCTTG TTCGAGTCT 720
CCTTCACTA CTTGGGCGCG GTGGTGCCCC TCACTGGGAA GCTCTCGGCC GCGGACAAAG 780
TGACCGAGTT CCGTCAAGAC CCGGATCGCT ACTACGACCC CAACGGCTTC AATGCCCAAT 840
ACCTCCGAAA CCTGCTCTTC TTGACCTGG GCTATGACAA CAGCTGGAC CCCAGCAGCC 900
CGCAGGTGCA GGAGCACATC CTGGAGGTGG AGCGTCGCTT CCACCTGGTG CTCTTCAAG 960
AGTACTTCGA CGAGTCCGCT GTGCTGCTGA AGGACCTGCT GTGCTGGGAG CTGGAGGACG 1020
TGCTCTACTT CAAGCTCAAC GCCCGCCGCG ACTGCCCCGT GCCCGGCTC TCGGGGAGC 1080

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| | | | | | | | |
|----|--|------------|-------------|-------------|------------|-------------|------|
| | TGTATGGGCG | CGCCACCGCC | TGGAACATGC | TGGACTCCCA | CCTCTACCGC | CACCTCAACG | 1140 |
| | CCAGCTTCTG | GGGCAAGGTG | GAGGCTCTCG | GGCGGGAGCG | CATGGCCCGC | GAGGTGGCCG | 1200 |
| | CCCTGGGCCA | TGCAACCGAG | CGCATGCGGA | CCATCTGCAT | CGACGGGGGC | CACGCCGTGG | 1260 |
| 5 | AGCGCGCGCG | CATCCAGGAC | GAGGCCATGC | AGCCCTGGCA | GCGCTGGGCG | ACCAAGTCCA | 1320 |
| | TCTGGGCTA | CAACTCAAG | AAGAGCATCG | GGCAGCGGCA | CGCGACGCTC | TGCCGGGCCA | 1380 |
| | TGCTCAGCGC | CGAGATCCAG | TACCTGATGG | ACCTGGGCGC | CAACCTGTGG | GTCAACCAAGC | 1440 |
| | TCTGGAAGTT | CATTGGGAT | TTCTGCGGT | GGTGACGTCC | CACCGCCAG | CGGCTTGCTT | 1500 |
| | GCTGCTCGC | TCCCTGCAGA | GGGGCTGAGC | AGGACGCGCG | TGGTGTGGCG | CGCCCCAGC | 1560 |
| 10 | CCCCCTCTGG | TGCCACCTCA | GACCCCGGGG | TGAGGGGGGG | CTCCCTGGGG | GGAGGCAGCC | 1620 |
| | AGCCAAAGCT | GGGCCCATCA | ACACAGAGAG | GGCTAAACCG | AGATCAGTAT | TTAACTAATT | 1680 |
| | ATACCAAGTT | TTATTAACCC | CCTTCCCTC | CCCGATAAAG | AATGTTCTAT | TTCTGCCTCC | 1740 |
| | CCTTAAAGGG | GAGACCTCAG | AAGTAAAGGA | ATTGTATGTT | GTGTTTTTGT | T | 1791 |
| 15 | Seq ID NO: 86 DNA Sequence | | | | | | |
| | Nucleic Acid Accession #: Eos sequence | | | | | | |
| | Coding sequence: 337..1878 | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| 20 | CTGCACAGGG | AGTTTGTCTT | GTGCAACAA | TTTCCAAGGC | AGCGTTTCT | TCCCTGCCTG | 60 |
| | GGAGTGCAGG | GCTCAGGCGC | TTCACTTTGG | AACTGACTCA | GAGACCTAAA | GAAGCCCAAC | 120 |
| | TGGCCAGCGG | GAAGGGGGGC | CGCGCGCGCC | TCCCGTTTT | GGGCAGCCCT | GGCCAGCTCC | 180 |
| | CTGTGGCCTT | GGAGGACTTC | CACCGGGCAG | CGCTTCCCAT | GATGCCAGGC | TACCAGGCGC | 240 |
| | GGGGGATTCC | TGCAGGCGCG | CGCTGCTTTT | CTTAGAACCC | CCTTCTTAGA | AAAGTACACC | 300 |
| 25 | TGGAAGTTTT | GCTTCAAGA | GAGGAGAGGC | AGCAGCATGG | CGAGTGTCTT | GTCCCGACGC | 360 |
| | CTTGGAAAGC | GGTCCCTCTT | GGGAGCCCGG | GTGTTGGGAC | CCAGTGCCTC | GGAGGGGCCC | 420 |
| | TGGGCTGGCC | CACCTCGGGA | GCCACTGCTA | GAAGGGGCGG | CTCCCCAGCC | TTTCAACACC | 480 |
| | TCTGATGACA | CCCCCTGCCA | GGAGCAGCCC | AAGGAAGTCC | TTAAGGCTCC | CAGCACCTCG | 540 |
| | GGCTTTCAGC | AGGTGGCTTT | TCAGCCTGGG | CAGAAGGTTT | ATGTGTGGTA | CGGGGGTCAA | 600 |
| 30 | GAGTGACAG | GACTGTGCGA | GCAGCACAGC | TGGATGGAGG | GTGAGGTGAC | CGTCTGGCTG | 660 |
| | CTGGAGCAGA | AGCTGCAGGT | CTGCTGCAGG | GTGGAGGAGG | TGTGGCTGGC | AGAGCTGCAG | 720 |
| | GGCCCTGTGC | CCAGGACACC | ACCCCTGGAG | CCCGAGGCCC | AGGCCCTGGC | CTACAGGCC | 780 |
| | GTCTCCAGGA | ACATCGATGT | CCCAAAGAGG | AAGTCGAGCG | CAGTGGAAAT | GGATGAGATG | 840 |
| | ATGGCGGCCA | TGGTGTGCTG | GTCCCTGTCC | TGCAGCCCTG | TTGTACAGAG | TCTCTCCGGG | 900 |
| 35 | ACCGAGGCCA | ACTTCTCTGC | TTCCCGTGGC | GCCTGGGACC | CATGGAAGGA | GAGTGGTGAC | 960 |
| | ATCTCGGAGA | CGGGCAGCAG | CACCTACCAGC | GGTCACTGGA | GTGGGAGCAG | TGGTGTCTCC | 1020 |
| | ACCCCTCTGC | CCCCCAACCC | CCAGGCCAGC | CCCAAGTATT | TGGGGGATGC | TTTTGGTTCT | 1080 |
| | CCCCAAACTG | ATCATGGCTT | TGAGACCGAT | CCTGACCCCT | TCTGCTGGGA | CGAACCAGCT | 1140 |
| | CCACGAAAAA | GAAAGAACTC | TGTGAAGGTG | ATGTACAAAT | GCCTGTGGCC | AAACTGTGGC | 1200 |
| 40 | AAAGTTCTGC | GCTCCATGTT | GGGCATCAAA | CGACACGTCA | AAGCCCTCCA | TCTGGGGGAC | 1260 |
| | ACAGTGGACT | CTGATCAGTT | CAAGCGGGAG | GAGGATTTCCT | ACTACACAGA | GGTGACAGTG | 1320 |
| | AAGGAGGAAT | CTGCTGTGCT | TGCTGTGCT | GCTGCCGCGG | GCACCCAGT | CCCTGGGACT | 1380 |
| | CCCACTCTCG | AGCCAGCTCC | CACCCCAAGC | ATGACTGGCC | TGCTCTGTCT | TGCTCTTCCA | 1440 |
| | CCACCTCTGC | ACAAAGCCCA | GTCCCTCGGC | CCAGAACATC | CTGCCCCGGA | GTCTCCCTTG | 1500 |
| 45 | CCCTCAGGGG | CTCTCAGCAA | GTGAGTCTCT | GGTCCCTTCT | GGCACATTCA | GGCAGATCAT | 1560 |
| | GCATACCAGG | CTCTGCCATC | CTTCCAGATC | CCAGTCTCAC | CACACATCTA | CACCAGTGTCT | 1620 |
| | AGCTGGGCTG | CTGCCCCCTC | CGCCGCTTGC | TCTCTCTCTC | CGGTCCGGAG | CCGGTGGCTA | 1680 |
| | AGCTTCAGCG | AGCCCCAGCA | GCCAGCACCT | GCGATGAAT | CTCATCTGAT | CGTCACTTCT | 1740 |
| 50 | CCACCCCGGG | CCCAGAGTGG | TGCCAGGAAA | GCCCGAGGGG | AGGCTAAGAA | GTGCCCGCAAG | 1800 |
| | GTGATAGGCA | TGAGACACCG | GGACCAGTGG | TGCACGGCCT | GCCGGTGGAA | GAAGGCTTGC | 1860 |
| | CAGGCTTTTC | TGGACTGAGC | TGTGCTGCAG | GTCTACTCT | GTTCCTGGCC | CTGCCGGCAG | 1920 |
| | CCACTGACAA | GAGGCCAGTG | TGTCAACAGC | CCTCAGCAGA | AACCGAAAGA | GAAAGAACGG | 1980 |
| | AAACACGGAG | TTTGGGCTCT | GTGGCTAAG | GTGTAACACT | TAAAGCAATT | TTCTCCCAT | 2040 |
| 55 | GTGCGAACAT | TTTATTTTTT | AAAAAAAGA | AACAAAATA | TTTTTCCCC | TAAATAGGA | 2100 |
| | GAGAGCCAAA | ACTGACCAAG | GCTATTACGC | AGTGAACAG | TGACCAAAGA | ATTAATTACC | 2160 |
| | CTCGTTTCC | CACATCCCA | CTCTTAGGG | GATTAGCTTG | TGCGTGTCAA | AAGAAGGAAC | 2220 |
| | AGCTCGTTCT | GCTTCTGCT | GAGTCGGTGA | ATTCTTTGCT | TTCTAAACTC | TTCCAGAAAG | 2280 |
| | GACTGTGAGC | AAGATGAATT | TACTTTTCTT | AAAAAAAGAA | AAAAAAAGAA | AAAAAAGAG | 2340 |
| | TTTCTGGCTG | ATGGGTGACT | CAGAGTGCAG | GACTGCCTGG | CCGTGGGGCA | GAGGGGTTTG | 2400 |
| 60 | CCCTTCTCGG | AGGGTACCTC | CTGTTCCCTG | TCTGAGCATC | CTGCATGGAA | GTCAAAGGAA | 2460 |
| | ATCCCTTTCT | TGGTGACGAC | TTAAATCTGG | GTCCCTCAG | ACATTGGGTT | GCACCCCAAC | 2520 |
| | AAATATTAAA | TGGCTTCTTC | TTAAAGCCCA | GAGAAAGAGG | TTTTTTAAAA | GACTGTGCGC | 2580 |
| | AAATAGCTGA | GCCAAAAGGC | TGATCAGAAT | TCACTTTTGG | GAATGTGGCA | GTTAAACACT | 2640 |
| | ACCTTGATCA | TTCTCTCCTC | TTTCTCGAG | GAACTCCTGG | AGGGTTTGAG | CGTCTGGAAG | 2700 |
| 65 | CTCTCTGCTC | TGACCCGAGG | AAGCACCTCT | CTGACGCGCG | CTTCTCCCGG | TTATTGAAAG | 2760 |
| | GACGCTCAG | AAATGCTTTG | TTTTCTTTTA | CGATGTATTC | AGAAGCCCTT | ACTGATTAAA | 2820 |
| | GTTTTCTTTT | ATTTGGGTGG | CCGGGAGAGA | CCCAGGGAGG | TTCTGGAGGT | TCCTTTCTGT | 2880 |
| | CTCCTGCCCC | CACCAGGGAT | TTCCCATTTT | CTGTTTGGCT | CCTGAAAGCA | GGATGAGGAA | 2940 |
| 70 | GGCCAAGGAG | AGTCTTGCA | CCCGTGAGCG | TCAGGATGAG | GAAATGACAG | GAGGAAGACG | 3000 |
| | TGGGTTTGGG | TTAGTGGCTG | CTGGCGTTTT | GGCCCTTGGT | GTTCCTGGAG | CCTCCAGGGA | 3060 |
| | TCTAGGGGAG | CCTGGGCTGC | GTGCATGTGC | ATAAGCAGAG | CTGTCTTGG | GGAGAAGGAG | 3120 |
| | GGAGGTCTCG | GGAGGTGAGC | ACCATGCCAA | CCAGCCCTGC | GCGAAGACAG | AGTGAGCCAC | 3180 |
| | GCCCGATAGG | CAGGGCATGT | TTCTGTTTTG | GTGTCTCACT | TTCTCCCAAG | CGTGACTTAT | 3240 |
| | TTGGGATATC | CTCAGGGCTC | ACTGGAATGT | GACTGCCCCA | TGCCAGCTG | CCTCGGGTAC | 3300 |
| 75 | AAGTCTTGGC | CCTATGTCCC | AGCTGTGAGG | GGCTCAGGGA | ATCCTACCCA | GCCACCTGTC | 3360 |
| | CTGGGATGGA | GTGTGAGCAT | CCACCCCTTG | GTGTGATCG | AGGCCGCCCT | CCCAGTCTCT | 3420 |
| | GGTGAAGATA | TTTGGGCCAC | CAGGCTCCCC | TTGGCCCTTT | CACGTAGGAA | ATAGACACGT | 3480 |
| | GCTTTTAAAT | GCAGSACACT | TTGAGTGTTA | CAAAATCTGT | AGACCTGGCA | GTAGGGTCTAT | 3540 |
| 80 | GATGTTGGGA | AGGGGTAGT | CCCTAGGTTT | GGTGACAGAA | GGGACAGACA | CTTGTGCACA | 3600 |
| | GGTGTCTTTG | GTGATGGGGT | TTTTTTTTTT | ATAACTTAGT | AAAAAAAGAA | AAATGTATGT | 3660 |
| | GGAAATCTGT | CTCTGGTAA | AGCTCAAAGC | CAGGCTAGCC | TGAGGTGGCG | CAGGGCTCTC | 3720 |
| | CTTCTGTCC | CTTGTCTCTC | CTTGAGAAAT | AAGAGCTGGC | AGCTGCTGAT | GGTGTTCCTC | 3780 |
| | AACCCCTCTC | ACTTCCCAAG | ACAACCCCA | GCTTCAGGTC | CTCATGGGGA | GGGGAGGGCA | 3840 |
| | CGTTCTTGAC | ACATGGGAAC | TTGGCTCAGG | AGGGCTCTCC | CTTCCCTCT | CCCTCAGAGT | 3900 |
| | TTTCACTGCC | GTCTGCTCTT | TAGAAAGCTG | TTTGAATTCC | CCCCGCCCCC | AGTTTGGACC | 3960 |

5
10
15

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GTGTAGATAT AACTGGATAT ACGGATTTTT CTCTTGTGC AGGCTTCTTA TGCCGTGGST 4020
ATACAGGGCA GGAAAGAGAG GAATAAAGGG AGAGAGCAGT GTGGAAACCA CGGTGGTTTT 4080
GCTTTGTCT TACTAGGTTT TGGTGCCACC TTCCCTGCCT GCGCTTGTGC CCCTCTCCT 4140
CCTTGGCACT GCGGGCTCC TTGCTCCCT TCCACCGTG CTGCCATCCC GTGCTGTGC 4200
TGTGTGTCT TCACACGTGC TCTGTCTCG GGTGTGTCC ATTCATGCCT TCTTGGAGGG 4260
TGAGGGTGGC TTGGGAACCG ACCCAGTGAT CATGCTACT TTCTTCTTG TATCTCCCTC 4320
CTTCCAGCC CACCCGGGCA GCAGACTCTG ATGGAAGGAA GGTGCGTAG GTGGGCTTT 4380
AGAAACTAAC GGGACTGGTT TTCAAAGCAG TTATCTTGGG AAACCTGTTA TTCCAGCGAT 4440
GTGACTTTTT TCAGAAATAT TCTTGAATC ATATTCAGAG TCTGGGCTG TGTGTGAGC 4500
AGCCTTAAGG ATGCTAGACA CTCAATTAGT GCCCAGGGAG TCCAGCGAAT GACGTCTGTG 4560
GCCAAGCGAG GTCTCAGGTG CAAAGCAAAA GGACCATTTA AAGTAAAAA GCTTGGATTG 4620
AATCATGTGA CTTTTAAATT GGCTCAGAAA GCAATTTTGT AATTTCAGAG AGTGTTTTGA 4680
GCCATGGCCA CGTTGTCAAT GTGAGTCTAT AGCTTGACTC CTGGAGAAC AATATTCAIT 4740
TGGTGTGGA GACTGATTTG CTGGGAGAAA TCTGTCTGT TACTTTCTG TCATCCAGG 4800
TTCTGACTTT TACCAGGGC AAAAAAAAAA AAAGCAAGAG GGAGATAAAT CCCATCTGTG 4860
AGTTTGTCTT ATTGGCGCT TTTTCTCAG CTGTCTTCCA AGTATTATT TTACTGTTAA 4920
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30
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Seq ID NO: 87 DNA Sequence
Nucleic Acid Accession #: Eos sequence

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1      11      21      31      41      51
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AGTGTGAAGG GAAGGCTAAG GACGCATCGG TGCTGGAGAG TTGAGAATAT GCCTTCCCCT 60
CCACCCCCAA CCCAGTCACC TTATTTGAAA AAAAATTAAA AAACACCTTT TATTTAAAAA 120
CCTAACCCCTG GAAGTTTGCT CGGGAAGGCA TTCTCTTCCT CTTCCTCCAG CTGCTGAAA 180
ATCATATGCG TGTTTTTCTC TGTTCCTGC TCTGTAGCTG ACATCAGGGG AGCAACGTGA 240
ACACAGGAAA ATGGAAATCA ACATTTGAAA CTTTAAATG GAAGCTTTAT TGGGGTTCCA 300
CATATGAAAA ACTGCAATA GCAGAAGTAT GTGACTCAAT AAATTATTCT GGAGTGACCA 360
CATCTCTAA CTGCTCCCA GGACAAGAG GAGAATGTGA ACAATGCTCC TGAAGCCCC 420
TTTCCCTCAA AGAATCACT CAATTGAAGG AAAAATGCTC CATGTCCCCT CTGCCAGTTG 480
GTGTTTATCA AAGGACAAGC GAGGAAGAGA GACAAGATGC CTGGATGTGT GTGTTAATCA 540
AGAGTTGTCA GGACCTGCCC TCTAAAGAAA AGCGCTAAAA TGATGCTTTT GACAAGACT 600
TTCTCAAGT GATGCACTG TAAGGTTGG AAAACAAGGC CCAATCAGGC TAGGTCTGAC 660
TTGTGCGCTG CTTTGTGAAA TAAAGTTTAA TTGGCTCACA GA 702

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50

Seq ID NO: 88 DNA Sequence
Nucleic Acid Accession #: Eos sequence

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1      11      21      31      41      51
|      |      |      |      |      |
AGTGTGAAGG GAAGGCTAAG GACGCATCGG TGCTGGAGAG TTGAGAATAT GCCTTCCCCT 60
CCACCCCCAA CCCAGTCACC TTATTTGAAA AAAAATTAAA AAACACCTTT TATTTAAAAA 120
CCTAACCCCTG GAAGTTTGCT CGCTGCCTGA AAATCATATG CGTGGTTTTT CCGTTTCTCT 180
GCTCTGTAGC TGACATCAGG GGAGCAACGT GAACACAGGA AAATGGAAAT CAACATTGTA 240
AACTTTTAAA TGGAAAGCTT ATTGGGGTTC CACATATGGA AAACGCAAA TAGCAGAAGT 300
ATGTGACTCA ATAAATTATT CTGGAGTGAC CACATCCTCT AACTGCCTCC CAGGACAAGA 360
CGGAGAATGT GAACAATGCT CCTGAAGGCC CCTTCCCTC AAAGAATCAC TGCAATTGAA 420
GGAAAAATGC TCCATGTCCC CTCTGCCAGT TGGTGTATAT CAAAGGACAA CGGAGGAAGA 480
GAGACAAAGT GCCTGGATGT GTGTGTTAAT CAAGAGTTGT CAGGACCCCT CCTCTAAAG 540
AAAGCGCTAA AATGATGCTT TTGACAGAC TTTTCTCAA GTGGATGCAG TCTAAGGGTT 600
GGAAAAACAG GCCAATCAG GCTAGGTCTG ACTTGTGCCG TGCTTTTGTA AATAAAGTTT 660
TATTGGCTCA CAGA 674

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55
60
65

Seq ID NO: 89 DNA Sequence
Nucleic Acid Accession #: Eos sequence

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1      11      21      31      41      51
|      |      |      |      |      |
AGTGTGAAGG GAAGGCTAAG GACGCATCGG TGCTGGAGAG TTGAGAATAT GCCTTCCCCT 60
CCACCCCCAA CCCAGTCACC TTATTTGAAA AAAAATTAAA AAACACCTTT TATTTAAAAA 120
CCTAACCCCTG GAAGTTTGCT CGCTGACATC AGGGGAGCAA CGTGAACACA GGAAAAATGGA 180
AATCAACATT TGAACATTTT AAATGGAAGC TTTATTGGGG TTCCACATAT GGAAAACTGC 240
AAATAGCAGA AGTATGTGAC TCAATAAATT ATTCTGGAGT GACCACATCC TCTAACTGCC 300
TCCAGGACA AGAAGGAGAA TGTGAACAA TCTCCTGAAG GCGCTTTCC CTCAAAGAAT 360
CACTGCAATT GAAGGAAAAA TGCTCCATGT CCCCTCTGCC AGTTGGTGT TATCAAAGGA 420
CAAGCGGAGA AGAGAGACAA AGTGCCTGGA TGTGTGTGT AATCAAGAGT TGTGAGGACC 480
CTGCCTCTAA AAGAAAGCGC TAAATATGAT CTTTGTACAA GACTTTTCTC AAAGTGGATG 540
CAGTCTAAGG GTTGGAAAAA AAGGCCAAT CAGGCTAGGT CTGACTGTGC GCCTGCTTTT 600
GTAATAAAG TTTTATTGGC TCACAGA 627

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Seq ID NO: 90 DNA Sequence
Nucleic Acid Accession #: AB058765.2
Coding sequence: 400..3492

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GGTAGGGCGA GAAAGAGCTG GGACCCCGCC GCAACTTCGG GATCGGCTGG GTGAGGCTGG 120
GCAGGCTGTA TGCTCAGGGG TTCGTGCGCG GAAGTTCAAG TCCTCGGACA ACCTCTCTCC 180
AGCTCTCCCG CGCGGTACC CACGCGCCAG TCTCCACCTG GGGAAACCCC CTTGGCGTGG 240
CTTGTTCGT TACAAGTTAT CCTGGTAGAG TGGGCATGAA GGCTCGGAG GCAACTGTGC 300
CTGCAGGTGT CCATCACCTT CAAGGACTTG GCCGTGCGGT TCTCGGAGGA GGAGTGGCGG 360
CTCCTGGAGG AGGGGACAGG GGAGTTCTAC CGAGACGTGA TCGGGAGAGG CTAACGAGACG 420
CTGCTCTCTG TGGGGACAGC TGAGCTGCTC CCCCTCTCTG CTTTCTGTGC ACCCTCAGAG 480
CCTGGAAGAG CTGTTGGGGG AGGGAGCCAC GCTGATGAGG GGCAGAGGCC TGCTGTTGT 540
GGAGATCCCC AGGGGGGACA GCGCGGCAC AGCTGCACC TCACAGCCCT GGTGCAGCTG 600
GTGAAGGAGA TCCAGAGATT CTGTTTGGG GAAGTCAAGG GCGCTATGGA CAGCCCCGAG 660

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| | | | | | | | |
|----|-------------|------------|------------|------------|------------|------------|------|
| 5 | AGCGAGAGCC | GGGGAGCCAG | CCTGGATGGA | GAGAGAGCGA | GCCCGGAGGC | AGCTGCGGCA | 720 |
| | AGAGAGCCCT | GCCCTCTCCG | AGGCTGCTCT | AGCTGCTCTC | CAGACGGCCC | TACCAGCCAG | 780 |
| | CCCCACCTGG | CCACCAACGC | CACCGACAGC | TCGTGTTCCA | GTGGCCCAAC | TGGTGACGGG | 840 |
| | GTCCAGGGAA | GTCTCTCTCC | CATCAAACT | GCCGACAAAC | CGTGGCTTAC | AAGGAAGGAA | 900 |
| | GGCCCAAGGAG | CCCTGGGGGG | GGAGCCCAAG | CCTCCCACTC | ATAGCCCCAG | CAGGAGGAAG | 960 |
| | AGCCACAGAG | GACAGGAGAG | AGGGAACCTA | GAGGCGGAA | TTTCTCTGG | GAACAGCCCC | 1020 |
| | TTGCAAGGCC | TCATCAACTG | TCTGAAGGAA | ATCCTTGTGC | CTGGGCCCCG | GCACCCCGAG | 1080 |
| | ACATCCCCAA | GCTTCTTGCC | ACCTCTCCCT | AGCCTGGGCA | CGTCCAGGCT | AACCAAGACA | 1140 |
| 10 | GACCTGGGGC | CTGGGAGCCC | GCCCTGGGCA | GTGAAGACCG | AGGCGGTTTC | AGGGGATTGT | 1200 |
| | CCCCCTCAGG | GTCTGTCTAC | CTGTCTGAAG | GAGCTCCCCG | AGGCCACAGG | CAGGCATCCC | 1260 |
| | AGTCCCTCAG | AAGTGGGGAA | CCGACGGCTA | CAGGAGAAAT | CAGGAGCCTG | GAAAGGGGTT | 1320 |
| | TCTGGAGGGC | CTGGATACCT | CCTGACCCCT | CCTCCCATC | CTGATCTTGG | AGCTGGCGGT | 1380 |
| | CTGCTCTCTG | TGAAGATGGA | GAACAGCTGG | GTCCAGAGCC | CCCCAGGACC | TGCATCCTGT | 1440 |
| 15 | CAGCTTGCCA | GGCAGCCCTC | CAGTCCCTCA | GCCACTGGAG | ACACCAGAGG | GGTCCCCCAA | 1500 |
| | CCCAAGCTGGG | GCCCTGAGGC | TCAAGCTGCC | AGTGCCTCAA | GCTCACCGCT | GGAGGCCCTG | 1560 |
| | GAAGCCTGTC | TGAAGGGGCA | TCCCCCAAAT | GGGTGCTCAC | CTTCCAGCT | GCCACCCACT | 1620 |
| | TCTTGTTCCT | AGAACCCCCA | GCCAGGAGAC | TCTAGGTCTC | AGAAGCCTGA | ACTGCAACCC | 1680 |
| | CACAGATCAC | ACAGTGAAGA | AGCGACCCAG | GAGCCTGTTC | TGCCTCTGGG | TCTGCAGAGC | 1740 |
| 20 | TGTGTGAGAG | ATGGGCCCGC | CAGGCCCTTG | GCCGCCCGAG | GAACCCCAAC | CAGCTTCTCC | 1800 |
| | TCATCCAGCA | GCACCCAGCT | GGACCTGGAT | TTTGGGAGTC | CTGTGGGGAA | CCAGGGGCGG | 1860 |
| | CATCCTGTGC | AAGGAAGGCA | ACCAGGAAGC | TCCCCACTGC | AGGGTCTGGA | GAATTGTCTC | 1920 |
| | AAGGAGATAC | CTGTGCCTGT | GCTGCGGCTT | GCTGGGCCCT | GCTCCTCAGC | AGCAGACAGG | 1980 |
| | GGACCGAGGA | GAGCAGAGCC | CAGGAACCTG | ACACGACACA | AGGAAGGACT | GAGGGCTGAG | 2040 |
| 25 | GCTGTGAGAG | ATGGCCCTCT | CGGGCAGGGT | AGGGGAGAA | CGCCCAACCG | GAGCCTCCAT | 2100 |
| | CTGGTCAGCC | CACAGGTGTT | CACCTCCAGC | TGCGTCCCGG | CCTGCCACCA | CGGGGGGTTT | 2160 |
| | AAAGACCTGC | GGGCCACCGC | GCCAGGAGTG | TGGAGGTGGC | TCCACAGAGG | GTCTGCCCCC | 2220 |
| | AAGCCCTCCC | CGCTGCACCT | CCTGGAGAGC | GCCCTGAGGG | GGATCTTGCC | TGTAAGGCC | 2280 |
| | TTGCGCTTGG | CCTGCGTGGG | AGGCCCCAGC | CCCAGCCCCA | GCCCCGGCTC | CAGCTCGAGC | 2340 |
| 30 | TTAGCGGCTG | CTTAAGGAGA | AGACCCGAGG | CCAGAGCCTG | AGCTCTGGAA | CGCGCTCCCC | 2400 |
| | CAGGAGAGGG | ACCGCCTTCC | CAGCTGTAA | CCTCCTGTCC | CTCTGTCCCC | ATGCTCTGGT | 2460 |
| | GGGACCCCTG | CTGGCAGCAG | TGGCGGAGC | CCTGGTGAAG | ACCCACAGAG | AACAGAGCCC | 2520 |
| | AGGTACTGCA | GCGGCTCCGG | TGCAGGTACA | GCTCAGGATC | CCTGCGCGGT | TTCTCAGCTG | 2580 |
| | GAGAAAGGCC | CCAGGGTTAG | TGAAGCATCC | AGAGGCTTGG | AGCTTGGACA | TGGAAGACCC | 2640 |
| 35 | AGAGTTGCAG | CCAAGACCCA | TGAGAGGCTG | CTCCCCCAGG | GCCCCGCTGA | GCTGCCCATG | 2700 |
| | GAGTCTCCCC | CTCCGAGGCT | GCCCCCTCCG | GAAGCTGCGC | CTCCTGTGTT | GCCAGCCTCC | 2760 |
| | TCCCTGAGCG | CGCCATGCTG | CTGTGGGAAG | CCCTGACAGC | AGGAGCTGCA | CAGCCTCGGT | 2820 |
| | GCTGCCCTTG | CGGAGAAGCT | GGATCGGCTC | GCCACAGCGC | TGGCAGGCCT | GGCTCAGGAA | 2880 |
| | GTGGCCACCA | TGAGGACCCA | GGTGAATCGG | CTGGGGAGGC | GCCCCCAAGG | CCCTGGGCCA | 2940 |
| 40 | ATGGGCCAAG | CTTCTGATG | GTGGACCTCT | CCACGGGGAC | CTGCTGGGG | TCATGGCCCT | 3000 |
| | GGTCACAGAC | ATCTGCCCTA | CTGGAGGCGG | AAGGGACCCA | CGAGGCTTAA | ACCAAGATC | 3060 |
| | CTGCGTGGG | AGGGAGAGAG | CTGACGGGCT | GGTGAACCTC | AAGGACTCTC | CAGAGGGACC | 3120 |
| | GCTCGCCGGG | CACGTCCGCT | GCCTCCAGAC | GCTCCCCCGG | CAGAACCTCC | TGGGCTCCAC | 3180 |
| | TGCAGCTCTT | CCACAGAGCT | GCTGTCTCTT | ACACCCAGCT | GCCATGTGTC | CGCGCTGACA | 3240 |
| 45 | CACCCCTCTC | TCGCACATAC | CGGGGGCCAC | CAGAGCCCCC | TTCCCCCTTT | AGTGCTGTCT | 3300 |
| | GCCTTACCCC | TGACGGGAGC | CTCTCTCTCT | GCAGCCAGTG | CAGATGCAGA | CGTGCCGACC | 3360 |
| | TCAAGAGTGG | CACCAAGCGG | GATCCCAGAG | CGGCCCAAGG | AGCCGAGCAG | CCTGCTGGGA | 3420 |
| | GGAGTGCAGA | GGGCCCTCCA | GGAAAGACTG | TGGGTGGGG | AGCACAGGGA | CCCGAGATGG | 3480 |
| | GGGGCGCAAT | GATGGCATTC | CTCTTCTCCA | CATCTGTCTG | TTCTTGGCGA | GGGTGCAGTG | 3540 |
| 50 | GTGGCGTGA | AGCCCTGTGA | CCCCACCCCA | GGCCACCTCT | TCCACAGAGA | CGCCATCTCC | 3600 |
| | CTTACTGTGG | CTGGGAGCCT | CGCCCTTTGT | CCCAACTGGG | TAGAGCCCCC | AGGTGCTGTT | 3660 |
| | TGCTCAGGAG | GCTGCTGTGG | GGGTGCTTTC | CTCAGCTCTT | GGCCCTCTTG | GCTCAGATTG | 3720 |
| | AATCAATGT | TGCTTCCCTC | TCTGTCTTTT | CCCACTGGAG | CGCCCAAGC | TTGTAGGTGG | 3780 |
| | GTGGTGTGCA | TAGGCCACGT | GTGCCCCACA | TATGCAGGGG | GTGCCCCACA | CAGCTAGAGC | 3840 |
| 55 | GGCCAGGAGA | GGCCCTCTTA | ACCACCAAGC | GTCTCTGATC | TCAGGAGCCT | TGAAGGGCTG | 3900 |
| | GGCTCTGCCC | TTCTTGGAGT | AAATATTGGC | ACAGATTCTA | TTTGAGAGAA | CTCAGCCCCC | 3960 |
| | TGGTCTAAGC | TGGACTTACC | TCTGTGGATT | CTGAAATTA | AGAAGTGAGT | TGCTAAGG | 4018 |

Seq ID NO: 91 DNA Sequence

Nucleic Acid Accession #: AL831935.1

Coding sequence: ..1854

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|----|------------|------------|------------|------------|------------|-------------|------|
| 60 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| | AGCCTGCTGG | TTGTGGAGAT | CCCCAGGGGG | GACAGCCCCG | GCACAGCCTG | CACCTCACAG | 60 |
| | CCCTGGTGCA | GCTGGTGAAG | GAGATCCCAG | AGTTCTTGTT | TGGAGAAATC | AAGGGCGCTA | 120 |
| 65 | TGGACAGCCC | CGAGAGCGAG | AGCCGGGGAG | CCAGCCTGGA | TGGAGAGAGA | GCGAGCCCCG | 180 |
| | AGGCTGCGGC | AAGAGAGCCC | TGCCCTCTCC | GAGGCCTGCT | CAGCTGCCTT | CCAGACGGCC | 240 |
| | CTACCAAGCA | GCCCCACCTG | GCCACCAGCG | CCACCGACAG | CTCGTGTTC | AGTGGCCCAA | 300 |
| | CTGGTGACGG | GGTCAGAGGA | AGTCCTCTCC | CCATCAAAAC | TGCCGACAAA | CCGTGGCCCTA | 360 |
| | CAAGGAAGGA | AGGCCACAGG | GCCCTGGGCG | GGGAGCCACG | CCCTCCCAAC | CATAGCCCCA | 420 |
| 70 | GCAGGAGGAA | GAGCCACAGA | GGACAGGAGA | GAGGGAACCT | AGAGGCCCGA | ATTCTCTCTG | 480 |
| | GGACAGCCCC | CTTGCAAGGC | CTCATCAACT | GTCTGAAGGA | AATCCTTGTG | CCTGGGCCCC | 540 |
| | GGCACCCCGA | GACATCCCCA | AGCTTCTTGC | CACCTCTCCC | TAGCCTGGGC | ACGTCACAGC | 600 |
| | TAAACAGAGC | AGACCTGGGG | CCTGGGAGCC | CGCCCTGGGC | AGTGAAGACC | GAGGCGGTTT | 660 |
| | CAGGGGATTG | TCCCTCCAG | GGTCTGTAC | ACTGTCTGAA | GGAGCTCCCC | GAGGCCACAG | 720 |
| 75 | ACAGGCATCC | CAGTCCCTCA | GGAGTGGGGA | ACCGACGGCT | ACAGGAGAA | CCAGGAGCCT | 780 |
| | GGAAAAGGGG | TTCTGGAGGG | CCTGGATACC | TCTGACCCCC | TCTTCCCCAT | CCTGATCTTG | 840 |
| | GAGCTGGGGG | CTGTCTCTCT | GTGAAGATGG | AGAACAGCTG | GGTCCAGAGC | CCCCAGGAC | 900 |
| | CTGCATCTCT | TCAGCTCTGG | AGGCAGCCCC | TAGTCTCTCT | AGCCACTGGA | GACACCAAG | 960 |
| | GGGTCCCCCA | ACCCAGCTGG | GGCCCTGAGG | CTCAAGCTGC | CAGTGCCTCA | AGCTCACCGG | 1020 |
| 80 | TGAAGGCCCT | GGAGGCTGT | CTGAAGGGCA | TCCCCCAAAA | TGGGTGCTCA | CCTTCCACAG | 1080 |
| | TGCCACCCAC | TTCTTGTTC | CAGAACCCCC | AGCCAGGAGA | CTCTAGGTCT | CAGAAGCCTG | 1140 |
| | AACCTGCAAC | CCACAGATCA | CACAGTGAAG | AAGGCACAG | AGAGCCTGTT | CTGCTCTGG | 1200 |
| | GTCTGCAGAG | CTGTGTGAGA | GATGGCCCCA | GCAGGCCCTC | GGCCCCCGA | GGAAACCCCA | 1260 |
| | CCAGCTTCTC | CTCATCCAGC | AGCACCGACT | GGGACCTGGA | TTTTGGGAGT | CCTGTGGGGA | 1320 |

| | | | | | | | |
|--------------------------------------|------------|-------------|-------------|-------------|------------|------------|------|
| | ACCAGGGGCA | GCATCCTGGA | AAAGGAAGCC | CACCAGGAAG | CTCCCCACTG | CAGGGTCTGG | 1380 |
| | AGAATTGTCT | CAAGAGAGATA | CCTGTGCCTG | TGCTGGGGCC | TGCTCCTCAG | | 1440 |
| | CAGCAGACAG | GGGACCGAGG | AGAGCAGAGC | CCAGGAACCTG | GACAGCAGAC | AAGGAAGGGT | 1500 |
| | CTGCCCCCAA | CGCTCCCGG | CTGCACTGCC | TGGAGAGCGC | CCTGAGGGGG | ATCTTGCTGG | 1560 |
| 5 | TAAGGCCCTT | GGCTTCGCC | TGCGTGGGAG | GCCCCAGCCC | CAGCCCCAGC | CCCGCTCCA | 1620 |
| | GCTCGAGCTT | CAGCGGTCTT | GAAGGAGAAG | ACCGGAGGCC | AGAGCTGAT | CTCTGGAAGC | 1680 |
| | CGCTCCCCCA | GGAGAGGGAC | CGCCTTCCCA | GCTGTAAGCC | TCCTGTCCCT | CTGTCCCAT | 1740 |
| | GTCTGGTGG | GACCCCTGCT | GGCAGCAGTG | GCGGCAGCCC | TGGTGAAGAC | CCCAGGAGAA | 1800 |
| | CAGAGCCGAG | GTACTGCAGC | GGCCTCGGTG | CAGGTGAGCC | TGGGTCTCC | TGAGGGGGGG | 1860 |
| 10 | CCCATGCGTT | CCCCAGAGGA | CCAGGAGTCC | AGACTGGATC | CTTTGAGTCC | TGCTGTGCG | 1920 |
| | TTTGCTGGC | TCTTGCCAGG | GAGTCTGCA | CATTGGCCGT | GCTTTAGTTC | CCTGTAAGGT | 1980 |
| | ACAGCTCAGG | ATCCCTGCCC | GGTTTCTCAG | CTGGAGAAAA | GGCCCCAGGT | TAGTGAAGCA | 2040 |
| | TCCAGAGGCC | TGGAGCTTGG | ACATGGAAGA | CCCAGAGTTG | CAGCCAAGAC | CCATGAGAGG | 2100 |
| | CTGCTCCCC | AGGCCCCGCC | TGAGCTGCCC | AGTGAGTCTC | CCCCCTCCGA | GCTGCCCTCT | 2160 |
| 15 | CGGGAAGCTG | CGCTTCTGT | GTTCGCAGCC | TCCTCCCTGC | AGCCGCCATG | CCACTGTGGG | 2220 |
| | AAGCCCTTGC | AGCAGGAGCT | GCACAGCCCT | GGTGTGCCCC | TTGCGGAGAA | GCTGGATCGG | 2280 |
| | CTGCGCCAGG | CGCTGGCAGG | CCTGGCTCAG | GAAGTGGCCA | CCATGAGGAC | CCAGGTGAAT | 2340 |
| | CGGCTGGGGA | GGGCCCCCA | AGGCCCTGGG | CCAATGGGCC | AAGCTTCTCT | GATGTGGACC | 2400 |
| | CTCCCCAGGG | GACCTCGCTG | GGCTCATGGC | CCTGTGCACA | GACATCTGCC | CTACTGGAGG | 2460 |
| 20 | CAGAAGGGAC | CCACGAGGCC | TAAACCAAG | ATCCTGCGTG | GCCAGGGAGA | GAGCTGCAGG | 2520 |
| | GCTGTGTACC | TGCAAGGACT | CTCCAGAGGG | ACCGCTGCCC | GGGCAAGTCC | GCTGCTCCA | 2580 |
| | GAGCTCTCAG | CGGCAAGAAC | TCCTGGGCTC | CACTGCAGCT | CTTCCAGCA | GCTGCTGCC | 2640 |
| | TCTACACCCA | GCTGCCATGC | TGGCCCGCT | GCACACCCCT | TCCTGCACA | TACCGGGGGC | 2700 |
| 25 | CACCAGAGCC | CCCTTCCCC | TTTAGTGCTT | GCTGCCTTAC | CCCTGCAGGG | AGCCTCTCCT | 2760 |
| | CCTGCAGCCA | CTGCAGATGC | AGACGTGCGG | ACCTCAGGAG | TGGCACCAGA | CGGGATCCCA | 2820 |
| | GAGCGGCCCA | AGGAGCCGAG | CAGCCCTGCT | GGAGGAGTGC | AGAGGGCCCT | CCAGGAAGAA | 2880 |
| | CTGTGGGAGT | GGGAGCACAG | GGACCCGAGA | TGGGGGGCGC | ATTGATGGCA | TTCTCTTCT | 2940 |
| | CCACATCTGC | TGCTTCTTGC | CGAGGGTGCA | GTGGTGGCGT | GGAAGCCCTG | TCACCCACCC | 3000 |
| | CCAGGCCACC | CTCTCCAGCA | GGACGCCATC | TCCCTTACTG | TTGCTGGAGG | CCTCGCCCTT | 3060 |
| 30 | TGTCCCAACT | GGGTAGAGCC | CCCAGTGTCT | GTTCGTCTAG | GAGGCTGTCT | TGGGGGTGCT | 3120 |
| | TTCTCAGCC | TTCTGCCCC | TTGGCTCAGA | TTCAATCAAA | TGTTGCTTCC | CTCTCTCTGC | 3180 |
| | TTTCCCACTG | GAGCCGCCCA | AGCTTGTAGG | TGGGTGGTGT | GCATAGGCCA | CGTGTGCCCC | 3240 |
| | ACATATGCA | GGGGTCCCC | ACACAGCTAG | AGCGGCCAGG | AGAGCGCCTC | CTAACCACCA | 3300 |
| 35 | GCCTTCTCTG | ATCTCAGGAG | CCTTGAAGGG | CTGGGCTCTT | GCCTTCTCTG | AGTAAATATT | 3360 |
| | GGCAGAGATT | TCATTGTAGA | GAACTCAGCC | CCCTGGTCTA | AGCTGGAGCT | ACCTCTGTGG | 3420 |
| | ATTCTGAAT | TAAAGAAGTG | AGTTGCCAAA | AAAAAAAAAA | AAAA | | 3464 |
| Seq ID NO: 92 DNA Sequence | | | | | | | |
| Nucleic Acid Accession #: BC029071.1 | | | | | | | |
| Coding sequence: ..771 | | | | | | | |
| 40 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| | CGGACGCGTG | GGCGGACCGG | TGGGCGGCTG | AGGAGTGGGG | TGATGATGCC | ACTGGCAGAA | 60 |
| | GCAGGGGCC | TGCCCCAAGG | AGGAGGCCCT | TCAGCAACGG | AGTGGGCTCT | CATTCTCGG | 120 |
| 45 | AGGAAGACCC | CCAGGCACAA | GCAGCCCAAC | TTACTGATGG | TCAGAGCATC | CAGAAGAAGT | 180 |
| | GGCAAGACTT | CAGCTGTCTT | CAAAGCAGGA | AGACAGAGTG | TTTCTGGCAG | AAAGAACAGC | 240 |
| | ACAAAGCAAG | ATCTGGTAAC | CCTAGGTGCC | TCCAGTTTGA | GGGAGGAGAG | AGGACACCCC | 300 |
| | CTCCACCCCA | GACATAGGAA | AGCAGTCCAC | CTGCGCACCA | GGGCGAGGAC | ACGTGGCTGG | 360 |
| | GTGCAGACGC | TGGCCCGGAT | GTGCGGGAGG | ACTCGCGGGC | CGGTAGAGCG | CGCGCGGGG | 420 |
| 50 | GGCGCGCGG | CGCGCGCGG | AGGAGACGCA | GGTCAAGCCC | CCTTCCACCC | ACCTCCCGCC | 480 |
| | GGCGCGGGG | CGCGCGCGG | GAGGAGCCCG | GGACAGGTGA | CTCCTAGAGG | ACTGGCTCTG | 540 |
| | GGCTCCCGG | GGCGGAGTGC | CCTTCTTGG | GGCTCTGCG | GGCCCTTGG | TCCCTCTCTG | 600 |
| | GGCTTCCGAG | AGTCTGACTC | AGCCAAGCCG | GCATCGCTTC | GGCTCTTACA | ACACACCCCG | 660 |
| | AGCGCGAGAA | GAAATTACAG | GATTGCAGGG | GCACGGCTAA | TGCGCTCTAA | TTACCCACCG | 720 |
| 55 | CGGCTGTCT | CGCGCGCGCT | CGCGCGCGCT | GGGCCAACGC | GGCTTAATTA | AGAGCGCGCT | 780 |
| | CGCGCGTCCC | GGAAACCTCC | CTTGGCCACC | CTCCACCCAC | CCACTCGCG | GTCCCCAGGA | 840 |
| | CCACTGGCTG | CCAACTCTCT | CGCGCTCTG | GGACTGCCCC | TCAGTCCGAG | GAGAGCTATG | 900 |
| | AGGCTCACT | GGGGGCAGAA | CTTGGGAGAA | CCGAAGCCCG | CCCTTCCACT | CCCCTAAACC | 960 |
| | TACAGTCTCT | GAAAGTCTCT | GCTGGAAGAG | ACTGGGAGAG | TGGGGAGGGG | CCAGGGACCT | 1020 |
| 60 | ATTTCGTTGA | CAGAAACAGT | GAGGTCTATT | GGAAAGTTAG | CCTTCAGTGG | GAGGAGTGGC | 1080 |
| | AAAGGCACGC | AGGGCAGCAG | TACCCCGCTT | TGGCACTTGA | GGCAGCGAGA | AGGGAAAGGA | 1140 |
| | AGTCCGCCCA | CCAGAACTC | CCAGACCCGC | TGCTTTAACA | GTGGCTTTAT | GAGCAGCAGC | 1200 |
| | ACGAGCTCCC | TCCCCTGGGG | GGGAAATTAC | CTTCTGCGCA | AGAAAGGTGA | CATCCCAGCC | 1260 |
| | ACAGACACGG | AGGCCCCCGC | TGCTGGCCAG | CTGTGGCCCG | CATAGGGGAG | CTGGTGAGGA | 1320 |
| 65 | GTGAGGTGGC | TCTGGCTCCC | CATGTCAAGT | AGGCTGAGAG | AGGCCCTGAA | GATAGAAGCC | 1380 |
| | AGGCCCGAAG | GGCAGAAATTA | AAGGGGTAGC | TGGGCCATCA | GCTCCTTCCC | CCAAAAACAG | 1440 |
| | GCTCAGAGCT | CTCCTCTATC | AGCAATTCTT | TCCTGAGGTC | CAGGGTGTGG | CAAACTCATG | 1500 |
| | GCCTTGGGCC | ACGTTTACC | TTCACTGAGG | TTTGTGTTGG | CTTGCAATGA | GTACATGGGT | 1560 |
| | TTTAGGTTGA | ATGTGAGAGT | CTGCAGACAA | TGTGGGTTCT | CCGACTGCCC | TCCCAGTGAA | 1620 |
| 70 | GGTGGACCTC | TGATTTAGAC | CGGCCCCGCTG | GGCCCCGTGCC | TACATCCTTT | TCCTCAGCGT | 1680 |
| | CAGGATCTTA | GTCCCCATCA | TTGCTGCCCC | TTTGTGGTCT | GCATGTTTCT | TGGTAAGGGT | 1740 |
| | GCCCACTCAA | GTGCTCTGG | GAGCCCCCTC | TTCTCTGTCA | TCGTCAAGCT | CCCCACTTGC | 1800 |
| | AGTGGCCGTG | GTGGCTGCAC | ATGCTCCCCG | ATACCCCTCC | AGCACTCCCT | TTTGTCTATC | 1860 |
| | TGAGTTTCAG | TCCGTGACTT | GGGTGGCACC | CTATCTTCTC | CATCAGGGAT | GGTAGCTATT | 1920 |
| 75 | TTTCTGCCAT | GAGACTAGAG | GTGCTTGGAG | AACAGGAAAT | TGGATCTCTC | CTTCAAGGCT | 1980 |
| | GGGATTTCAC | TAGGGCTGG | AGAAGGGGGG | AATATGGGAG | GATTATCTCC | TATCACAGGG | 2040 |
| | AGCGCTCTGA | GGGCAAGGCT | GTGCTCCGA | TTCACTGCA | CGTTCCTCT | AGGATGGGGC | 2100 |
| | TGTTTCTCCC | CTCCGACTGG | GGCTCCCTGA | GGATGGGGCT | GTTTCTCCCC | TCCGACTGGG | 2160 |
| | GCTCCCTGAG | GACAGGGCTG | TGTCTCCCC | CAGCCTGGGG | CTCCCTGAGT | CAGGGCTGTG | 2220 |
| 80 | TCTCCCTCTA | GACTGGGGCT | CCCTGAGGAC | GGGGCTGTGT | CTGCCTCAGA | CTGGGAATCC | 2280 |
| | CTGAAGATGG | GGCGGTGTCT | CCCTCAAAGT | GGGGCTCCCT | CAGGACAGCG | TTGTGTCTCC | 2340 |
| | CCTCAGACTG | CGGCTCCCTG | AGGACGGGGC | TGTGTCTCCC | TCAGACTGGG | GCTCCCTGAA | 2400 |
| | GAAAGGGCTG | CTTCTCCCTC | AGACTGGAGC | TCCCTGAAGA | TGGGGCTGTG | TCCCCCTCAG | 2460 |
| | ACTGGGGCTG | CCTGAGGAGC | AGGCTGCATC | TCCCTCAGA | CTGGAGCTCC | CTGAGGGCAG | 2520 |

Seq ID NO: 93 DNA Sequence
Nucleic Acid Accession #: NM_002104.1
Coding sequence: 41..835

Seq ID NO: 94 DNA Sequence
Nucleic Acid Accession #: NM_052947.1
Coding sequence: 199..4794

673

| | | | | | | | |
|----|------------|-------------|-------------|-------------|------------|-------------|------|
| | GGGGTTGACA | CGCACAACTC | CACAGGCCAA | ATTCATGACG | TCCCTGAAAA | TGACATAGTT | 3000 |
| | GAGCCAGAG | AGCGTCAGTA | TGTGTTTCT | GTTCACAGA | AAAGGGGAAC | TATTGAGAT | 3060 |
| | GAGCGTGGGA | AACCTTTGCC | CTCTTCTCCT | GATCTTACCA | GGTTCCTTG | TACTTTCATCT | 3120 |
| 5 | CTGTAAGGAA | ATGTACAGAA | CTTTTGTATA | AGCCACAAA | TGGAGGAACC | TAAAAATAGAG | 3180 |
| | GTGCTTCAAA | TTGGGGAAAC | CAAAACCCCA | AGCTCATCTA | GCTCCTCAGC | GAAGACCTTG | 3240 |
| | GCATTATTTT | CAGGAGAACG | TGAGTTAGAG | AAAGCCCCCTA | AGTTACTGCA | GGATCCATGT | 3300 |
| | CAAAAAGGCA | CCCTGGGCTG | TGCGAAAAAG | TCCAGGGAGA | GAGAGAAGTC | CCTGGAAGCC | 3360 |
| | CGAGCAGGCA | AATCGCCAGG | GACCTTCACA | GCAGTGACGG | GGTCAGAGGA | GGTCAAGAGG | 3420 |
| | AAGCCAGAAG | CCCCAGGCAG | TGGACATTTA | GCTGAGGGAG | TAAAGAAGAA | AATTTTGTCT | 3480 |
| 10 | AGGGTGGCAG | CACTGAGGCT | GAAACTGGAA | GAAAAGGAAA | ATATCAGAAA | GAACTCAGCC | 3540 |
| | TTTCTTAAAA | AGATGCCCAA | ACTCGAAACA | TCATTATCAC | ACACAGAGA | GAAAACAGAC | 3600 |
| | CCAAAAAGAC | CATCTTGCAA | AAGAGAAGGA | AGAGCTCCAG | TATTACTGAA | AAAAATCCAA | 3660 |
| | GCTGAGATGT | TCCCTGAACA | CTCTGGAAT | GTAAATTTAA | GCTGCCAATT | TGCAGAAATT | 3720 |
| | CATGAAGATT | CTACTATCTG | CTGACAAAA | GATTCAAAGT | CCATAGCCCA | AGTGCAGAGA | 3780 |
| 15 | AGTGCAGGGG | ACAACTCCAC | TGTTTCTTT | GCCATCGTGC | AAGCCAGTCC | GAAGGACCAG | 3840 |
| | GGACTCTATT | ACTGCTGCAT | CAAGAACAGC | TACGGAAAG | TGACTCGTGA | ATTAAACCTC | 3900 |
| | ACAGCTGAAG | TTCTCAAAAC | GCTGTCAAGT | CGCCAGGATA | CTAAAGGATG | TGAAGAGATT | 3960 |
| | GAATTCAGCC | AACTCATCTT | CAAAGAAGAC | TTCTCCATG | ACAGCTACTT | TGGGGGCCGC | 4020 |
| | CTGCGTGGTC | AGATCGCCAC | GGAGGAGCTG | CACCTTGGAG | AAGGGTTTCA | CCGCAAGGCC | 4080 |
| 20 | TTCCGACGCA | CAGTGATGCA | CGGCCCTCATG | CCTGTCTTCA | AACTCGGCCA | TGCTGTGTG | 4140 |
| | CTTAAGGTGC | ACAAATGCCAT | TGCCTATGGG | ACCAGAAATA | ATGATGAGCT | CATCCAAAGG | 4200 |
| | AACTCAAAAC | TGCTGACCCA | GGAATGCTAT | GTTCAAAATA | CTGCCAGGTA | TTATGCAAG | 4260 |
| | ATCTAAGCTG | CTGAAGCACA | GCCTCTGGAA | GGCTTTGGAG | AAGTACCTGA | GATCATTCTCT | 4320 |
| 25 | ATTTTTCTTA | TCCATCGGCC | TGAGAACAAT | ATCCCGTATG | CTACAGTGA | GGAGGAGCTG | 4380 |
| | ATTGAGAGAT | TTGTGAAGTA | TTCCATCAGG | GATGGGAAAG | AAATAAACTT | CTTGAGAAGA | 4440 |
| | GAATCAGAA | TGCTGCAGAA | ATGTTGCACC | TTCCAGCACT | GGGTGTACCA | GAAAAACAAGT | 4500 |
| | GGCTGCCTCC | TGGTGAACGA | CATGCAAGGT | GTAGGAATGA | AGCTAACTGA | CCTTGGCATA | 4560 |
| | GCAACGCTGG | CTAAAGGGTA | CAAGGGATT | AAAGGCAACT | GTTCATGAC | CTTCATTGAT | 4620 |
| 30 | CAGTTTAAAG | CACACACCA | GTGTAACAAG | TATTCAAAA | TGCTGGGACT | GAAATCCCTT | 4680 |
| | CAAAACAAAC | ACCAAGAAAC | GAAGCAGCCG | AGCATTGGGA | AAAGCAAAGT | TCAAAACAAAC | 4740 |
| | TCTATGACAG | TAAAGAAAGC | AGGGCTCAG | ACCCAGGCG | AAAAGAAAC | CTAACGTCCT | 4800 |
| | TGGTAACTCT | AATGGCCACT | GGCTAGCAGC | ACACAATCTC | GCCAGGGAAA | ATCTGAGGCC | 4860 |
| | ACACAGGAGA | GAATATACAG | CCTGCAGAGA | GTGCGTGGCA | ATCCTTACCC | CCAGCCGACT | 4920 |
| 35 | GTGCGCCAG | ATGCTTCTAA | ACCCATCACC | TGCTGTCTTC | ACTCAAATGA | TTTCAGAAC | 4980 |
| | GGATTGCGA | CCAGGTTTAT | GGGGAGATTG | AATCAACGAT | TGGTCTCAAA | GACAGGCCAT | 5040 |
| | TCTTTATATA | CACGTTTAGC | ATTTTATCCA | ACCTCACATC | ATGTGTATAT | TTGTGTATT | 5100 |
| | GCACATGGTT | GTGCTGTGCA | GGACCTGGTG | CTGAGAAGAG | TCTGTTTACA | GCCAAATTC | 5160 |
| | TTCCCATGTT | CATTCTTAAC | CTGGGATTTC | TAGACACATC | CTGCTGTGAT | GTAAACAGAA | 5220 |
| 40 | ATCACGAATT | CGCTCACTGG | ATCAAGTTGT | TCCACTGGTG | TCTAATACGC | TATTGTTGCC | 5280 |
| | GGAGGTGGGT | TCTGTGAGCT | GAAGCCATT | CCCATCATTC | AACAGCCAGT | TACAAATTTT | 5340 |
| | TGTTTAATTA | AATTCATATT | TAAACAAAA | AAAAA | | | 5375 |

Seq ID NO: 95 DNA Sequence

Nucleic Acid Accession #: NM_134421.1

Coding sequence: 527..1108

| | | | | | | | |
|----|------------|-------------|------------|-------------|------------|-------------|------|
| 45 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| | AGCTTCTGCC | AAGGGTGGGG | GCCCAAGCGG | AGGCGATCCG | CTCGTTCCTC | CCAGGGCCAT | 60 |
| | GGGGGAGGA | GGAGAGCCCT | GGCCTCCCGC | CGACCCGAC | CGCGACCTGG | GCCAGAGCGG | 120 |
| 50 | CCACCTTCCC | CGGTGCGGGT | TGCTTCTCT | TTAAAAATGAG | GACAGCTCCT | CCCTTGGGGG | 180 |
| | CTGTGGTGAC | AGGTGAAATG | AGAAGCAGCT | GAAGCAGCT | CTTGGTCCAA | AGCCCCGAC | 240 |
| | ACAGGCGATG | GTCTAGTGGC | CCAGTCAGGA | CGCGGAAACA | CTCCCTGGAG | GTTCTGACCC | 300 |
| | ACTCCCTCTC | AGCCTCGGCC | TGGTCTCTGG | GTTGGCTGTT | CCAGCTCCAA | AGAGAAGGAG | 360 |
| | GAACCTTTTC | CTTCTGACAG | CCCTCCCCAC | CAGCTCCATT | CCTTAGCTGG | GGTCAGACCT | 420 |
| 55 | GGGGTCTCCA | CTGCACTGGG | CCTCTGGCAG | CGTTCTCAGG | CTAGCCCTCC | CTGCTGAAAA | 480 |
| | GAGAACCGTG | TGGGACTCAC | AGGTGTAGTC | GCGCGCCGCA | GCCGCCATGG | GCAAAACAGAA | 540 |
| | CAGCAAGCTG | CGGCCGAGG | TGCTGCAGGA | CTGCGGGAG | AACACGGAGT | TCACCGACCA | 600 |
| | CGAGCTGCAG | GAGTGGTACA | AGGGCTTCCT | CAAGGACTGC | CCCAACGGCC | ACCTGACCGT | 660 |
| 60 | GGACGAGTTC | AAGAAGATCT | ACGCCAACTT | CTTCCCTTAC | GGCGACGCTT | CCAAGTTGCG | 720 |
| | CGAGCAGCTC | TTCCGACCTT | TCGACACCAA | CGGCGACGGC | ACCATCGACT | TCGGGAGTT | 780 |
| | CATCATTGCG | CTGAGCGTGA | CCTCGCGGGG | CAAGCTGGAG | CAGAAGCTCA | AGTGGGCCCT | 840 |
| | CAGCATGTAC | GACCTGGACG | GCAACGGCTA | CATCAGCCGC | AGCGAGATGC | TGGAGATCGT | 900 |
| | GCAGGCCATC | TACAAGATGG | TGTCGTCTGT | GATGAAGATG | CCGAGGATG | AGTCCACCCC | 960 |
| | GGAGAAGCGC | ACAGACAAGA | TCTTCAGGCA | GATGGACACC | AACAATGAGC | GCAAACTGTC | 1020 |
| 65 | CTTGAAGAA | TTTCATCAGAG | GTGCCAAGAG | CGACCCCTCC | ATCGTCCGCC | TGCTGCAAGT | 1080 |
| | CGACCCGAGC | AGTGCCAGTC | AGTTCTGAGC | GAGCGGCCCC | TGGACAGTTG | CAGAGAAACA | 1140 |
| | CAGGCTTGTC | GTGCGGTTTA | AGCTTTGCTT | GCAAGAGTGG | ATGCCCGCA | ATCGTTCCCT | 1200 |
| | CTCTCCCGGG | CCCCGGGCTT | GGGGCATGGG | TTGCACCTGC | CCGGCCCGGT | GGCTGCGCCT | 1260 |
| 70 | CCCTCTCCCA | CCTGACCAAC | GCGACATTCC | TCCCTTCACG | CCTGGCCCGG | TCCCTTCCAG | 1320 |
| | GGCAACTCCC | AGGAGTGTGG | TGACATGCAG | GGTTCAAGTG | TTCTTGGTTC | CAGGCACCTC | 1380 |
| | CGGCTCACG | GGGAGCTCAG | AGGTCCATGC | CGAGGAGACC | AGGCAGGACC | TCCCGAGGCT | 1440 |
| | GCGCCCCGGC | CGGCCCATGC | GTTTTGTGAT | CCCAAGTGAC | TCTGTGGGAA | GGTGGGGGAC | 1500 |
| | GAGGCGTCGG | GAGGGTATAC | AGGGAGCCCC | TCCGTCGAT | GGCTGCCCCC | CCGTTTCATT | 1560 |
| 75 | TTCTCCACAC | AGCGCCTTGC | ACGTATAGAT | ACTGTGGTCC | CTTTCTTTT | AATATATAAA | 1620 |
| | TTATGTATGG | TGAAGTGGAG | TGTATTGTGT | AGGTCCCGTA | TTTAAAGCCT | CTGACTGCCT | 1680 |
| | TTGAAGCGCA | GCCTCTGTG | GCCCGCAGCC | CCCTGAGCCT | GGCTGTTGTG | TGGTATTAT | 1740 |
| | GCTCTCTTTG | TCTGCTCTTT | TCTAAGGAAA | TGCAATGTGT | CCCTGAGCCG | TGATGATCCT | 1800 |
| 80 | CCCATCCGTG | TTGTGAGCAC | AGGCATTGT | GTCTGGTCTG | TCCTCCCTGT | TGATTGGTCT | 1860 |
| | GGCATTTCGG | GTATTAATAA | GATAAATAA | ATGGCATTTC | CTGAAAAAAA | AAAAAAAAAA | 1920 |

Seq ID NO: 96 DNA Sequence

Nucleic Acid Accession #: NM_002149.2

Coding sequence: 375..956

1 11 21 31 41 51

| | | | | | | | |
|----|------------|------------|-------------|------------|-------------|------------|------|
| | CGGCGGCGGC | GGGCAGCGGA | CGGGCGGACT | GACGGGGGCC | TCCACCTTGC | TCCCTCCCTG | 60 |
| | GCTGCGGGCT | TCCTTTTGTG | TTTCTGGGCG | GCGATGAGCG | CAGGGCCGGC | GCACGAGCTG | 120 |
| | CGGGCGCAGG | GAGGCCGCGG | CTGCTAGTCA | CTCCTCCCGG | CCTGGGCGCG | CTTGTCCCGG | 180 |
| 5 | GCAGCGGCCC | GGGCGCGCTG | CAGCGCGCGC | CGGGCGGAA | CTTGGGCTCG | GGAAAGCGGC | 240 |
| | GGACGCGGTC | CTGCGCGGGA | GCAGGGGCAT | GGTCTAGTGG | CCCACTCAGG | ACGCGGAAAC | 300 |
| | ACTCCCTGGA | GTTTCTGACC | CACTCCCTCT | CAGCCTCCGC | CTGGTCTCTG | GTGTAGTCCG | 360 |
| | CGCCGCGAGC | CGCCATGGGC | AAACAGAACCA | GCAAGCTGCG | GCCCGAGGTG | CTGCAGGACC | 420 |
| | TGCGGGAGAA | CACGGAGTTC | ACCGACCACG | AGCTGCAGGA | GTGGTACAAG | GGCTTCCTCA | 480 |
| 10 | AGGACTGCCC | CACCGGCCAC | CTGACCGTGG | ACGAGTTCAA | GAAGATCTAC | GCCAACTTCT | 540 |
| | TCCCCTAGCG | CGAGCGTTCC | AAGTTCCGCG | AGCACTCTTT | CCGCACTTTC | GACACCAACG | 600 |
| | GCGAGCGCAC | CATCGACTTC | CGGGAGTTCA | TCATTGCGCT | GAGCGTGACC | TGCGGGGCA | 660 |
| | AGCTGGAGCA | GAAGCTCAAG | TGGGCCTTCA | GCATGTACGA | CCTGGACGGC | AACGGCTACA | 720 |
| | TCAGCGCAG | CGAGATGCTG | GAGATCGTGC | AGGCCATCTA | CAAGATGGTG | TCGTCTGTGA | 780 |
| 15 | TGAAGATGCC | GGAGGATGAG | TCCACCCCGG | AGAAGCGCAC | AGACAAGATC | TTCAGGCAGA | 840 |
| | TGGACACCAA | CAATGACGGC | AAACTGTCTT | TGGAAGAATT | CATCAGAGGT | GCCAAGAGCG | 900 |
| | ACCCCTCAT | CGTCCGCTTG | CTGCAGTGG | ACCCGAGCAG | TGCCAGTCAG | TTCTGAGCGA | 960 |
| | GGGCGCCCTG | GACAGTTGCA | GAGAAACACA | GGCTTGTGCT | GCCGTTTAAAG | CTTTGCTTGC | 1020 |
| | AAGAGTGAT | CGCCGCAAT | CGTTCTGTCT | CTCCGGGCGC | CGGGCCTGG | GGCATGCGTT | 1080 |
| 20 | GCACCTGCCC | GGCCCGGTGG | CTGCGCTTCC | CTCCTCCACC | TGACCAACGC | GACATTCTCT | 1140 |
| | CCCTCACGCC | TGGCCGGTGC | CCTTCCAGGG | CAACTCCAG | GGATGTGGTG | ACATGCAGGG | 1200 |
| | TTCAAGTGT | CTTGTGTCCA | GGCACTTCCC | GGCTCACGGG | GAGCTCAGAG | GTCCATGCCG | 1260 |
| | AGGAGACGAC | GAGGACCTTC | CGGAGGCTGC | GCCCGGCGCG | GCCCATGCGT | TTTGTGATCC | 1320 |
| | CAAGTGACTC | TGTGGGAAGG | GTGGGGAGCA | GGCGTCGGGA | GGGTATACAG | GGAGCCCTCT | 1380 |
| 25 | CCGTGCATGG | CTGCCCGCCC | GTTCAATTTT | TCCACCACAG | CGCTTGCCAC | GTATAGATAC | 1440 |
| | TGTGTGCTCC | TTTCTTTTAA | TATATAAATT | ATGTATGGTG | AAGTGGAGTG | TATTGTGTAG | 1500 |
| | GTCCCGTATT | TAATGCCTCT | GACTGCCTTT | GAAGCGCAGC | CCTCTGTGGC | CCGAGCCCTC | 1560 |
| | CTGAGCCTGG | CTGTGTGTGT | GTATTATATG | TCTCTTTGTC | TGCCTGTTTC | TAAGGAAATG | 1620 |
| | CATGTGTGCT | CTGCGCGTGG | ATGATCTCTC | CATCCGTGTT | GTGAGCACAG | GCATTTGTGT | 1680 |
| 30 | CTGGTCTGTC | CTCCCTGTTG | ATTGGTCTGG | CATTTCGGGT | ATTAAATGA | TAAATAAAT | 1740 |
| | GGCATTTTCT | GAAAAAATAA | AAAAAATAA | | | | 1769 |

Seq ID NO: 97 DNA Sequence

Nucleic Acid Accession #: Eos sequence

| | | | | | | | |
|----|-------------|-------------|------------|------------|-------------|-------------|------|
| 35 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | GCTGACTCTG | AGGACCCCGT | GGACATTAAA | GAAAAATGAA | CAGGTTTTTC | TTAAAGCACC | 60 |
| | AACTGCTCT | TTAAACAAAA | TTATGAAAGG | TTAAAAAGAG | TCTATAAAAA | CTTACCTTAT | 120 |
| | GGTCAACACAT | GAAAAATTGG | ATAAATATGT | CTACAAGGTT | TTATTAATAAT | TAAGTTTAAC | 180 |
| 40 | ATTAATAACA | CACATAATATA | AAGGTAAAT | TTAGCTTATC | TGGTATAAAA | GTACATACAGG | 240 |
| | AAGCATTAGT | AAATATAAAA | TAGCGTTTAG | CTTTCTTTTG | TCTAAAAAAT | AATAAAAAAT | 300 |
| | GGTGCTAAAG | GAAGCATTCA | TTTTACTAGA | GGATCATAAA | AGTTAAAGAC | TTAAAAACAA | 360 |
| | CTTTGGCAAT | TAAGACAGCA | TACCAAGATG | CAATAGCCTG | GTGGAATAGG | ATCAAAATAT | 420 |
| | CCATCTGACG | GTTAAACAAA | AGCAATTAGC | ATGCTTGTGC | ACATGGCAGC | CCAGAGACCC | 480 |
| 45 | TGATTGTCCC | CCTTCCACTA | AGGTGGTCTT | CCAGTGCACC | AGGCATGGGC | TGCATGGTAG | 540 |
| | CTCTTTTCCA | GGATTCTACA | GCCTGGAGTA | ATAAGTCATG | CCAAGCTCTC | TCTGCTATAT | 600 |
| | CCTGAAGTCC | CTGCGGGTCA | GCCCGGAGG | GCCATCCAGC | TTCGCTCTCC | CAACACTAAG | 660 |
| | TTCACTTCTT | GTCTCTCATG | GCAGGGAGGA | GACTTAGCAT | TCCTTGGAGA | CCTGAAGGGA | 720 |
| | TGCACTGAGC | TTAAGAAATT | TCAAGAGCTT | ATCAATCAGT | CAGCCCTTGT | TCATCCCGGA | 780 |
| 50 | GCGGATGTGT | GGTGGTATTG | TGGTGCACCT | TTATTGGGCA | CTCTGCCGAA | TAACATAGAT | 840 |
| | GGCACTTGTG | CTTTAGCCTA | TTTGGCTATC | CCTTTACCC | TGGCATTTC | TCAACAGAG | 900 |
| | GAAGGAAAAA | AAAAATAATA | AGACATCGTA | AAGCGAGAGA | AGCCCTTAT | GGGTCTTCA | 960 |
| | ACTCTCACAT | CTATTAGAT | GCAATCGAAG | CCCCGCAAGG | AACACCATAG | CAATTTAAAG | 1020 |
| 55 | TCCGAAATCA | AATAGCTACA | GGATTAAAGT | CAATATTTTG | GTAGATGAGA | GTCAATAAAA | 1080 |
| | ATGTAGATTA | GATAAACTGC | ATCTATTACA | CCCAACAGCA | ATGAGCTTTT | CATGAGTTGA | 1140 |
| | AAAAAGAAAA | AACTCATGTC | GGCCCCAGCC | CTGAGGCTAC | CTGACCTGAC | AAAACTCTTT | 1200 |
| | ACACTCTATG | TGTGAGAAAG | AGAAAAAATG | GCAGTTGGAG | TTTTAACCCA | GACTGTAGGG | 1260 |
| | CCCTGGCCAA | GGCCAGTGGC | CTATCTCTCA | AAACAACTAG | ACGGGGTTTC | CAAGGGCTGG | 1320 |
| | CCCCCATGAC | CAAGGGCCCT | GGCAGCAATA | GCCCTGTTAG | CACAAGAAGC | AGATAAGCTA | 1380 |
| 60 | ACTCTTAGGC | AAAACTTAAA | CATAAAGTCC | CCCATGCTG | TGGTAACTTT | AATAAATACC | 1440 |
| | AAAGGACATC | ATTAGCTAAT | GAATGCTAGA | CTGACTGACT | AGATACCAAA | GCTTGTCTCTG | 1500 |
| | TGAAAAATCC | TGCATAACCG | TGGAAGTTTG | CAACACCTTA | AACCCAGCCA | CCTTACTCCT | 1560 |
| | GGTATCAGAG | AGCCCAAGTG | AACATAACTG | TGTAGAGTTA | TTGGACTCAG | TTTATTCTAG | 1620 |
| | TGGGTCCAAC | TCCAAGACCA | TCCTTAAACA | TCAGTAGACT | GGGAGCTGTA | CGTGGATGGG | 1680 |
| 65 | AGCACTGTCG | CCAACCCCTG | CAAAGTGATT | CTGAAGAAGA | CGACAAGCGC | TGCTCCAGTC | 1740 |
| | ACACCCGGAA | GCTGACTGGT | CCACTCATGG | CCGAGCATGA | GGAACTCAT | CGCGGACTC | 1800 |
| | ATTTTCCTTA | AAATTGGAC | TTGCACAGTA | AGGACTTCAA | CTGACCTTCC | TCAGACTGAG | 1860 |
| | GACTGTTCCC | AGGATATACA | TCAAGTCACT | GAGGTAGGGA | AAAAAGGTTG | CTACAGTCTT | 1920 |
| | ATTATTTTAT | AGTTATTATG | AATGCCTAGG | AACTCCAAAA | GGAACTTGTT | TGTACAATAA | 1980 |
| 70 | CACTCAGTAC | AAAGTATGTA | ATCCAGGAAG | TGACCAAGCT | GAAGCGTGT | ATGACTCACT | 2040 |
| | GTAAGCTCTC | CATGATTAAG | GACTGATCCT | TTTCTAAGTG | ACAGAAGTAG | AGTAATAGCT | 2100 |
| | AAAAAATAA | AAAAAATAA | CGAGC | | | | 2125 |

Seq ID NO: 98 DNA Sequence

Nucleic Acid Accession #: NM_003946.2

Coding sequence: 98..724

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| 75 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | GGCAGGAGGG | AGAGGAGGGA | GGACACCGAG | TTCCCCGTGT | TGGCCTCCAG | GTCTGTGCT | 60 |
| | TGCGGAGCGG | TCCGCGGCGT | GGGATCGAGC | CCCGACAATG | GGCAACGCGC | AGGAGCGGCC | 120 |
| 80 | GTGAGAGACT | ATCGACCGCG | AGCGGAAACG | CCTGGTCCAG | ACGCTGCAGG | CGGACTCGGG | 180 |
| | ACTGCTGTTG | GACGCGCTGC | TGGCGCGGGG | CGTGCTCACC | GGGCCAGAGT | ACGAGGCATT | 240 |
| | GGATGCAGCTG | CCTGATGCGG | AGCGCAGGGT | GCGCCGCTTA | CTGCTGTGCG | TGCAGGGCAA | 300 |
| | GGGCGAGGCC | GCCTGCCAGG | AGCTGCTACG | CTGTGCCAG | OGTACCGCGG | GCGCCGCGGA | 360 |

CCCCCTTGG GACTGGCAGC ACGTGGGTCC GGGCTACCGG GACCCGAGCT ATGACCCCTCC 420
 ATGCCAGGCG CACTGGAGCG CGGAGGCACC CGGCTCGGGG ACCACATGCC CGGGTTGCC 480
 CAGAGCTTCA GACCCCTGACG AGGCCGGGGG CCTGAGGGG TCCGAGGCGG TGCAATCCGG 540
 GACCCCGGAG GAGCCAGAGC CAGAGCTGGA AGCTGAGGCC TCTAAGAGG CTGAACCGGA 600
 GCGGAGGCA GAGCCAGAGC TGAACCCGA GGCTGAAGCA GAACCAGAGC CGGAAGTGA 660
 GCCAGAACCG GACCCAGAGC CCGAGCCGGA CTTCGAGGAA AGGACGAGT CCGAAGATTC 720
 CTGAAGGCCA GAGCTCTGAC AGGCGGTGCC CCGCCCATGC TGGTAGGAC CTGGGATGCT 780
 GCTGGAGCTG AATCGGATGC CACCAAGGCT CGGTCCAGCC CAGTACCGCT GGAAGTGAAT 840
 AAATCCGGA GGGTGGAGC GGACTGGGC TCTCTCCAG ATTCTGGCTG TTTGCCCAGG 900
 AACTTAGGGT GGGTACCTCT GAGTCCAGG GACCTGGGCA GGCCCAAGCC CACCAGAGC 960
 ATCATCCAGT CCTCAGCCCT AATCTGCCCT TAGGAGTCCA GGCTGCACCC TGGAGATCCC 1020
 AAACCTAGCC CCTAGTGGG ACAAGGACCT GACCCCTCTG CCGCATACA CAACCCATT 1080
 CCCCCTGGTA GCCACTTGGC AGCATATGTA GGTACCAGCT CAACCCACG CAAGTTCCCTG 1140
 AGCTGAACAT GGAGCAAGGG GAGGTGACT TCTCTCCACA TAGGGAGGGC TTAGAGCTCA 1200
 CAGCCTTGGG AAGTGAGACT AGAAGAGGGG AGCAGAAAGG GACCTTGAGT AGACAAAGGC 1260
 CACACACATC ATTGTCAAT TGTCTTAAAT TGTCTGGCTT CTCTCTGGAC TGGGAGCTCA 1320
 GTGAGGATTC TGACCAATGA CTTACACAAA AGGCGCTCTA TACATATTAT AATATATTGC 1380
 CTTACTAAAT GAAAAAATA AAAAAAATA A 1411

20 Seq ID NO: 99 DNA Sequence
 Nucleic Acid Accession #: NM_004207.1
 Coding sequence: 63..1460

1 11 21 31 41 51
 25 GGCAGAGGCG GGGCTGAGGC GGGCCAGCGG CGGCAGGTGA GGCAGAACCA ACCCTCCTGG 60
 CCATGGGAGG GGGCTGAGGC GGCAGGAGCC CCACAGGCGT CAAGGCCCTG GACGGGGGCT 120
 GGGGCTGGGC CGTGTCTTTC GGCTGTTTCG TCATCACTGG CTCTCTCTAC GCCTTCCCA 180
 AGGCCGTGAG TGTCTTCTTC AAGGAGCTCA TACAGGAGTT TGGGATCGGC TACAGGACA 240
 CAGCCTGGAT CTCTCTCATC CTGCTGGCCA TGCTCTACGG GACAGGTCCG CTCTGCACTG 300
 TGTGCGTGA GGGCTTGGG TGCGGGCCCG TCATGCTTGT GGGGGTCTC TTTGGCTGCG 360
 TGGGATGGT GGCCTGCTCC TTTTGGCGGA GCATCATCCA GGTCTACCTC ACCACTGGGG 420
 TCATCAAGGG GTTGGGTTTG GCACTCAACT TCCAGCCCTC GCTCATCATG CTGAACCGCT 480
 ACTTCAGCAA CGGGCGCCCC ATGGCCAAAG GGCTGGCGGC AGCAGGTAGC CCTGTCTTCC 540
 TGTGTGCCCT GAGCCCGCTG GGGCAGCTGC TGCCAGGACG CTACGGCTGG CGGGGGGGCT 600
 35 TCCTCATCTT GGGCGGCGCT CTGCTCAACT GCTGCGTGTG TGCCGCACTC ATGAGGCCCC 660
 TGGTGGTCA GGGCCAGCGG GGCTGGGGGC CGCCGGGACC CTCCGGCGGC CTGCTAGACC 720
 TGAGGTCTT CGGGAGCGAG GGCTTGTGTC TTTACGCGGT GGGCGCTCG GTCATGGTGC 780
 TGGGCTCTT GTGCCGCCCC GTGTTGGTGG TGAGCTACGC CAAGGACCTG GGGCTGCCCG 840
 40 ACACCAAGGC CGCCTTCTCT CTACCATCC TGCGCTTCAT TGACATCTTC CGCGGGCCCG 900
 CGCGGGGCTT CGTGGCGGGG CTTGGGAAGG TGCGGCCCTA CTCCGTCTAC CTCTTCAGCT 960
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 GGCTCGTGT CTCTGTCATC TCTTTGGCA TCTCTACGG CATGGTGGGG GCCTGCACTG 1080
 TCGAGGTGCT CATGGCCATC GTGGGCACCC ACAAGTCTC CAGTGCCTAT GGCCTGGTGC 1140
 TGCTGATGGA GGGCGTGGCC GTGCTGCTCG GGGCCCTTTC GGGAGGCAAA CTCTGGATG 1200
 45 CGACCCAGCT CTACATGTAC GTGTTCACTC TGCGGGGGGC CGAGGTGCTC ACCTCTCTCC 1260
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 AGGTGGCGGC CGGGAGAGAG GAGAAGCTCC ACAAGCTCC TGCAAGTCC GGGTGGACT 1380
 TGCGGGAGGT GGAGCATTTT CTGAAGGCTG AGCCTGAGAA AAACGGGAG GTGTTTACA 1440
 CCGCGGAAC AAGTGTCTGA GTGGCTGGGC GGGGCGGCA GGCACAGGGA GGAGGTACAG 1500
 50 AAGCGGCAAA CGCTTGTCTAT TTATTTTACA AACTGGAGCT GCTCAGGAG GGCACGGCT 1560
 GGGCTCCAGC TGCGGGCCCA GCGGATCGTC GCGGATCAG TGTTTTGAAG GGAAGGTGG 1620
 CGGGTGGGA ACGGTGTCT TCCAGAGTGG ATCTGCGGTG AAGCCAAGCC GCAAGTTAC 1680
 AAGGCATCT CACCAGGGGC CCGGCTGCT GCTCCAGGT GGCCTGCGGC CACTGCTATG 1740
 CTCAAGGACC TGAAGACCA TGCTTGAGGA CAAGGTGACT TTAATGGAG GGTGGGTGG 1800
 55 CCGCAGAGAG GCTGGCAGGG CAGGTGCTGC GTGGGGCCCT CTCAGCCCG TCCTACCTCG 1860
 GGCTCACATG GGGCCTGTGC CCACCCCTCT TGAGTGTCTT GGGGACAGCT CTCTCCACCC 1920
 CTGGAAGATG GAAATAAAC TGCGTGTGGG TGAGTGTTC TCGTCCGAA TTCAAAAGC 1980
 TT 1982

60 Seq ID NO: 100 DNA Sequence
 Nucleic Acid Accession #: NM_018325.1
 Coding sequence: 163..1590

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 CCAAGAACTT TCGAGATCTG CGGTCTGGGG TCTGGTTGAA AGATGGCGGC CCTCACTACC 180
 CTGTTTAAAT ACATAGATGA AAATCAGGAT CGCTACATTA AGAACTCGC AAAATGGGTG 240
 GCTATCCAGA GTGTGTCTGC GTGGCCGGAG AAGAGAGGCG AAATCAGGAG GATGATGGAA 300
 70 GTTGTCTGTG CAGATGTTAA GCAGTGGGGG GGCTCTGTGG AACTGGTGA TATCGGAAAA 360
 CAAAAGTCC CTGATGGCTC GGAGATCCCG CTCCCTCTTA TCTGCTCGG CAGGCTGGGC 420
 TCCGACCCAC AGAAGAAGAC CGTGTGCATT TACGGGCACC TGATGTGCA GCCTGCAGCC 480
 CTGGAGGACG GCTGGGACAG CGAGCCCTTC ACCCTGGTGG AGCGAGACGG CAAGCTGTAT 540
 GGGAGAGGTT CGACTGATGA TAAGGGCCCG GTGGCCGGCT GGATAAACGC CCTGGAAGCG 600
 75 TATCAGAAAA CAGGCCAGGA GATTCTGTTC AACGTCCGAT TCTGCCTCGA AGGCATGGAG 660
 GAGTCAGGCT CTGAGGGCTC AGACGAGCTG ATTTTGTCCC GGAAGACAC ATTCTTTAAG 720
 GATGTGACT ATGTCTGCAT TTCTGACAA TACTGGCTGG GAAAGAAGAA GCCCTGCATC 780
 ACCTACGGCC TCAGGGGCA TTTGCTACTT TTCTACGAGG TGGAGTGCAG CAACAAAGAC 840
 CTCCATTCTG GGGTGTACGG GGGCTCGGTG CATGAGGCCA TGACTGATCT CATTTTGTCT 900
 80 ATGGGCTCTT TCGTGTGACA GAGGGGGAAC ATCCTGATCC CCGGCATTAA CGAGGCGCGT 960
 GCGCGCGTCA CGGAAGAGGA GCACAAGCTG TACGACGACA TCGACTTTGA CATAGAGGAG 1020
 TTTGCCAAGG ATGTGGGGGC GCAGATCCTC CTGCACAGCC ACAAGAAGA CATCCTCATG 1080
 CACCGATGGC GGTACCGCTC TCTGTCCCTC CATGGCATCG AAGGCGCCTT CTCTGGGTCT 1140
 GGGGCAAGA CCGTGATTCC CAGGAAGGTG GTTGGCAAGT TCTCCATCAG GCTCGTCCCG 1200

AACATGACTC CTGAAGTCGT CGGCGAGCAG GTCACAAGCT ACCTAACTAA GAAGTTTGCT 1260
 GAACTAGCA GCCCAATGA GTTCAAGGTG TACATGGGCC ACGGTGGGAA GCCCTGGGTC 1320
 TCCGACTTCA GTCACTCTCA TTACTTGGCT GGGAGAAGAG CCATGAAGAC AGTTTTGGT 1380
 GTTGAGCCAG ACTTGACCA GGAAGGCGGC AGTATTCCCG TGACCTTGAC CTTTCAGGAG 1440
 5 GCCACGGGCA AGAAGCTCAT GCTGCTGCCT GTGGGGTCAG CGGATGACGG AGCCCACTCC 1500
 CAGAATGAAA AGCTCAACAG GTATAACTAC ATAGAGGGAA CCAAGATGCT GGCCGCGTAC 1560
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 GAAGGAATCC TGCCCTCACC TCACCCCTTT CCAACTTGCC CAGGGAAGTG GAGGTTCCCT 1680
 CTTTCTTTC CTTCTGTCA GGTCACTCCAT GACTTTAGAG AACAGACACA AGTGTATCCA 1740
 10 GCTGTCCAGG GGTGGAGCTA CCGTTGGGC TTATAGTGA CTGGAGTGA CAGCTGAGTC 1800
 ACCCTGGGTA AGTTCTCAGA GTGGTCAGGA TGGCTTGACC TGCAGAAGAT ACCCAAGGTC 1860
 CAAAAGCACA AGGTCTCGCG AAGTTCTGG TTGTCCGGTG GGCACCACGG CTCACACCTA 1920
 TAATCGAGCA CTTTGGGAGG CCAAGACAGG AGGATCACTT GAGGCCAGGA GTCTGAGACA 1980
 AGCTTAGGCA ACAAACAAG ACTCTGTCTC TACAAAAAGT TTAAGAAATG AGCCAGACAT 2040
 15 GGTGGTGTAT GCCTGTAGTC CCAGCCACTC AGAAGGCTGA GGCAGGAGGA TCGCTTGAGA 2100
 CCAAGAGTTT GAGCCTCGCG TGAGCTGTGA ATGCACCAAG GCACCTCAAG CTGGGCAATG 2160
 TAGCAAGATC CTGTCTCTAC AAGAAATTTT TAAAAATGA GCCAAGTGTG GTGGTGCAATG 2220
 CCTGTAGTTC CAGCTACTCA GGACACTGAC GTAGGAGGGT TGCTTGAGAC TGAGAGTTGG 2280
 AGGCTGGCAT CCGCTATGAA TGCCCACTG CACTCCAGCC TGGGCGACAG AACGAGACCC 2340
 20 CATCTCAAAA AAAATAAGTT CTGGTTGTCA TTGAATTTGG ATAAACAGAG AGCTTGATGC 2400
 TTTCTGCCCT CTGTCTCAGG TGATGCATTG CACATTTGGG ATATTGGAA AGGAAATGAG 2460
 GAAAGAAATT AGGGCTCCTT CTGATCTCTC GCTATCTGCG GGTCTGTGCC TTTTCTCAAG 2520
 ACCTTCACCA TTACTGGCAT TTCTCTGTCT TCTCTTAGT ATGATCCCTC AAAACCTCAC 2580
 25 TAACTGGAAG GATGATTTTG TCTCAGTTTG TACTCCTAAA TAAAAAGTAA ACATGACACC 2640
 TCT 2643

Seq ID NO: 101 DNA Sequence
 Nucleic Acid Accession #: AF258592
 Coding sequence: 93..1268

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 ACATAGATGA AAATCAGGAT CGCTACATTA AGAAACTCGC AAAATGGGTG GCTATCCAGA 180
 35 GTGTGTCTGC GTGGCGCGAG AAGAGAGGCG AAATCAGGAG GATGATGGAA GTTGCTGCTG 240
 CAGATGTTAA GCAGTTGGGG GGCTCTGTGG AACTGGTGA TATCGGAAAA CAAAAGGAGA 300
 TTCTGTCAA CGTCCGATTG TGCTCGAAG GCATGGAGGA GTCAGGCTCT GAGGGCCTAG 360
 ACCGAGCTGAT TTTTGCCTGG AAAGACACAT TCTTTAAGGA TGTGAGTAT GTCTGCATT 420
 40 CTGCAATTA CTGGCTGGGA AAGAAGAAGC CCTGCATCAC CTACGCCCTC AGGGGCATT 480
 GCTACTTTTT CATCGAGGTG GAGTGCAGCA ACAAAGACCT CCATTCTGGG GTGTACGGGG 540
 GCTCGGTGCA TGAGGCCATG ACTGATCTCA TTTTGTCTGAT GGGCTCTTTG GTGCAAGA 600
 GGGGGAACAT CTTGATCCCC GGCATTAAAG AGGCCGTGGC CGCCGTCAAG GAAGAGGAGC 660
 ACAAAGCTGA CGACGACATC GACTTTGACA TAGAGGAGTT TGCCAAGGAT GTGGGGCGC 720
 45 AGATCTTCTC GCACAGCCAC AAGAAAGACA TCCTCATGCA CCGATGGCGG TACCCGTCTC 780
 TGTCCTCCA TGGCATCGAA GGCGCTTCT CTGGTCTGG GGCCAAGACC GTGATTCCA 840
 GGAAGGTGTT TGGCAAGTTC TCCATCAGGC TCGTGCCGAA CATGACTCTT GAAGTGTCTG 900
 CCGAGCAGGT CACAAGCTAC CTAACAAAGA AGTTTGCTGA ACTACGCAGC CCCAATGAGT 960
 TCAAGGTGTA CATGGGCCAC GGTGGGAAGC CTTGGGTCTC CGACTTCAGT CACCTCATT 1020
 50 ACCTGGCTGG GAGAAGAGCT ATGAAGACAG TTTTGGTGT TGAGCCAGAG TTGACCAGGG 1080
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 TGCTGCTGT GGGGTGAGG GATGACGGAG CCCACTCCCA GAATGAAAAG CTCACAGGT 1200
 ATAACTACAT AGAGGGAACC AAGATGCTGG CCGGTACCT GTATGAGGTC TCCAGCTGA 1260
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 55 ACCCTTTCTC AACTTGCCCA GGGAAAGTGA GGTTCCTCT TCTTTCTCC TCTTGTCAAG 1380
 TCATCCATGA CTTTAGAGAA CAGACACAAG TGTATCCAGC TGTCACCGG TGGAGCTACC 1440
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 GGTGAGGATG GCTTGACCTG CAGAAGATAC CCAAGGTCCA AAAGCACAAG GTCTGCGGAA 1560
 AGTTCTGGTT GTGCGCTGGG CACCAAGGCT CACACCTATA ATCGAGCACT TTGGGAGGCC 1620
 60 AAGACAGGAG GATCACTTGA GGCCAGGAGT CTGAGACAAG CCTAGGCAAC AAAACAAGAC 1680
 TCTGTCTCTA CAAAAGTTT AAGAAATGAG CCAGACATGG TGGTGTATGC CTGTAGTCCC 1740
 AGCCACTCAG AAGGCTGAGG CAGGAGGATC GCTTGAGACC AAGAGTTTGA GCCTGCGGTG 1800
 AGCTGTGAAT GCACCAAGGC ACTCAAGCCT GGGCAATGTA GCAAGATCCT GTCTCTACAA 1860
 GAAATTTTTT AAAAATGAGC CAAGTGTGGT GGTGATGCC TGTAGTTCCA GCTACTCAGG 1920
 65 ACACCTAGCT AGGAGGGTTG CTTGAGACTG AGAGTTGGAG GCTGCGATGA GCCATGAATG 1980
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 GGTGTGCTT GAATTTGGAT AAACAGAGAG CTTGATGCTT TCTGCTTCT GTCTCAGGTG 2100
 ATGCAATTGA CATTGGGAT ATTGGAAAG GAAATGAGGA AAGAAATTAG GGCCTCCTCT 2160
 GATCTCTGCG TATCTGCGGG TCCTGTCTCT TTCTCAAGAC CTTCAACATT ACTGGCATT 2220
 70 TCCTGTCTCT TCTTTAGTAT GATCCCTCAA AACCTCACTA ACTGGAAGGA TGATTTTGTG 2280
 TCAGTTTGTG CTCCTAAATA AAAAGTAAAC ATGACACCTC TAAAAAATAA AAAAAAATAA 2340
 AAAAAAATAA 2349

Seq ID NO: 102 DNA Sequence
 Nucleic Acid Accession #: Eos sequence

75 1 11 21 31 41 51
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 TTTTTCACAA AGGGAATTA AATTGTGAGG ATGATGGCAT ATCATCAGTG AGATGCTTCT 60
 ACGTTGATGT GCACTTGTGT ATGCATGTAT TATACATACC CTCATGATGG GAACTGGAGT 120
 CAATAAATTT CTTTCTTTTC TTAGGACAC TTTCTAGAT CTTTCCACTG TTAACCCAAC 180
 80 CATCCAGATC TCCTAAACTC TCTGAGAAC TTAGAAATTA ACTCTTTCC TCTTCCCTAT 240
 TTGGCTGGCG TAATAGAGCA GGCATGCAAT ACTAAGCTTC ACAGCTAGGT GTCCTCATAA 300
 TGCAATGACT TCCTTTGGCA GCCTAGTCAT TGACAGCTGA CTTTGAGTCA AGAAAGTAAG 360
 TTTTCTCTCT CCTTATGTT TAAATTTCTAT TTAGGAGAT TCCTTATGAG GGATACCTAT 420
 GAAGGCCACT TTCCTCTGTC TATGTGCTCA GAGCTAACTC CATATTTTCC TGTAAGTTTA 480

TAAGTAGCTT GCAATTCACT TAGGTGTCCA CCAATG

516

Seq ID NO: 103 DNA Sequence
Nucleic Acid Accession #: NM_018401.1
Coding sequence: 65..1309

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| 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | |
| GTCCACATC | CGCATCCGG | CATCCACGG | GCCGGGCATG | TAGCAGCGGC | AGCAACGGCG | 60 |
| GAATATGGGC | GGGAACCACT | CCCAACAGCC | CCCCGTGTTT | GACGAGAATG | AGGAAGTCAA | 120 |
| CTTTGACCAT | TTTCAGATTG | TGCGGGCCAT | TGGTAAAGGG | AGTTTGGGAA | AGGTATGCAT | 180 |
| CGTGCAAGAG | CGAGACACTA | AGAAAATGTA | TGCAATGAAG | TACATGAACA | AGCAGAAGTG | 240 |
| CATCGAGAGG | GATGAGGTTT | GGAAATGTTT | CCGGGAGCTG | CAGATCATGC | AAGGGCTGGA | 300 |
| GCACCCCTTC | CTGGTCAATC | TGTGGTACTC | CTTCCAGGAT | GAGGAGGACA | TGTTTCATGGT | 360 |
| GGTGGACCTG | CTCCTGGGAG | GCGACCTGGG | CTACCATCTG | CAGCAGAATG | TGCATTTTAC | 420 |
| AGAGGGGACT | GTGAACTCT | ACATCTGTGA | GCTGSCACTG | GCCCTGGAGT | ATCTTCAGAG | 480 |
| GTACCACAT | ATCCACAGAG | ACATCAAGCC | AGACAATATC | CTGCTGGATG | AACACGGACA | 540 |
| TGTTTCACTT | ACAGACTTCA | ACATAGCGAC | GCTAGTGAAG | GGAGCAGAAA | GGGCTTCTCT | 600 |
| CATGGCTGGC | ACCAAGCCCT | ACATGGCTCC | AGAAGTATTC | CAGGTGTACA | TGGACAGAGG | 660 |
| CCCGGATAC | TGCTACCTCT | TGCACTGGTG | GTCCCTGGGC | ATCACAGCCT | ATGAGCTGCT | 720 |
| GCGGGGCTGG | AGGCCGTACG | AAATCCACTC | GGTCACGCCC | ATCGATGAAA | TCCTCAACAT | 780 |
| GTTCAAGGTG | GAGCGTGTC | ACTACTCCTC | CACGTGGTGC | AAGGGGATGG | TGGCCCTGCT | 840 |
| GAGGAAGCTC | CTGACCAAGG | ATCCTGAGAG | CCGCGTGTC | AGCCTTCATG | ACATACAGAG | 900 |
| CGTGCCCTAC | TTGGCCGACA | TGAACCTGGG | CGCGTGTTT | AAGAAGGCAC | TGATGCCCGG | 960 |
| CTTTGTGCCC | AATAAAGGGA | GGTTGAACCT | CGATCCACCA | TTTGAGCTTG | AAGAGATGAT | 1020 |
| TCTAGAAATC | AAGCCACTTC | ACAAAAAGAA | GAAGCGATTG | GCAAGAAGCA | GATCCAGGGA | 1080 |
| TGGCACAAGG | GACAGCTGCC | CGCTGAATGG | ACACCTGCAG | CACCTGTTGG | AGACTGTCCG | 1140 |
| GGAGGAATTC | ATCATATTCA | ACAGAGAGAA | GCTCAGGAGG | CAGCAGGGAC | AGGGCAGCCA | 1200 |
| GCTCTTGAG | ACCGCAGGCC | GAGGGGGAGG | CCAGGCCCAA | AGCAAGCTCC | AGGACGGGTG | 1260 |
| CAACAACAAC | CTCCTCACCC | ACACCTGCAC | CGGTGGCTGC | AGCAGCTGAG | CCACACATTG | 1320 |
| TGTGTGCTCA | ACAGACTGCG | ACTCGTCTCT | GCCCTGCCCA | CCCAGAGCCC | CTCTTGTGTC | 1380 |
| CCTGATGGTC | CCTGTCTCAC | CCCTGAAAAC | ATCAGATGCA | GA AAAAGCCC | TGGACTTGA | 1440 |
| GCTGGGAAGT | GTGGGTTCTG | GTCCCATCTC | CATGACTGAT | TCACGTGTGA | CCTCAGACAA | 1500 |
| GTACCGCCCT | CTCTGTGCTT | CGGTTTCTG | CATCTGCCAA | AGGGGTTAAA | CACCTTCTGCC | 1560 |
| CCACTTCAAA | TACAAAGATT | ATGGGGAGAA | CCCAATTAGG | TAGGAAACAT | GA AAAACCTT | 1620 |
| TGATATTAT | AAAATCATTT | TACGTGCAAA | AATATAACCT | TAATATTGGA | AGTGACCCCC | 1680 |
| ATTCGCCAAA | GCAATCAAAC | CGTCATGACT | TTGCAATTGG | GCACATCCTA | GCTTGTGAGA | 1740 |
| GGGCACTTCC | GA AAAACACA | GCCCTGACAG | CA AAAATAAG | GTCTGATATG | TTGGCCCTTT | 1800 |
| CTATGGAAGC | AACGCTGCCA | AATCCTGGAG | CA AAAACCTGA | AGTGTCTTCA | TGTGCATTCT | 1860 |
| CTGGCAGGCC | CAGACTCTGA | GCTTGTAAAG | TGGTGCAGCA | TGCAGACCAG | ACTTGTCCCC | 1920 |
| AAGGTCTCAG | CGCTGCGGTC | TCACTCCTCC | CCTCATTTAA | GAAGACTATC | CTTACCTTTT | 1980 |
| AGTTTCAGCA | GTCCCTCACA | CCACCATATC | CCCAGTGCTG | GGATGGCACA | CAGGTGTGCT | 2040 |
| TTCAATGATG | AGTTGGGTGG | CTGAGCATTG | GTTACTCCTG | CAGAGTGTA | TCAGCACCCC | 2100 |
| ATCCAATCTG | CCCGAAAGCC | CAGACCTGCA | GCAGAACTCT | CCAACCTCTC | ATCAGCTTTC | 2160 |
| AGGGTTTTCT | CTCCTGGGAA | GGGTGTAAAA | TCAGCTTGTC | AGATTCTTCT | TACAGAGAGT | 2220 |
| ATCCAATCGG | TATTGGTGGG | GCGGCTCCCT | ATTTATACAA | TAGGAAGCAT | GGGTGCTTAG | 2280 |
| AAAGTTTATT | TCAGGAGGAA | AATGGGTTC | CACAAAAGC | AAACTACATT | CTGATCTGCT | 2340 |
| CAGGGAGAAG | CTTGCCCTTG | AACCTGGAAG | TGTTGGGATG | AGCAGGGAAA | GCTTAGACTT | 2400 |
| TGGAGTCAGG | TTTGTTTCA | GAATCCAGCC | CTGCTGGCTA | CTAACTAACT | GGGAGACCTT | 2460 |
| AGGCAAGGCA | TGCAATCCCT | CTGAATGGCA | GTTTCTCAT | TTTTAAACAG | GGATAATAAA | 2520 |
| ACTAATATTG | CAGGGGAGTT | ACAGGGTTAA | ATAAGATCCT | GTGTGTAACC | CCAAGCATTG | 2580 |
| GATGACTCAT | AGAATGGCCT | TTTTTGTGAG | CATAATCGTC | ATCATTATT | AGATACCTTC | 2640 |
| TTCTTCTACT | CACCCAGCAG | GTCAAGTTTT | TGTGCAACAA | AACTGTTTAA | GGATTCTTCC | 2700 |
| AAATGCTCTT | CCTGGGGTCT | TTGATATTG | TTTGTATCAT | CCTGCTGAAG | TTGAGCTGTG | 2760 |
| TTTTTATTTT | TTTATCCAACT | TTCCATTTTT | CACCTTTTAC | ATGATTACTC | AATCCTTGGG | 2820 |
| GCTGTCCATG | TCATCTCTTA | GATTTCCTAA | AAGACATTTT | AATGTATGGT | TAGGTTTTAT | 2880 |
| ATTTTTTATT | TTTAAAAAAG | AAATAGTCAG | TGTTTTCTCT | CTTCAACCG | AGACTATTTC | 2940 |
| TGGATTGTGT | GCTCCTCGTC | AGTTGACTTG | TTTTGCACAC | TTTTCTTTAC | TTTATGTCCT | 3000 |
| CATCAACAAC | CGTCTGCTC | CCCACTCCC | CCAGGAAATA | AGGGGCTGTC | TCCTCTCCCT | 3060 |
| ACTGTGACCC | TGGAGGCTCT | TAAGATGATG | ATGGTTTTTT | TTATGGGCT | GAGTTACAGA | 3120 |
| ATTAGGGGCA | GGAGCTGGAA | GTGCGCCTAG | GAACACCAGA | TTTCTGGT | CTGTTCAAGT | 3180 |
| TGGCATTCT | TGTTTGGGAA | AAACTATTTC | TTGGACATTC | CTTC | | 3224 |

Seq ID NO: 104 DNA Sequence
Nucleic Acid Accession #: NM_004207.1
Coding sequence: 63..1460

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75
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|------------|------------|------------|------------|------------|------------|------|
| 1 | 11 | 21 | 31 | 41 | 51 | |
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| CCATGGGAGG | GGCCGTGGTG | GACGAGGGCC | CCACAGCGGT | CAAGGCCCTC | GACCGCGGCT | 120 |
| GGGGCTGGGC | CGTGCTCTTC | GGCTGTTTGG | TCATCACTGG | CTTCTCTTAC | GCCTTCCCCA | 180 |
| AGGCCGTCAG | TGTCTTCTTC | AAGGAGCTCA | TACAGAGATT | TGGGATCGGC | TACAGGAGCA | 240 |
| CAGCCTGGAT | CTCCTCCATC | CTGCTGCCCA | TGCTCTACGG | GACAGGTCCG | CTCTGCAGTG | 300 |
| TGTGCGTGAA | CCGCTTTGGC | TGCCGGCCCG | TCATGCTTGT | GGGGGTCTC | TTTGCGTGGC | 360 |
| TGGGCATGGT | GGCTGCGTCC | TTTTGCCGGA | GCATCATCCA | GGTCTACCTC | ACCACTGGGG | 420 |
| TCATCAGCGG | TTTGGGTTTG | GCACTCAACT | TCCAGCCCTC | GCTCATCATG | CTGAACCGCT | 480 |
| ACTTCAGCAA | CGGGCGCCCC | ATGGCCAAAG | GGCTGGCGGC | AGCAGGTAGC | CCTGTCTTCC | 540 |
| TGTGTGCCCT | GAGCCCGCTG | GCGCAGCTGC | TGCAGSACCG | CTACGGCTGG | CGGGGCGGCT | 600 |
| TCCTCATCCT | GGGCGGCTCG | CTGCTCAACT | GCTGCGTGTG | TGCCGCACTC | ATGAGGCCCC | 660 |
| TGGTGGTCAC | GGCCAGCGCG | GGCTCGGGGC | CGCCGCGACC | CTCCCGGCGC | CTGCTAGACC | 720 |
| TGAGGCTCTT | CCGGGACCGC | GGCTTTGTGC | TTTACGCGGT | GGCCGCTCTG | GTGATGGTGC | 780 |
| TGGGCTCTTT | CGTCCCGCCC | GTGTTCTGTC | TGAGCTACGC | CAAGGACCTG | GGCGTGCCCG | 840 |
| ACACCAAGGC | CGCTTCTCTC | CTCACCATCC | TGGGCTTCAT | TGACATCTTC | GCGCGGCGCG | 900 |
| CCGCGGGCTT | CGTGGCGGGG | CTTGGGAAGG | TGCGGCCCTA | CTCGTCTAC | CTCTTCAGCT | 960 |
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| | GCCTGGTGGT | CTTCTGCATC | TTCTTTGGCA | TCTCTACGG | CATGGTGGGG | GCCCTGCAGT | 1080 |
| | TGGAGGTGCT | CATGGCCATC | GTGGSCACCC | ACAAAGTTCTC | CAGTGCCATT | GGCCTGGTGC | 1140 |
| | TGCTGATGGA | GGCGGTGGCC | GTGCTCGTCG | GGCCCCCTTC | GGGAGGCAAA | CTCCTGGATG | 1200 |
| | CGACCCACGT | CTACATGTAC | GTGTTTCATC | TGGCGGGGGC | CGAGGTGCTC | ACCTCCTCCC | 1260 |
| 5 | TGATTTTGGT | GCTGGGCAAC | TTCTTCTGCA | TTAGGAAGAA | GCCCAAGAG | CCACAGCCTG | 1320 |
| | AGGTGGCGGC | CGCGGAGGAG | GAGAAGCTCC | ACAAGCCTCC | TGCAGACTCG | GGGGTGGACT | 1380 |
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| | CTCAAGGACC | TGGAACCCCA | TGCTTCGAGA | CAACGTGACT | TTAATGGGAG | GGTGGGTGGG | 1800 |
| | CCGCAGACAG | GCTGGCAGGG | CAGGTGCTGC | GTGGGGCCCT | CTCCAGCCCG | TCCTACCCCTG | 1860 |
| 15 | GGCTCACATG | GGGCTGTGTC | CCACCCCTCT | TGAGTGTCTT | GGGACACAGT | CTTTCCACCC | 1920 |
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| | TT | | | | | | 1982 |
| 20 | Seq ID NO: 105 DNA Sequence | | | | | | |
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| 30 | CACCTTCATC | GGCGTCTACC | TGCCGTGCC | CGAAGAACATC | CTGGGCGTCA | TCCTCTCTCT | 420 |
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| 35 | GACCATCGAG | ATTTTCTGTA | CGTACATCTC | CCCGGGTGGG | GCCATCTTCC | AGGCGGAGGC | 720 |
| | TGCAAGTGGC | GAGGCGGCCG | CCATGCTGCA | CAACATGCGT | GTGTACGGCA | CGTCAACGCT | 780 |
| | OGTGTCTATG | GGCCTGGTGG | TCTTGGTGGG | CGTCAAGTAT | GTCAACAAGC | TGGCGCTGGT | 840 |
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| 40 | CTTGGATGCC | TGGGTCAAGG | CCTACGGCAT | CCACAACAAC | TCAGCCACCT | CCGCGCTCTG | 1020 |
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Seq ID NO: 108 DNA Sequence
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Seq ID NO: 109 DNA Sequence
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Nucleic Acid Accession #: NM_001250
Coding sequence: 48..881

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Seq ID NO: 112 DNA Sequence
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Seq ID NO: 113 DNA Sequence
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| | CGACACAAGA | ACATCATCAA | CCTGCTTGGT | GTCTGCACCC | AGGAAGGGCC | CCTGTACGTT | 1800 |
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| 75 | GGCCCCGACC | TACGCCCCGA | CGGTCTCTGG | AGCAGTGAGG | GGCGGCTCTC | CTTCCAGTTC | 1920 |
| | CTGGTCTCCT | GGGCTTACCA | GGTGGCCCGA | GGCATGCAGT | ATCTGGAGTC | CCGGAAGTGT | 1980 |
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| | GCGCTCTCTG | AGGAGTACCT | CGACCTCCGC | CTGACCTTCG | GACCCCTATT | CCCTCTGTGT | 2460 |
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Nucleic Acid Accession #: NM_022963.1
Coding sequence: 157..2445

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Coding sequence: 1..4359

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CCATGGATGC CATCAGGTTT TCTCATGCTG GTGAATGCCT CTGGGAGACC TGAGGGGCGA 240
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| | GGACACCTTG | ACCCAGATAC | AGAATATGAG | ATTAGTGTGC | TCCTGACCAG | GCCAGGGGAG | 1080 |
| 5 | GGTGGCACTG | GCTCTCTGG | TCCAGCTCTC | AGGACAAGAA | CAAAGTGTGC | TGATCCCATG | 1140 |
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| 10 | CTCATGAACC | CAGAGGGCCG | GAAGGAAAGC | CAAGAACTCA | TAGTGCAGAC | AGATGAAGAC | 1440 |
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| | ACCAAAATAT | CAGCACCCTC | TATGCCAGCT | TATGAACTTG | AGACACCTTT | GAATCAAACT | 1800 |
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| 20 | AAGTGTAC | CAGTGCCAAT | TCACTTCCAG | AATGCTTCTC | TGCTGAATC | ACAGTACTAC | 1980 |
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Seq ID NO: 116 DNA Sequence

Nucleic Acid Accession #: NM_016551.1

Coding sequence: 38..1750

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 55 CAGGCCACTT CTGCTCTGTC CAGGACGGGG ACCACTGCGC CGCGTCCGCG GCTTACGCCA 720
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 60 TATGTGTGAA AACAAGAAAG CCAAGGGGTG ATGTAGTCAA GGTGATCGTC TCGTCCAGC 1020
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Seq ID NO: 118 DNA Sequence
 Nucleic Acid Accession #: Eos sequence
 Coding sequence: 42..1070

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| 5 | TCCACATCTT | CATCGTGTTC | AGCTTCTTCC | TGGTCTTCTC | CATCATCTCT | TTCTGCAACC | 660 |
| | TGGTCATCAT | CGGTACCTTG | CTCATGCAGC | CGGTGCAGCA | GCAGCGCAAC | GCTGAAGTCA | 720 |
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| 15 | CTCACCTGGG | CAGGGATGAT | GGCAGAGCCA | GGCTGTTGGA | AAATCCAGAA | CTCAATGAG | 1260 |
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| 20 | AAGAGATGGA | GACCATCTG | GCCAACATTG | TAAAACCCCA | TCTCTACTAA | AACATACAAA | 1560 |
| | AATTAGCCGG | GCATGGTGG | ACACGCCCTG | AGTCCAGCT | ACTCAGGAGG | CTGAGGCAGG | 1620 |
| | AGAATCGCTT | GAACTGGGGA | GGCAGAGGTT | GCAGTGAACC | TAGATTGCAC | CATTGCATCT | 1680 |
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| 25 | TGTTAGGCAC | TACCTTGGGG | CAGACTTTTG | AGCTAAGATG | TTGCCATCTT | CTCTCCACCC | 1860 |
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| | GCTAGGACAA | GAGCTTGCTT | CCCAAGACAG | ACGTGTCTGT | CTGCAAGGCG | CTTGCTCTA | 2040 |
| | GTCCAGTCAG | CTCTGGGGGA | GTGGGAAGGA | GATGCCACCC | TCTCTTTTCT | GTCTCAACAA | 2100 |
| 30 | TAGTCCCTAA | TTAAGTACCT | TCTGTGGGGC | AGCCACCCAC | TGAGGGTGGG | CAAGGCCCCC | 2160 |
| | TTGAAAGCAA | AATTGGGGCT | GGGCTCAGTG | GCTCATGGCT | ATAATCCAG | CACCTTGGGA | 2220 |
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| | GGAGGCTGAG | TGGGGCCGAT | CATTGGAAGT | TAGGAGTTTG | AGACCAGCCT | GACCAATATG | 2400 |
| 35 | GTAAACCCCT | GTCTCTACTA | AAAATACAAA | AAAATTAGCC | TGGCGTGGTG | GCGCATGCCT | 2460 |
| | GTAGTCCCAT | AGGCTGTAGC | TACTGGGAGG | AGGCGGAGCT | TGCAGTGAGC | CGAGATCAGC | 2520 |
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| | AAAAAAGCCA | AAATTGGAGC | GTGCCAGGCC | AGGACACCCC | GATGTCCAGG | GGCTTCCATA | 2640 |
| | CGAACAGGCA | CATGGGCTGG | GAAGTACATG | AGGCCCTCTG | GTAGAAGGGT | CTGTCACTTC | 2700 |
| 40 | TCTCTCTCCT | TGCCCTCTTG | GAGGTCCTTC | CTAACATAGC | TTCCAGGAGG | TGGGAGGAGC | 2760 |
| | AGTTACTGTG | AGCAGGTGTC | AGCCAGGTGT | CAGCTTCTCC | TGGGGATCTC | TAGATGTCTG | 2820 |
| | CTTGATGATT | TTGGCAAGTA | TATGCAAAATG | AGCCTCTCTC | CCTGCCCTGA | GACAAGTATC | 2880 |
| | TGCAGTGTGA | ACTCTGCAGC | CTCAGACCCA | AGGGGCTCAG | AGGAAACTTC | TCTGGTTTCT | 2940 |
| | AGAGCTCTGT | GCTCCTTCAG | AGAAGTCTTC | CTTCTTCCCA | GTCAGTGTCC | CTGTGAAGCT | 3000 |
| 45 | GGGATACTCA | TTTCTGTGTG | ACCGGGCAAA | CACCGGATTG | CTGATTTTGA | GAATAGCCTC | 3060 |
| | TCGATGGACC | TGTAACCTGC | TGGAGTCTGG | GATGGTAGCT | TGGGGCTGGA | CTTGGCTGAT | 3120 |
| | GGGATGACCC | GGTGGCTAGT | GCAGCATCAC | ACAAGCCTGG | TTCAAGTCTT | GGCTGTGTCA | 3180 |
| | TTTCTCTGCT | AGGGACCAGG | CACGTAAATT | CCTACCTCTT | AGGGTCATTA | CCTATGAGGT | 3240 |
| | TAAAGCTACC | TCATGGGATT | GTATACGCC | ACTAATGTGG | AGGCAGACAC | CTCTTGGCAG | 3300 |
| 50 | GGTGACTGCT | CATCTTAGAC | CCTCCCCTTT | TCTGCGAATT | TGGGCCCTTT | GATCCTCTGA | 3360 |
| | TGGGAGCTGA | AAGGATGAGA | GGTGGGCATC | TAGATTTAGG | GAGGCTGTTC | AGGCTTTGCA | 3420 |
| | GGTCCCTTAC | CTGAACACAT | AGAAACCCCTG | GAGCTGTGAC | TGTGTCCATG | TGTGTGTGTT | 3480 |
| | TGTCGTGTGT | TGTTGGCGGG | GATGGGCACC | TGCATGAATG | TGGTAGAGAA | AATGGCTCTG | 3540 |
| | CTCAGAGGGA | AGATAGCAT | AGCAAGGCAG | GGACCAAGAG | AATCACAGGC | GCCTGGAGAG | 3600 |
| 55 | CAGCGGGGCA | CCGCCTCCAG | GGACCTGCCG | GCTTCCCTCA | GTCTCCAGG | GGCCAGCAC | 3660 |
| | TCTTCTTTTA | GGCCCTGTGA | GGCTCCCTTG | TCAGGATACA | TTCTCTCATT | TGCTGGAAGC | 3720 |
| | TGATTGTGATT | GGGTGTCTGT | TTCTCGCAGC | CAAAAGAGCT | CTGAATGAGG | AAAGTGCTTC | 3780 |
| | TGTGTAACT | CCCGCGGTCT | CCTGAATTTT | AGTCATTAT | GTACCCGCGT | CGAAATTTT | 3840 |
| 60 | GCAATATCTG | TGTAACCACT | GTCCATTAT | TTAATAAAGA | AGTTTTCTTT | AAATTAAGTC | 3900 |
| | ACTTTTAA | | | | | | 3908 |

Seq ID NO: 119 DNA Sequence
Nucleic Acid Accession #: NM_003271.2
Coding sequence: 137..853

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| | ACTGAAGCGC | TGCGGCATGG | CGCGCGCCTG | CCTCCAGGCC | GTCAAGTACC | TCATGTTGCG | 180 |
| 70 | CTTCAACCTG | CTCTTCTGGC | TGGGAGGCTG | TGGCGTGTG | GGTGTGCGCA | TCTGGCTGGC | 240 |
| | CGCCACACAG | GGGAGCTTCG | CCACGCTGTC | CTCTTCTTTC | CCGTCCCTGT | CGGCTGCCAA | 300 |
| | CCTGCTCATC | ATCACCGGCG | CCTTTGTTCAT | GGCCATCGGC | TTCGTGGGCT | GCCTGGGTGC | 360 |
| | CATCAAGGAG | AACAAGTGCC | TCCTGCTCAC | TTTCTTCTGT | CTGCTGCTGC | TGGTGTTCCT | 420 |
| | GCTGGAGGAC | ACCATCGCCA | TCCTTCTTCT | CGCCTACACG | GACAAGATTG | ACAGGTATGC | 480 |
| | CCAGCAAGAC | CTGAAGAAAG | GCTTGCACTT | GTAAGGACAG | CAGGGCAACG | TGGGCCTCAC | 540 |
| 75 | CAAGCCTGCG | AGCATCATCC | AGACCGACTT | CGCTGCTGT | GGCGTCTCCA | ACTACACTGA | 600 |
| | CTGGTTCGAG | GTGTACAACG | CCACGCGGGT | ACCTGACTCC | TGCTGCTTGG | AGTTCACTGA | 660 |
| | GAGCTGTGGG | CTGCAGCGCC | CCGGCACCTG | GTGGAAGGCG | CCGTGCTACG | AGACGGTGAA | 720 |
| | GGTGTGGCTT | CAGGAGAACC | TGCTGGCTGT | GGGCATCTTT | GGGCTGTGCA | CGGCGCTGGT | 780 |
| | GCAGATCCTG | GGCTGACCTT | TCGCCATGAC | CATGTACTGC | CAAGTGGTCA | AGGCAGACAC | 840 |
| 80 | CTACTGCGCG | TAGGCGCGCC | ACCGCCGCTC | TCTCTGCCAA | AAGGAACGCC | ACGGGAGATG | 900 |
| | GGCGGCACCC | ACAGCTGCCT | TTCCACCCAC | CAGCCTCGGT | GCTCTGCCCC | ATGCTGGGAG | 960 |
| | GAGGGAGGGA | GGGACAGGTG | CCTGGAGCCC | CGGGAACCTT | GTTTCTGGAA | GGCCCTAGCT | 1020 |
| | CAGGTGGCTT | CAGGGCTCTC | GGAACCCGCC | TGGGAGGGGT | GGCCACGTGC | TGGCTGGGGA | 1080 |
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 Coding sequence: 639..2546

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 15 CCGGCGCGGG GCGCGCGGCC ACAGGCCCTT GCTCCGGCGG TCGTTTGAGC ACCGCGGGCG 240
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CGGGTTCCCA CGCAGAGGGG AGGCTGTCTC ACCCTACTCT TCCTCCCTTG CTCCAGCAG 720
CGGAAGCGCC TCTGACCCCTT GGCTTGAGTC CCACGTGGGG GAGGAGGAGG CAGGCAGCAC 780
CAGCAGGGGT CCACCAAGAG CCCAGACCAG CCCCTCTGCC CTCTACCCG GGCCTCGAAG 840
GGTGTGGCAG AGGCTACGTG TTGAGCGTGG CTTAGCTGAG CCAACAAGAA GCAGGGCGCT 900
CTGAGTGCCA AGGAGCGTGG CGGGCTCCAC GTTAGCCAG GCTCTGAGAG CCAGCCCAGG 960
GGCGGGCGTG CTCAGCTTGG GCTGGTCCAG GGCTGCCCA GGTGGGGGCA CCTTTGCCCT 1020
CTGAGGCGCA GCGCACTCTT CCCTGCCCA AGCCTACTGC TCCCGCTGC GCGCAGTACC 1080
CCCTCCAGCC CCACACTGG GCTCCCTCT GCACTCCCC TCCTTGTCTC CCCTCTGTCC 1140
CCAGGGATCA AACAGAAGCA GCGTGGGCA AAATACAATT TCATTTAACA AATTGAAAAA 1200
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1260
AAAAAAAAAA AAAAAAAAAA AAAA 1284

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Seq ID NO: 123 DNA Sequence
Nucleic Acid Accession #: Eos sequence

55
60
65

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1 11 21 31 41 51
| | | | |
TCTTGACTGA AATTCTCTCC TGATGCTGAG CCCTGCACCC CACCTTCTCT TTCCTAACTA 60
TGAATTGATG GCAAGTCCCA CTCAAAACA CCAGTTAAGT GCTCAGAGA GAGTAGTCAA 120
GCACCTCCAG AAAGAAACCG GGTTTTGTGT CACATAGCAG GAAGTGACTC CCTGGGTGGT 180
AATTATCTTT GGAACAACAG GTAGATTGGC AGAAAAACCG GAACATGTAG GTACCCGAT 240
GTTGGTGATG GTCCATTACT TTGGGATAGG CTTTCTCAGT CTTTCTCAA ATGATAGTTG 300
AGCCAGTTTT CCAGTGGCAA TTCTGAGTGA CTTGCGCTTG TCTTATGGTG TGGTCAAGGG 360
ACGTTCAAGG ATACGGAAGA CTTTACTGTA AACAGCGAAG CAGAGTATAC CGGCATGAGA 420
GGGAAGATGA AACTCACCT ATGTACCACT CTTTGACAA ATATATAGTA TTTCTCAAT 480
CAGTCTCAAG ACTGATCCTG TCTCAGAAAC GACCATTTGT CTCTCATTTT TCTAATACGG 540
TGAGAGGAAC ACTCTGAATA AAGGCTAAGT GGTGGAGCAT GCAA 584

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Seq ID NO: 124 DNA Sequence
Nucleic Acid Accession #: NM_002204.1
Coding sequence: 74..3229

70
75
80

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TCCGCTGGCA GCCATGGGCC CCGGCCCCAG CCGCGCGCCC CGCGCCCCAC GCCTGATGCT 120
CTGTGGCTGC GCCTTGATGG TGGGGGCGGG CGGCTGCGTC GTCTCCGCTT TCAACCTGGA 180
TACCCGATTG CTGGTAGTGA AGGAGGCGGG GAACCCGGGG AGCCTCTTCG GCTACTCGGT 240
CGCCCTCCAT CGGCAGACAG AGCGGCAGCA GCGCTACCTG CTCCTGGGTG GTGCCCCCG 300
GGAGCTCGCT GTGCCCGATG GCTACACCAA CCGGACTGGT GCTGTGTACC TGTGCCACT 360
CACTGCCAC AAGGATGACT GTGAGCGGAT GAACATCACA GTGAAAAATG ACCCTGGCCA 420
TCACATTATT GAGGACATGT GGCTTGAGT GACTGTGGCC AGCCAGGGCC CTGCAGGAG 480
AGTTCTGGTG TGTGCCACCC GCTACACCA GGTGCTGTGG TCAGGGTCAG AAGACGAGCG 540
GCGCATGGTG TGCAAGTGCT ACGTGGAGG CAATGACCTA GAGCTGGAAT CCAGTGATGA 600
CTGGCAGACC TACCACAACG AGATGTGCAA TAGCAACACA GACTACCTGG AGACGGGCAT 660
GTGCCAGCTG GGCACGACCG GTGGCTTAC CCAGAACACT GTGTACTTCG GCGCCCCCGG 720
TGCTCAACAC TGGAAAGGAA ACAGCTACAT GATTCAAGCG AAGGAGTGGG ACTTATCTGA 780
GTATAGTTAC AAGGACCCAG AGGACCAAGG AAACCTCTAT ATTGGGTACA CGATGCAGGT 840

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| | | | | | | | |
|---------------------------------------|-------------|-------------|-------------|------------|-------------|------------|------|
| | AGGCAGCTTC | ATCCTGCACC | CCAAAAACAT | CACCATTGTG | ACAGGTGCCC | CACGGCACCG | 900 |
| | ACATATGGGC | GCGGTGTTCT | TGCTGAGCCA | GGAGGACGGC | GGAGACCTGC | GGAGGAGGCA | 960 |
| | GGTGTCTGGG | GGCTGCGAGG | TGGGCGCCTA | TTTTGGCAGC | GCAATTGGCC | TGGCAGACCT | 1020 |
| | GAACAATGAT | GGGTGGCAGG | ACCTCTGGT | GGGCGCCCCC | TACTACTTCG | AGAGGAAAGA | 1080 |
| 5 | GGAAGTAGGG | GGTGGCATCT | ATGTCTTCAT | GAACCAGGCG | GGAACTCTCT | TCCCTGCTCA | 1140 |
| | CCCTCACTC | CTTCTTCATG | GGCCAGTGG | CTCTGCCTTT | GGTTTATCTG | TGGCCAGCAT | 1200 |
| | TGGTGACATC | AAACCAGGATG | GATTTTCAGGA | TATTGCTGTG | GGAGCTCCGT | TTGAAGGCTT | 1260 |
| | GGGCAAAAGTG | TACATCTATC | ACAGTAGCTC | TAAGGGGCTC | CTTAGACAGC | CCCAGCAGGT | 1320 |
| | AATCCATGGA | GAGAAGCTGG | GACTGCCTGG | GTGGCCACC | TTGGCTATT | CCCTCAGTGG | 1380 |
| 10 | GCAGATGGAT | GTGGATGAGA | ACTTCTACCC | AGACCTTCTA | GTGGGAAGCC | TGTACAGACA | 1440 |
| | CATTGTGCTG | CTGCGGGCCC | GGCCAGTCA | CAACATCGTC | CACAAGACCT | TGGTGCCCGA | 1500 |
| | GCCAGCTGTG | CTGGACCCCTG | CACCTTGCAC | GGCCACCTCT | TGTGTGCAAG | TGGAGCTGTG | 1560 |
| | CTTGTCTTAC | AACCAGAGTG | CGGGAAACCC | CAACTACAGG | CGAAACATCA | CCCTGGCCTA | 1620 |
| | CACCTCTGGG | GCTGACAGGG | ACCGCCGGCC | GCCCCGGCTC | CGCTTGGCCG | GCAGTGAGTC | 1680 |
| 15 | CGCTGTCTTC | CACGGCTTCT | TCTCCATGCC | CSAGATGGCC | TGCCAGAACG | TGGAGCTGCT | 1740 |
| | CCTGATGGAC | AACTCCGTG | ACAAATCCG | CCCCATCATC | ATCTCCATGA | ACTACTCTTT | 1800 |
| | ACCTTTGGGG | ATGCCGATC | GCCCCCGCT | GGGGCTGGGG | TCCCTGGACG | CCTACCCGAT | 1860 |
| | CCTCAACCAG | GCACAGGCTC | TGGAGAACCA | CACCTGAGTC | CAGTCCAGAA | AGGAGTGCGG | 1920 |
| | GCCTGACAA | AAGTGTGAGA | GCAACTTGCA | GATGCGGGCA | GGCTTCGTGT | CAGAGCAGCA | 1980 |
| 20 | GCAGAAGCTG | AGCAGGCTCC | AGTACAGCAG | AGACGTCCGG | AAATTGCTCC | TGAGCATCAA | 2040 |
| | CGTGAGGAAC | ACCCGAGACT | CGGAGCGCTC | CGGGGAGGAC | GCCCCACGAG | CGCTGCTCAC | 2100 |
| | CCTGGTGGTG | CCTCCGCGCC | TGCTGTCTGC | CTCAGTGCCG | CCCCCGGGGG | CCTGCCAAGC | 2160 |
| | TAATGAGACC | ATCTTTTGGG | AGCTGGGGAA | CCCCCTCAAA | CGGAACAGAA | GGATGGAGCT | 2220 |
| | GCTCATCGCC | TTTGAGGTCA | TGGGGGTGAC | CCTGCACACA | AGGACCTTTC | AGGTGCAGCT | 2280 |
| 25 | GCAGCTCTCC | ACGTGAGTCA | ACCAGGACAA | CCTGTGGGCC | ATGATCCTCA | CTCTGCTGGT | 2340 |
| | GGACTATACA | CTCCAGACCT | CGCTTAGCAT | GGTAAATCAC | CGCTACAAA | GCTTCTTTGG | 2400 |
| | GGGGAAGTGT | ATGGGTGAGT | CTGGCATGAA | AACTGTGGAG | GATGTAGGAA | GCCCCCTCAA | 2460 |
| | GTATGAATTC | CAGGTGGGGT | CAATGGGGGA | GGGGCTGGTG | GGCTGGGGGA | CCCTGGTCTT | 2520 |
| | AGGTCTGGAG | TGGCCCTACG | AAGTCAGCAA | TGGCAAGTGG | CTGCTGTATC | CCAAGGAGAT | 2580 |
| 30 | CACCGTCCAT | GGCAATGGGT | CCTGGCCCTG | CCGACCACTC | GGAGACCTTA | TCAACCTCTT | 2640 |
| | CAACCTCACT | CTTTCTGACC | CTGGGGACAG | GCCATCATCC | CCACAGCGCA | GGCGCCGACA | 2700 |
| | GCTGGATCCA | GGGGGAGGCC | AGGGCCCCCC | ACCTGTCACT | CTGGCTGCTG | CCAAAAAAGC | 2760 |
| | CAAGTCTGAG | ACTGTGCTGA | CCTGTGCCAC | AGGGCGTGCC | CACCTGTGTG | GGCTAGAGTG | 2820 |
| | CCCCATCCCT | GATGCCCCCG | TTGTCAACAA | CGTGACTGTG | AAGGCACGAG | TGTGGAACAG | 2880 |
| 35 | CACCTTCATC | GAGGATTACA | GAGACTTTGA | CCGAGTCCGG | GTAAATGGCT | GGGCTACCTT | 2940 |
| | ATTCTCTCGA | ACCAGCATCC | CCACCATCAA | CATGGAGAAC | AAGACCACTG | GCTTCTCTGT | 3000 |
| | GGACATTGAC | TGGAGCTGGG | TGGAGGAGCT | GCCGGCCGAA | ATCGAGCTGT | GGCTGGTGTG | 3060 |
| 40 | GGTGCGGTG | GGTGCGGGC | TGCTGCTGCT | GGGGCTGATC | ATCTCTCTGC | TGTGGAAGTG | 3120 |
| | CGGCTTCTTC | AAGCCAGCCG | GCACTCGGCG | CCTGTATGAA | GCTAAGAGGC | AGAAGGGCGA | 3180 |
| | GATGAAGAGC | CAGCCGTCAG | AGACAGAGAG | GCTGACCGAC | GACTACTGAG | GGGGCAGCCC | 3240 |
| | CCCGCCCCCG | GCCCCACTGG | TGTGACTTCT | TTAAGCGGAC | CCGCTATTAT | CAGATCATGC | 3300 |
| | CCAAGTACCA | CGCAGTGGCG | ATCCGGGAGG | AGGAGCGCTA | CCCACCTCCA | GGGAGCACCC | 3360 |
| | TGCCACCAAA | GAAGCACTGG | GTGACCAGCT | GGCAGACTCG | GGACCAATAC | TACTGACGTC | 3420 |
| 45 | CTCCCTGATC | CCACCCCTCG | CTCCCCAGT | GTCCCTTTTC | TTCTTATTTA | TCATAAGTTA | 3480 |
| | TGCCCTCTGAC | AGTCCACAGG | GGCCACCACC | TTTGCTGGGT | AGCAGCAGGC | TCAGGCACAT | 3540 |
| | ACACCTCGTC | AAGAGCATGC | ACATGCTGTC | TGGCCCTGGG | GATCTTCCCA | CAGGAGGGCC | 3600 |
| | AGGCTGTGGG | ACCTTACAA | GCCGAGTGCA | CTGCATTCTT | GTGCCCTAGA | TGCAGTGGG | 3660 |
| | GCCCACTGCT | CGTGGAAGT | GCTGTGTCAT | CACGGATGGT | GCATGGGCTC | GCCGTGTCTC | 3720 |
| 50 | AGCCTCTGCC | AGCGCCAGCG | CCAAACAAG | CCAAAGAGCC | TCCCAACAGA | GCCGGGAGGA | 3780 |
| | AAAGGCCCTT | GCAATGTGGT | GACACCTCCC | CTTTCACACC | TGGATCCATC | TTGAGAGCCA | 3840 |
| | CAGTCACTGG | ATTGACTTTG | CTGTCAAAAC | TACTGACAGG | GAGCAGCCCC | CGGGCGCTG | 3900 |
| | GCTGGTGGGC | CCCCAATTGA | CACCCATGCC | AGAGAGGTGG | GGATCCTGCC | TAAGGTTGTC | 3960 |
| | TACGGGGGCA | CTTGGAGGAC | CTGGCGTGCT | CAGACCCAAC | AGCAAGGAA | CTAGAAAGAA | 4020 |
| 55 | GGACCCAGAA | GGCTGTCTTT | CTGCACTCTC | TGTGAAGCCT | CTCTCCTTGG | CCACAGACTG | 4080 |
| | AACTCGCAGG | GAGTGCAGCA | GGAAAGAAAC | AAGACAGGCA | AACGGCAACG | TAGCCTGGGC | 4140 |
| | TCACTGTGCT | GGGGCATGGC | GGGATCTCTC | ACAGAGAGGA | GGGAGCCAAT | TCTGGACAGA | 4200 |
| | CAGATGTTGG | GAGGATACAG | AGGAGATGCC | ACTTCTCACT | CACCACTACC | AGCCAGCCTC | 4260 |
| | CAGAAGGCC | CAGAGAGACC | CTGCAAGACC | ACGGAGGGAG | CCGACACTTG | AATGTAGTAA | 4320 |
| 60 | TAGGCAGGGC | GCCCTGCCAC | CCCATCCAGC | CAGACCCAGC | CTGAACCATG | CGTCAGGGGC | 4380 |
| | CTAGAGGTGG | AGTTCTTAGC | TATCCTTGCC | TTTCTGTGCC | AGCCTGGCTC | TGCCCTCTCC | 4440 |
| | CCATGGGCTG | TGTCTTAAGG | CCCATTTGAG | AAGCTGAGGC | TAGTTCCAAA | AACTCTCTCT | 4500 |
| | GACCCCTGCC | TGTTGGCAGC | CCACTCCCA | GCCCCAGCCC | CTTCCATGCT | ACTGTAGCAG | 4560 |
| | GGGAATTCCC | TCCCTCTCCT | TGTGCTTCT | TTGTATATAG | GCTTCTCACC | GCGACCAATA | 4620 |
| 65 | AACAGCTCCC | AGTTTGT | | | | | 4637 |
| Seq ID NO: 125 DNA Sequence | | | | | | | |
| Nucleic Acid Accession #: NM_005501.1 | | | | | | | |
| Coding sequence: 74..3274 | | | | | | | |
| 70 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | AGGTGAACAG | GTCTTCACGC | CCAGCTCCGC | CCCCTCACGC | GCTCTCGCCG | GGACCCCGCT | 60 |
| | TCCGCTGGCA | GCCATGGGCC | CCGGCCCCAG | CCGGCCGCCC | CCGCCCCCAC | GCCTGATGCT | 120 |
| | CTGTGCGCTC | GCCTTGTATG | TGGCGGCGCG | CGGCTGCGTC | GTCTCCGCCCT | TCAACCTGGA | 180 |
| | TACCCGATTC | CTGGTAGTGA | AGGAGGCGCG | GAAACCCGGG | AGCCTCTTCG | GCTACTCGGT | 240 |
| 75 | CGCCCTCCAT | CGGCAGACAG | AGCGGCAGCA | GCGTACCTG | CTCTGGCTG | GTGCCCCCGG | 300 |
| | GGAGCTCGCT | GTGCCCGATG | GCTACACCAA | CGGACTGGT | GCTGTGTAAC | TGTGCCCACT | 360 |
| | CACCTGCCAC | AAGGATGACT | GTGAGCGGAT | GAACATCACA | GTGAAAAATG | ACCCTGGCCA | 420 |
| | TCACATTATT | GAGGACATGT | GGCTTGGAGT | GACTGTGGCC | AGCCAGGGCC | CTGCAGGCAG | 480 |
| 80 | AGTTCTGGTG | TGTGCCCAAC | GCTACACCCA | GGTGTGTGG | TCAGGCTCAG | AAGACCAAGC | 540 |
| | GCGCATGGTG | GGCAAGTCT | ACGTGCGAGG | CAATGACCTA | GAGCTGGACT | CCAGTGTATG | 600 |
| | CTGGCAGACC | TACCAACAAC | AGATGTGCAA | TAGCAACACA | GACTACCTGG | AGACGGGCAT | 660 |
| | GTGCCAGCTG | GGCACCAGCG | GTGGCTTAC | CCAGAACACT | GTGTACTTCG | GCGCCCCCGG | 720 |
| | TGCTTACAA | TGAAAGGAA | ACAGCTACAT | GATTGAGCG | AAGGAGTGGG | ACTTATCTGA | 780 |
| | GTATAGTTAG | AAGGACCAAG | AAACCTCTAT | ATTGGGTACA | CGATGCAGGT | | 840 |

| | | | | | | | |
|----|-------------|-------------|------------|------------|------------|------------|------|
| | AGGCAGCTTC | ATCCTGCACC | CCAAAAACAT | CACCATTGTG | ACAGGTGCCC | CACGGCACCG | 900 |
| | ACATATGGGC | GCCTGTCTT | TGCTGAGCCA | GGAGGCAGGC | GGAGACTGCG | GGAGGAGGCA | 960 |
| | GGTGTCTGGAG | GGCTCGCAGG | TGGGCGCCTA | TTTTGGCAGC | GCAATTGCCC | TGGCAGACCT | 1020 |
| 5 | GAACAATGAT | GGGTGGCAGG | ACCTCTGGT | GGGCGCCGCC | TACTACTTCG | AGAGGAAAGA | 1080 |
| | GGAAGTAGGG | GGTGCCATCT | ATGTCTTCAT | GAACCCAGGG | GGAACTCTCT | TCCCTGCTCA | 1140 |
| | CCCTCTACTC | CTTCTTCATG | GCCCCAGTGG | CTCTGCCCTT | GGTTTATCTG | TGGCCAGCAT | 1200 |
| | TGGTGACATC | AACCAGGATG | GATTTGAGGA | TATTGCTGTG | GGAGCTCGT | TTGAAGGCTT | 1260 |
| | GGGCAAGTGT | TACATCTATC | ACAGTAGCTC | TAAGGGGCTC | CTTAGACAGC | CCCAGCAGGT | 1320 |
| 10 | AATCCATGGA | GAGAAGCTGG | GACTGCTGCG | GTTCGCCACC | TTCCGCTATT | CCCTCAGTGG | 1380 |
| | GCAGATGGAT | GTGGATGAGA | ACTTCTACCC | AGACCTTCTA | GTGGGAAGCC | TGTCAGACCA | 1440 |
| | CATTGTGCTG | CTCGGGGCCC | GGCCAGTCA | CAACATCGTC | CACAAGACCT | TGGTGCCAG | 1500 |
| | GCCAGCTGTG | CTGGACCCCT | CACTTTGAC | GGCCACCTCT | TGTGTGCAAG | TGGAGCTGTG | 1560 |
| | CTTTGCTTAC | AACCAGAGTG | CCGGGAACCC | CAACTACAGG | CGAAACATCA | CCCTGGCCTA | 1620 |
| 15 | CACTCTGGAG | GCTGCAGAGG | ACCCCGGCCC | GCCCCGGCTC | CGCTTTGCCG | GCAGTGAGTC | 1680 |
| | CGCTGTCTTC | CGCGCTTCT | TCTCCATGCC | CGAGATGCGC | TGCCAGAAGC | TGGAGCTGCT | 1740 |
| | CCTGATGAGC | AACTCCGTG | ACAACTCCG | CCCCCATCAT | ATCTCCATGA | ACTACTCTTT | 1800 |
| | ACCTTTGGCG | ATGCCCGATG | GCCCCGGCT | GGGGCTGGCG | TCCCTGGAGC | OCTACCGAT | 1860 |
| | CCTCAACAGC | GCACAGGCTC | TGGAGAACCA | CACGTAGGTC | CAGTTCAGAG | AGGAGTGCGG | 1920 |
| 20 | GCCTGACAA | AAGTGTGAGA | GCAACTTGCA | GATGCGGGCA | GCCTTCGTGT | CAGAGCAGCA | 1980 |
| | GCAGAAGCTG | GTGGATGAGC | AGTACAGCAG | AGACGTCCCG | AAATTGCTCC | TGAGCATCAA | 2040 |
| | CGTAGCAAC | ACCCGAGCTC | CGGAGCGCTC | CGGGAGGAGC | GCCCAAGAGG | CGCTGCTCAC | 2100 |
| | CCTGTGTGTG | CTCGCCGCCC | TGCTGCTGTC | CTCAGTGC | CCCCCGGGG | CCTGCCAAGC | 2160 |
| | TAATGAGACC | ATCTTTTGG | AGCTGGGGA | CCCCCTCAA | CGGAACAGAG | GGATGGAGCT | 2220 |
| 25 | GCTCATCGCC | TTTGAGGTCA | TCCGGGTGAC | CCTGCACACA | AGGGACCTTC | AGGTGCAGCT | 2280 |
| | GCAGCTCTCC | ACGCTGAGTC | ACCAGGACAA | CCTGTGGCCC | ATGATCCTCA | CTCTGCTGGT | 2340 |
| | GGACTATACA | CTCCAGACCT | CGCTTAGCAT | GGTAAATCAC | CGGCTACAAA | GCTTCTTTGG | 2400 |
| | GGGACAGATG | ATGGGTGAGT | CTGGCATGAA | AACTGTGGAG | GATGTAGGAA | GCCCCCTCAA | 2460 |
| | GTATGAATTC | CAGGTGGGCC | CAATGGGGGA | GGGGCTGGTG | GGCCTGGGGA | CCCTGCTCCT | 2520 |
| 30 | AGGTCTGGAG | TGGCCCTAGC | AAGTCAGCAA | TGGCAAGTGG | CTGCTGTATC | CCACGGAGAT | 2580 |
| | CACGTCTCAT | GAGCAATGGGT | CCTGGCCCTG | CCGACCACTT | GGAGACCTTA | TCAACCTCT | 2640 |
| | CAACCTCACT | CTTCTGACC | CTGGGGACAG | GCCATCATCC | CCACAGGCA | GGCGCCGACA | 2700 |
| | GCTGGATCCA | GGGGGAGGCG | AGGGCCCCC | ACCTGTCACT | CTGGCTGCTG | CCAAAAAAGC | 2760 |
| | CAAGTCTGAG | ACTGTGCTGA | CCTGTGCCAC | AGGGCGTGCC | CACGTGTGTG | GGCTAGAGTG | 2820 |
| 35 | CCCCATCCCT | GATGCCCCCG | TTGTCAACAA | CGTGACTGTG | AAGGCACGAG | TGTGGAACAG | 2880 |
| | CACCTTCATC | GAGGATTACA | GAGACTTTGA | CCGAGTCCCG | GTAATGGCTG | GGGCTACCTT | 2940 |
| | ATTCTCTCGA | ACCAGCATCC | CCACCATCAA | CATGGAGAAC | AAGACCACTG | GGTCTCTCTG | 3000 |
| | GGACATTGAC | TCCGAGCTGG | TGGAGGAGCT | GCCGGCCGAA | ATCGAGCTGT | GGCTGTGCT | 3060 |
| | GGTGGCCGTG | GGTGACGGGC | TGCTGCTGCT | GGGGCTGATC | ATCCTCTCTG | TGTGGAAGTG | 3120 |
| 40 | TGACTTCTTT | AAGCGGACCC | GCTATTATCA | GATCATGCCC | AAGTACCAAG | CAGTGCGGAT | 3180 |
| | CCGGGAGGAG | GAGCGCTAGC | CACCTCCAGG | GAGCAACCTG | CCCACCAAGA | AGCACTGGGT | 3240 |
| | GACCACTGGG | CAGACTCGGG | ACCAATACTA | CTGACGTCTT | CCCTGATCCC | ACCCCTCTCT | 3300 |
| | CCCCAGTGT | CCCCCTTCTT | CCTATTATC | ATAAGTTATG | CCTCTGACAG | TCCACAGGGG | 3360 |
| | CCACCACCTT | TGGCTGGTAG | CAGCAGGCTC | AGGCACATAC | ACCTCGTCAA | GAGCATGCAC | 3420 |
| 45 | ATGCTGTCTG | GCCTCTGGGA | TCTTCCCA | GGAGGGCCAG | CGCTGTGGAC | CTTACACGCG | 3480 |
| | CGAGTGCACT | GCATTCTGTG | GCCCTAGATG | CACGTGGGGC | CCACTGTCTG | TGGACTGTGC | 3540 |
| | TGGTGTCATC | CGGATGGTGC | ATGGGCTCGC | CGTGTCTCAG | CCTCTGCCAG | CGCCAGCGCC | 3600 |
| | AAACAAGACC | AAAGAGCCTC | CCACCAGAGC | CGGAGGAA | AGGCCCTCGT | AATGTGGTGA | 3660 |
| | CACCTCCCCT | TTACACCTG | GATCCATCTT | GAGAGCCACA | GTCAGTGGAT | TGACTTTGCT | 3720 |
| 50 | GTCAAAACTA | CTGACAGGGA | GCAGCCCCCG | GGCCGCTGGC | TGGTGGGCCC | CCAATTGACA | 3780 |
| | CCCATGCCAG | AGAGGTGGGG | ATCCTGCCTA | AGGTTGTCTA | CGGGGGCACT | TGGAGGACCT | 3840 |
| | GGCGTGCTCA | GACCAACAGC | CAAGGAACT | AGAAAGAAGG | ACCCAGAAGG | CTTGCTTTCC | 3900 |
| | TGCACTCTCG | TGAAGCCTCT | CTCCTTGSCC | ACAGACTGAA | CTCGCAGGGA | GTGCAGCAGG | 3960 |
| | AAGGAACAAA | GACAGGCAAA | CGGCAACGTA | GCCTGGGCTC | ACTGTGCTGG | GGCATGGCGG | 4020 |
| 55 | GATCTCTCC | AGAGAGGAGG | GGACCAATTC | TGGACAGACA | GATGTTGGGA | GGATACAGAG | 4080 |
| | GAGATGCCAC | TTCTCACTCA | CCACTACCA | CCAGCCTCCA | GAAAGGCCCA | GAGAGACCTT | 4140 |
| | GCAAGACCA | GGAGGGAGCC | GACACTTGAA | TGTAGTAATA | GGCAGGGGGC | CCTGCCACCC | 4200 |
| | CATCCAGCCA | GACCCAGCT | GAACCATGCG | TCAGGGGCTT | AGAGGTGGAG | TTCTTAGCTA | 4260 |
| | TCCTTGCTCT | TCTGTGCCAG | CCTGGCTCTG | CCCCCTCCCC | ATGGGCTGTG | TCCTAAGGCC | 4320 |
| 60 | CATTGAGAA | GCTGAGGCTA | GTTCCAAAA | CCTCTCTCTG | CCCCTGCTGA | TTGGCAGCCC | 4380 |
| | ACTCCCCAGC | CCCAAGCCCC | TCCATGGTAC | TGTAGCAGGG | GAATTCCCTC | CCCCCTCTTG | 4440 |
| | TGCTTCTTT | GTATATAGGC | TTCTCACCGC | GACCAATAAA | CAGCTCCAG | TTTGT | 4495 |

Seq ID NO: 126 DNA Sequence

Nucleic Acid Accession #: NM_003786

Coding sequence: 71..4654

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| | CCTCGGCCCC | ATGGACGCCC | TGTGCGGTTT | CGGGGAGCTC | GGCTCCAAGT | TCTGGGACTC | 120 |
| 70 | CAACTGTGCT | GTGCACACAG | AAAACCCGGA | CCTCACTCCC | TGCTTCCAGA | ACTCCCTGCT | 180 |
| | GGCTGGGTG | CCCTGCATCT | ACCTGTGGGT | CGCCCTGCC | TGCTACTTGC | TCTACCTGCG | 240 |
| | GCACCATTTG | CGTGGCTACA | TCATCTCTCT | CCACCTGTCC | AAGCTCAAGA | TGGTCTCTGG | 300 |
| | TGTCCTGTCT | TGCTGGCTGT | CCTGGGCGGA | CCTTTTCTT | TCTTCCATG | GCCTGGTCCA | 360 |
| | TGGCGGGGCC | CCTGCCCTCT | TTTTCTTTGT | CACCCCTTGG | GTGGTGGGGG | TCACCATGCT | 420 |
| 75 | GCTGGCCACC | CTGCTGATAC | AGTATGAGCG | GCTGCAGGGC | GTACAGTCTT | CGGGGGTCTT | 480 |
| | CATTATCTTC | TGGTTCCTGT | GTGTGGTCTG | CGCCATCGTC | CCATTCCGCT | CCAAGATCCT | 540 |
| | TTTAGCCCAAG | GCAGAGGGTG | AGATCTCAGA | CCCCCTCCCG | TTCAACACCT | TCTACATCCA | 600 |
| | CTTTGCCCTG | GTACTCTCTG | CCCTCATCTT | GGCCTGCTTC | AGGGAGAAAC | CTCCATTTTT | 660 |
| | CTCGCAAAAG | AATGTGAGCC | CTAACCCCTA | CCCTGAGACC | AGCGCTGGCT | TTCTCTCCCG | 720 |
| 80 | CCTGTTTTTC | TGGTGGTTCA | CAAAGATGGC | CATCTATGGC | TACCGGCATC | CCCTGGAGGA | 780 |
| | GAAGGACCTC | TGGTCCCTAA | AGGAAGAGGA | CAGATCCAG | ATGGTGGTGC | AGCAGCTGCT | 840 |
| | GGAGGCATGG | AGGAAGCAGG | AAAAGCAGAC | GGCAGCAGAC | AAGGCTTACG | CAGCACCTGG | 900 |
| | GAATAATGCC | TCCGGCGAGG | ACGAGGTGCT | GCTGGGTGCC | CGGCCAGGCG | CCCGGAAGCC | 960 |
| | CTCCTTCTCG | AAGGCCCTGC | TGGCCACCTT | CGGCTCCAGC | TTCTCTATCA | GTGCTGTGCT | 1020 |

| | | | | | | | |
|----|-------------|------------|-------------|------------|-------------|-------------|------|
| | CAAGCTTATC | CAGGACCTGC | TCTCCTTCAT | CAATCCACAG | CTGCTCAGCA | TCCTGATCAG | 1080 |
| | GTTTATCTCC | AACCCCATGG | CCCCCTCTG | GTGGGGCTTC | CTGGTGGCTG | GGCTGATGTT | 1140 |
| | CCTGTGCTCC | ATGATGCAGT | CGCTGATCTT | ACAACACTAT | TACCACTACA | TCCTTGTGAC | 1200 |
| | TGGGGTGAAG | TTTGGTACTG | GGATCATGGG | TGTCTCTAC | AGGAAGGCTC | TGGTTATCAC | 1260 |
| 5 | CAACTCAGTC | AAACGTGGGT | CCACTGTGGG | GGAAATTGTC | AACCTCATGT | CAGTGGATGC | 1320 |
| | CCAGCGCTTC | ATGGACCTTG | CCCCCTTCT | CAATCTGCTG | TGGTCAGCAC | CCCTGCAGAT | 1380 |
| | CATCCTGGCG | ATCTACTTCC | TCTGGCAGAA | CCTAGGTCCC | CTGTCTCTGG | CTGGAGTGGC | 1440 |
| | TTTCATGGTC | TTGTGATTTC | CACTCAACGG | AGCTGTGGCC | GTGAAGATGC | GCGCCTTCCA | 1500 |
| | GGTAAAGCAA | ATGAAATTGA | AGGACTCGCG | CATCAAGCTG | ATGAGTGAGA | TCCTGAACGG | 1560 |
| 10 | CATCAAGGTG | CTGAAGCTGT | ACGCTTGGGA | GGCCAGCTTC | CTGAAGCAGG | TGGAGGGCAT | 1620 |
| | CAGGCAGGGT | GAGCTCCAGC | TGCTGGCGAC | GGCGGCTTAC | CTCCACACCA | CAACCACTT | 1680 |
| | CACCTGGATG | TGCAGCCCTT | TCTTGGTGAC | CCTGATCACC | CTCTGGGTGT | ACGTGTACGT | 1740 |
| | GGACCCAAAC | AATGTGCTGG | ACGCCGAGAA | GGCCTTTGTG | TCTGTCTCCT | TGTTTAAATAT | 1800 |
| | CTTAAGACTT | CCCCTCAACA | TGCTGCCCCA | GTTAATCAGC | AACTGACTCT | AGGCCAGTGT | 1860 |
| 15 | GTCTCTGAAA | CGGATCCAGC | AATTCTCTGAG | CCAAGAGGAA | CTTGACCCCC | AGAGTGTGGA | 1920 |
| | AAGAAAGACC | ATCTCCCCAG | GCTATGCCAT | CACCATACAC | AGTGGCACCT | TCACCTGGGC | 1980 |
| | CCAGGACCTG | CCCCCACTCT | TGCACAGCCT | AGACATCCAG | GTCCCGAAAG | GGGCACCTGT | 2040 |
| | GGCCGTGGTG | GGGCGTGGG | GCTGTGGGAA | GTCTCCCTG | GTGTCTGCC | TGCTGGGAGA | 2100 |
| | GATGGAGAG | CTAGAAGGCA | AAGTGACAT | GAAGGGCTCC | GTGGCTATG | TGCCCCAGCA | 2160 |
| 20 | GGCATGGATC | CAGAACTGCA | CTCTTCAGGA | AAACGTGCTT | TTCCGCAAG | CCCTGAACCC | 2220 |
| | CAAGCGCTAC | CAGCAGACTC | TGGAGGCTGT | TGCTTGTCTA | GCTGACCTGG | AGATGCTGCC | 2280 |
| | TGGTGGGAT | CAGACAGAGA | TGGAGAGAA | GGCATTAAAC | CTGTCTGGGG | GCCAGCGGCA | 2340 |
| | GCGGTCAGT | CTGGCTGAG | CTGTTACAG | TGATGCCGAT | ATTTTCTTGC | TGGATGACCC | 2400 |
| | ACTGTCCCGG | GTGACTCTC | ATGTGGCCAA | GCACATCTT | GACCACTGCA | TCCGGCCAGA | 2460 |
| 25 | AGGCGTGTCT | GCAGGCAAGA | CGCGAGTGCT | GGTGACGCAC | GGCATTAGCT | TCCTGCCCA | 2520 |
| | GACAGACTTC | ATCATTTGTC | TAGCTGATGG | ACAGGTGTCT | GAGATGGGCG | CGTACCCAGC | 2580 |
| | CCTGCTGCAG | CGCAACGGCT | CTTTTGCCAA | CTTCTCTGCG | AACTATGCC | CCGATGAGGA | 2640 |
| | CCAAGGGCAC | CTGGAGGACA | GCTGGACCCG | GTGGAAGGT | GCAGAGGATA | AGGAGGCACT | 2700 |
| | GCTGATTGAA | GACACACTCA | GCAACCAAC | GGATCTGACA | GACAATGATC | CAGTCACTTA | 2760 |
| 30 | TGTGGTCCAG | AAGCAGTTTA | TGAGACAGCT | GAGTGCCCTG | TCCTCAGATG | GGGAGGGACA | 2820 |
| | GGGTCCGCTC | GTACCCCGGA | GGCACCTGGG | TCCATCAGAG | AAGGTGCAGG | TGACAGAGGC | 2880 |
| | GAAGGCAGAT | GGGGCACTGA | CCAGGAGGGA | GAAAGCAGCC | ATTGGCACTG | TGGAGCTCAG | 2940 |
| | TGTGTTCTGG | GATTATGCCA | AGGCCGTGGG | GCTCTGTACC | ACGCTGGCCA | TCGTCTCTCT | 3000 |
| | GTATGTGGGT | CAAACTGCGG | CTGCCATTGG | AGCCAATGTG | TGGCTCAGTG | CCTGGACAAA | 3060 |
| 35 | TGATGCCATG | GCAGACAGTA | GACAGAACA | CACCTCCCTG | AGGCTGGGCG | TCTATGCTCG | 3120 |
| | TTTAGGAATT | CTGCAAGGGT | TCTTGGTGAT | GCTGGCAGCC | ATGGCCATGG | CAGCGGGTGG | 3180 |
| | CATCCAGGCT | GGCCGTGTGT | TGCACCAAGG | ACTGCTGCAC | AACAAGATAC | GCTGCCACCA | 3240 |
| | GTCCCTCTTT | GACACACAC | CATCAGGCCG | CATCCTGAAC | TGCTTCTCCA | AGGACATCTA | 3300 |
| | TGTGTTGAT | GAGGTTCTGG | CCCCGTGCT | CCTCATGCTG | CTCAATTCTT | TCTTCAACGC | 3360 |
| 40 | CATCTCCACT | CTTGTGGTCA | TCATGGCCAG | CACGCCGCTC | TTCATGTGG | TCATCTGCC | 3420 |
| | CCTGGCTGTG | CTCTACACCT | TAGTGACGCG | CTTCTATGCA | GCCACATCAC | GGCAACTGAA | 3480 |
| | GCGGCTGGAA | TCAGTCAGCC | GCTCACCTAT | CTACTCCAC | TTTTCGGAGA | CAGTGACTGG | 3540 |
| | TGCCAGTGTG | ATCCGGGCTT | ACAACCGCAG | CGGGGATTTT | GAGATCATCA | GTGATACTAA | 3600 |
| 45 | GGTGGATGCC | AACCAAGAG | GCTGCTACCC | CTACATCATC | TCCAACCGGT | GGCTGAGCAT | 3660 |
| | CGGAGTGGAG | TTGCTGGGGA | ACTGCGTGGT | GCTCTTTGCT | GCACTATTGT | CGTCTATCGG | 3720 |
| | GAGGAGCAGC | CTGAACCCGG | GGCTGGTGGG | CCTTCTGTGT | TCCTACTCCT | TGCAGGTGAC | 3780 |
| | ATTTGCTCTG | AACTGGATGA | TACGAATGAT | GTGAGATTG | GAATCTAACA | TCGTGGCTGT | 3840 |
| | GGAGAGGGTC | AAGGAGTACT | CCAAGACAGA | GACAGAGGCG | CCCTGGGTGG | TGGAAGGCAG | 3900 |
| 50 | CCGCCCTCCC | GAAGTTGGCG | CCCCACGTGG | GGAGGTGGAG | TTCCGGAATT | ATTCTGTGCG | 3960 |
| | CTACCGGCGG | GGCCTAGACC | TGGTGCTGAG | AGACCTGAGT | CTGCATGTGC | ACGGTGGCGA | 4020 |
| | GAAGGTGGGG | ATCGTGGGCG | GCACTGGGGC | TGGCAAGTCT | TCCATGACCC | TTTGCTCTGT | 4080 |
| | CGCATCTCTG | GAGGCGGCAA | AGGGTGAAT | CCGCTTGTAT | GGCCTCAATG | TGGCAGACAT | 4140 |
| | CGGCTCCCAT | GACCTGGGCT | CTCAGCTGAC | CATCATCCCG | CAGGACCCCA | TCCTGTTCTC | 4200 |
| | GGGGACCCCTG | CGCATGAACC | TGGACCCCTT | CGGCAGCTAC | TCAGAGGAGG | ACATTGGTGG | 4260 |
| 55 | GGCTTTGGAG | TGCTCCACC | TGCACACGTT | TGTGAGCTCC | CAGCCGCGAG | GCTTGGACTT | 4320 |
| | CCAGTGCTCA | GAGGGCGGGG | AGAATCTCAG | CGTGGGCCAG | AGGCAGCTCG | TGTGCCCTGGC | 4380 |
| | CCGAGCCCTG | CTCCGCAAGA | GCGCATCCT | GTTTATAGAC | GAGGCCACAG | CTGCCATCGA | 4440 |
| | CCTGGAGACT | GACAACCTCA | TCCAGGCTAC | CATCCGACCC | CAGTTTGATA | CCTGCACTGT | 4500 |
| | CCTGACCATC | GCACACCGGC | TTAACACTAT | CATGGACTAC | ACCAGGGTCC | TGGTCTGGA | 4560 |
| 60 | CAAAGGAGTA | GTAGCTGAAT | TTGATTCTCC | AGCCAACCTC | ATTGCAGCTA | GAGGCATCTT | 4620 |
| | CTACGGGATG | GCCAGAGATG | CTGGACTTGC | CTAAAATATA | TTCTGAGAT | TTCTCTCTGG | 4680 |
| | CCTTCTCTGG | TTTTCATCAG | GAAGGAAATG | ACACCAATA | TGTCCGCAGA | ATGGACTTGA | 4740 |
| | TAGCAAAAC | TGGGGGCACC | TTAAGATTTT | GCACCTGTAA | AGTGCCCTTAC | AGGGTAACTG | 4800 |
| | TGCTGAATGC | TTTAGATGAG | GAATGATCC | CCAAGTGGTG | AATGACACGC | CTAAGGTCAC | 4860 |
| 65 | AGCTAGTTTG | AGCCAGTTAG | ACTAGTCCCC | CGGTCTCCCG | ATTCCCAACT | GAGTGTATT | 4920 |
| | TGCACACTGC | ACTGTTTCA | AATAACGATT | TTATGAAATG | ACCTCTGTCC | TCCCTCTGAT | 4980 |
| | TTTTCATATT | TTCTTAAAGT | TTGTTTCTG | TTTTTAAATA | AAAAGCTTTT | TCCTCTGGA | 5040 |
| | ACAGAAGACA | GCTGCTGGGT | CAGGCCACCC | CTAGGAACCT | AGTCTGTAC | TCTGGGGTGC | 5100 |
| | TGCTGAATC | CATTAAAAAT | GGGAGTACTG | ATGAAATAAA | ACTACATGTT | CAAGAGTAAA | 5160 |
| 70 | AAAAAAAAAA | AAAAAA | | | | | 5176 |

Seq ID NO: 127 DNA Sequence

Nucleic Acid Accession #: NM_002701.1

Coding sequence: 102..899

| | | | | | | | |
|----|------------|------------|------------|------------|------------|------------|-----|
| 75 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| | GTAGTCTTT | GTTACATGCA | TGAGTCAGTG | AACAGGGAAT | GGGTGAATGA | CATTGTGGG | 60 |
| | TAGGTTATTT | CTAGAAGTTA | GGTGGGCGAG | TGGGAAGGCA | GATGCATCTC | TACAGACTAT | 120 |
| | TCCTTGGGGC | CACACGTAGG | TTCTTGAATC | CCGAATGGAA | AGGGGAGATT | GATAACTGGT | 180 |
| 80 | GTGTTTATGT | TCTTACAAGT | CTTCTGGCCT | TTAAATCCCA | GTCCAGGAC | ATCAAAGCTC | 240 |
| | TGCAGAAAGA | ACTCGAGCAA | TTTGCCAAGC | TCCTGAAGCA | GAAGAGGATC | ACCCTGGGAT | 300 |
| | ATACACAGGC | CGATGTGGGG | CTCACCCCTG | GGGTTCTATT | TGGGAAGGTA | TTACGCCAAA | 360 |
| | CGACCATCTG | CGCTTTTGG | GCTCTGCAGC | TTAGCTTCAA | GAAATGTGT | AAGCTGCGG | 420 |
| | CCTTGCTGCA | GAAGTGGGTG | GAGGAAGCTG | ACAACAATGA | AAATCTTCAG | GAGATATGCA | 480 |

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AAGCAGAAAC CCTCGTGACG GCCCGAAAGA GAAAGCGAAC CAGTATCGAG AACCGAGTGA 540
GAGGCAACCT GGAGAAATTG TTCTGTCAGT GCCCGAAACC CACACTGCGAG CAGATCAGCC 600
ACATCGCCCA GCAGCTTGGG CTGAGGAAGG ATGTGTCGCG AGTGTGGTTC TGTAAACCGGC 660
GCCAGAAGGG CAAGCGATCA AGCAGCGACT ATGCACAACG AGAGGATTTT GAGGCTGCTG 720
GGTCTCCTTT CTAGGGGGGA CCAGTGTCTT TTCTCTGGC CCCAGGGCCC CATTTTGGTG 780
CCCCAGGCTA TGGGAGCCCT CACTTCACTG CACTGTACTC CTGGTCCCTT TTCCCTGAGG 840
GGGAAGCCCT TCCCTCTGTC TCTGTACCA CTCTGGGCTC TCCTTGCAT TCAAACTGAG 900
GTGCTCTGCT GCCCTTCTAG GAATGGGGGA CAGGGGGAGG GGAGGAGCTA GGGAAAGAAA 960
ACCTGGAGTT TGTGCCAGGG TTTTGGATT AAGTTCTTCA TTCACTAAGG AAGGAATTGG 1020
GAACACAAAG GGTGGGGCCA GGGGAGTTTG GGGCAACTGG TTGGAGGGAA GGTGAAGTTC 1080
AATGATGCTC TTGATTTTAA TCCACATCA TGTATCACTT TTTTCTTAAA TAAAGAAGCT 1140
TGGGACACAG TAGATAGA 1158

Seq ID NO: 128 DNA Sequence

Nucleic Acid Accession #: Eos sequence

1 11 21 31 41 51
| | | | |
AAATAAGTAT ATCTGTCAAA AATCATATTT TTATGAGATG TGTCAATACT GGTCTCGTGT 60
CATTTAGGCT ACTTGGAAAA AAGATAAAAA AAATCCTGTT TGGCTCCAAA AAGGAAAAAT 120
CAGCCCCCTC TGCGATGAGT GGAGCTGCAA CCCTTTAGAA CTGATAATCA CAAACCCCTC 180
AGAAACCAAG TGAATGAAAG GAAATATGT AACATTAGGC ATTGATGGAA GAGGACTAGA 240
TCTAGTGTGA AGCATCTTAA TAAAAGGAGG GGTTCAAAGA TGCTCTCCAG AACCACTATT 300
TCAGACTTCC TATGATAAAC TAAATGTGCC AGTACCAGAG ACTCCAGGAA AAACCAAGAA 360
TTTGTTTTGG CAATTAGCCG AGCATGTAGT CCAGTCTTTA AATGTCAATT CATGTTATGT 420
TTGTGGAAAA ACTGTAGTAA GAGTTTCCAT AAGAAGAACT TCCATAAGAA GCCCAAGAAT 480
TAGTTCCCTAC AGACCCAGTT CCTGATGAAT TCCCAGCCCA AAAGAACCAC CCTGACAAAT 540
TTTAGGTTCT AAAAGTCTGA ATTATTAGAC AGTATTGCAT AGCTAGAGAA GGAAAAGGAT 600
TCACTCATCC TATAAGGCGG CTAGTTGTTC TTAGGCAAAA GCTGTATAAT GGTACCACAA 660
ATACAGTTAC ATGGTGGAGT TCCAATTACA CAGAAAGAGA TCCATTCACT CAATTTCCAA 720
GGTTCGACAG TGCTTGGGCC CACCCAGAAT TCCACCGGGA CTGGACGGCC CCCACCAGGT 780
TATACCTGAT ATGTGGGCAC AGAGCTTATG CTAAGCTGCC TGATCAGTGG ACAGGTAGCT 840
GTGTAATTGA CACCATTAAG CCATCTTTCT TCTTACTGCC CATAAAAGCA GGGGAACCTC 900
TGGGCTTCCC AGTCTATGCT TCCCGCAAAA AACAAAGCAT AGCCATAGGT GATTGGAAAG 960
ATGATAAATG GCCCCCTGAA AGAATCATA AATACTATGG ACCCACCCTT TGGGCACAAG 1020
ATGACTCTTG GGGATATCGG ACCCCCATCT ACATGCTCAA CGGAATCATA CGGTTACAAG 1080
CTGTTTTTGA AATTATTACT AATACAACCG GTCAAGCCTT GACTGTTCTT GCCCAGCAGG 1140
AGACTCTGAT GAGAAATGCT ATCTATCAAA ATAGACTAGC TCTTGACTAC TTGCTAGCAG 1200
CTGAAAGAGA AGTTTGTGAA AAATTTAACT TTACTAATTG TTTTCTACAC ACAGGTGATC 1260
AAGGGCAAGT AGTTAAAAAT ATAGTTAAAG ATATAACAAA ACTGGCAGAT GTACCCATAC 1320
AAGTGTGGCA CGGACTCAAT CCAGGATCCA TGTTTAAAAA TTAGTTCCCA GCAATAGGAA 1380
GATTTAAAAA TCTTATAATA GGAGTTATAA TAGTAATAAA AACCTGCTTA CTGCTCCCTT 1440
GTTTACTACT TTTACTTCTA CAAATGATAA AAAGCTTCAT TGCTACCTTA GTTCACCAAA 1500
ATGCTTCAGC ACAGGTGTAC TATATGAATC ACTATCAATC TATTGCACAA AAAGACATAA 1560
GTAGCAAAAA TAAGAGTGAG AACTCCCACT AATAAAAAAGT GAGAGTCTCA AAGGGGGAAA 1620
ATGAGGAAAG AGAGCGACCC TCTCATATTG TCTATATTG TTTTATACTC AGTACCTGTT 1680
TTAAGGAAAA AACAAACAGG AAGTAAAAATC AAAGACAGGC AGCCACGCGC CAGGCCCAAA 1740
ACCAGGCTTG GGCTGCGCTG GCCTAAACCC AGTAGTTAAA AATCAACTCA TAACCTTAGAA 1800
ACTGATGTGA TTCAATAGAT CCAGACATTT TATAGAAGAA CATTTGTGTA CTCCTGCCC 1860
TGTTCTGTTT CTCTCTGACT GCCCGTGATG GCAGCCCTTG TCACGTACCG CCTGCTTGCT 1920
CAAAATCAATC ACGACCTTCT CATGTGAAAT GTTTAGTGTG GTGAGCCCTT AAAAGGGACA 1980
GAAATCGTGC ACTCGGGGAG CTCAGATTTT AAGGCAGTAG TTTGCTGATG CTCCTCAGCTG 2040
AATAAAGCCC TTCCTTCTAC AAAAAAAA 2068

Seq ID NO: 129 DNA Sequence

Nucleic Acid Accession #: Eos sequence

1 11 21 31 41 51
| | | | |
TTTTTTTTTT TTTTTTTTTT TTTCTGTAA CACTTTATGT TTATTAGCAG TCTGGTTTTA 60
GCCTAAAGT CACAACTTTT TTGGAAGTTT TCCCTAACCA GTCACCCAG ATTAGGCACA 120
TGCTCTAGG TTAGAGTCCCT GTACCCAGAG ATTGATCACA CTGATTGTG ATTGTTAGAC 180
AACTGTCTCA TTCAATAGAC TGTCAAGTTC TGGAGGGCAG AGATCTTGTC TCTGTTGTTT 240
CTCTTTTAAAT CCCAGTGTG TAGCATCTCA GAGACACTTG TTGAATGAAT TCATTAAACGA 300
CTGGCTGAAT AATGAGCAAT TCATGAAAAA ACACTTTATA TTCACAGGTT TTGGTAAGA 360
CAGTAGCTCC CTTAAACAC ACACACACTC TCTATGGTAT GTCACAGAAC TACAGTCTAC 420
ACTCAGTGCA AAGGGTTTCA AAATCCAGTA GGAAGGACAA ATATTGTCCC TCTTCTGTCC 480
TTGGAGAAGA TATTGTGCAA GTGTGGAGTT CTCTGGGAGA AATATTCTTT TTTTCTTTT 540
GAGATGGAGT TCACTCTTG TTGCCAGGC TGAGTGCAA TGGCACGATC TTAGTCACT 600
GCAACCTCTG CCTCATGGT TGAAGCAAT CAAGACCTGC CTTAGCCTCC TGGGTAGCTG 660
GAATTACAAG CACCCACCAC CACATCCAGC TAATTTTTTG TAATTTCACT AGAGATGGG 720
TTTCACTATA TTGGCCAGGC TGGTCTCGAA CTCTGACTT CAGACAATCC ACCCGCTCA 780
ATCTCCCAAA GTGCT 795

Seq ID NO: 130 DNA Sequence

Nucleic Acid Accession #: NM_005458.1

Coding sequence: 461..3286

1 11 21 31 41 51
| | | | |
GCCGCCCTCG AGCAGCCTCG CCTTGGCCTC CCGCGTTTCC TGCGGTCCGC CCTCCCCCGG 60
CCGAGCTCCA GGGGCTCGCG CTTAGCAGCT CCGCGCGGGA GAGCGGTTCA GAGCGCGCAC 120
GGGGCGCGGC GGAAGCGCGG CGGTGCGGGG CCGCGCGGCT GGAGAGAGGC GCGCGCGGAG 180
ACGCGGCCCC CCTCTCCGCG GTTGTCTGCG TTGCTCCCGC CCTCCCGCAC TCCGCTCGCT 240
CCCAACCCCTT CCGGCGGTGA TTGATCCGTC ACGGCGCGCG CCGCTGCGCG CGCCGCGGCG 300
GCGGCGGTTT TGAGCCGAGC CGGAACCTTA GCCCGAGACG GAGCGCGGGC CCGGCGCGGC 360
GCCATTGCGC GGGGCGCGCG GGAAGACCTT GCGCGGGGCG GCGGCGCGCG GCCAGGCCAT 420

| | | | | | | | |
|----|------------|-------------|------------|------------|------------|-------------|------|
| | GCGGGCCGAG | TGAGCCGGGG | CCGCGAGCCC | GCGGCGCGGC | ATGGCTTCCC | CGCGAGCTC | 480 |
| | CGGGCAGCCC | GGGCGCGCGC | CGCCGCGCCC | ACGCGCGCCC | GCGCGCTGCG | TACTGCTACT | 540 |
| | GCTGTCGCCG | CTGCTGCTGC | CTCTGGCGCC | CGGGCGCTGG | GGCTGGGCGC | GGGGGCGCCC | 600 |
| | CGGGCGCGCG | CCGAGCAGCC | CGCGGCTCTC | CATCATGGGC | CTCATGCGCG | TCACCAAGGA | 660 |
| 5 | GGTGGCCAAG | GGCAGCATCG | GGCGCGGTGT | GCTCCCGGCC | GTGGAACCTG | CCATCGAGCA | 720 |
| | GATCCGCAAC | GAGTCACTCC | TGCGCCCTTA | CTTCTCTGAC | ATAAAATACG | GGCCTAACCA | 780 |
| | GTGCGACAA | GCAAAAGGGT | TGAAAGCCTT | CTACGATGCA | ATGGAATACG | GGCCTAACCA | 840 |
| | CTTGATGGTG | TTTGGAGGGG | TCTGTCCATC | CGTCACATCC | ATCATTTGCG | AGTCCCTCCA | 900 |
| | AGGCTGGAAT | CTGGTGACGC | TTTCTTTTGC | TGCAACCAAG | CCTGTTCTAG | CCGATAAGAA | 960 |
| 10 | AAAAATACCT | TATTTCTTTC | GGACCGTCCC | ATCAGACAAT | GCGGTGAATC | CAGCCATTCT | 1020 |
| | GAAGTTGCTC | AAGCACTACC | AGTGAAGGCG | CGTGGGCACG | CGTGCCCAAG | ACGTTCCAGG | 1080 |
| | GTTCCTGAG | GTGCGGAATG | ACCTGACTGG | AGTTCTGTAT | GGCGAGGACA | TTGAGATTTT | 1140 |
| | AGACACCGAG | AGCTTCTCCA | ACGATCCCTG | TACCACTGTC | AAAAAGCTGA | AGGGGAATGA | 1200 |
| | TGTGCGGATC | ATCCTTGCGC | AGTTTGACCA | GAATATGGCA | GCAAAAGTGT | TCTGTTGTGC | 1260 |
| 15 | ATACGAGGAG | AACATGTATG | GTAGTAAATA | TCAGTGGATC | ATTCGGGGCT | GGTACGAGCC | 1320 |
| | TTCTTGGTGG | GAGCAGGTGC | ACACGGAAGC | CAACTCATCC | GGATTTGCGG | CCCTGAGCT | 1380 |
| | GCTTGTCTGC | ATGGAGGGCT | ACATTGGCGT | GGATTTGCGG | CCCTGAGCT | CCAAGCAGAT | 1440 |
| | CAAGACCATC | TCAGGAAAGA | CTCCACAGCA | GTATGAGAGA | GAGTACAACA | ACAAGCGGTC | 1500 |
| | AGGCGTGGGG | CCGACCAAGT | TCCACGGGTA | CGCCTACGAT | GGCATCTGGG | TCATCGCCAA | 1560 |
| 20 | GACACTGCAG | AGGGCCATGG | AGACACTGCA | TGCCAGCAGC | CGGCACCGAG | GGATCCAGGA | 1620 |
| | CTTCAACTAC | ACGACACACA | CGCTGGGCGG | GATCATCTCT | AATGCCATGA | ACGAGACCAA | 1680 |
| | CTTCTTGGGG | GTACGCGGTC | AAGTTGTATT | CCGGAATGGG | GAGAGAATGG | GGACCATTA | 1740 |
| | ATTTACTCAA | TTTCAAGACA | GCAGGGAGGT | GAAGGTGGGA | GAGTACAACG | CTGTGGCCGA | 1800 |
| | CACACTGGAG | ATCATCAATG | ACACCATCAG | GTTCGAAGGA | TCCGAACCAA | CAAAAGACAA | 1860 |
| 25 | GACCATCATC | TGGAGCAGC | TGCGGAAGAT | CTCCCTACTT | CTCTACAGCA | TCCTCTCTGC | 1920 |
| | CCTCACCATC | CTCGGGATGA | TCATGGCCAG | TGCTTTTCTC | TTCTTCAACA | TCAAGAACCG | 1980 |
| | GAATCAGAAG | CTCATAAAGA | TGTCGAGTTC | ATACATGAAC | AACCTTATCA | TCCTTGGAGG | 2040 |
| | GATGCTCTCC | TATGCTTCCA | TATTTCTCTT | TGGCCTTGAT | GGATCCTTTG | TCTCTGAAAA | 2100 |
| | GACCTTTGAA | ACACITTTGA | CGCTCAGGAC | CTGGATTCTC | ACCGTGGGCT | ACACGACCGC | 2160 |
| 30 | TTTGGGGGCC | ATGTTTGCAA | AGACCTGGAG | AGTCCACGCC | ATCTTCAAAA | ATGTGAAAAAT | 2220 |
| | GAAGAAGAAG | ATCATCAAGG | ACCAGAAACT | GCTTGTGATC | GTGGGGGGCA | TGCTGCTGAT | 2280 |
| | CGACCTGTGT | ATCCTGATCT | GCTGCGAGCG | TGTGGACCCC | CTGCGAAGGA | CAGTGGAGAA | 2340 |
| | GTACAGATGC | GAGCGGAGCC | CAGCAGGACG | GGATATCTCC | ATCCGCGCTC | TCCTGGAGCA | 2400 |
| | CTGTGAGTA | ACCCATATGA | CCATCTGGCT | TGGCATCGTC | TATGCTTACA | AGGGACTTCT | 2460 |
| 35 | CATGTTGTTT | GGTGTGTTCT | TAGCTTGGGA | GACCGCAAC | GTACGATCC | CCGCACTCAA | 2520 |
| | CGACAGCAAG | TACATCGGGA | TGAGTGTCTA | CAACGTGGGG | ATCATGTGCA | TCATCGGGGC | 2580 |
| | CGCTGTCTCC | TTCTTGACCC | GGGACCAAGC | CAATGTGCGC | TTCTGCATCG | TGGCTCTGGT | 2640 |
| | CATCATCTTC | TGCAGCAGCA | TCACCTCTGT | CCTGGTATTC | GTGCGGAAGC | TCATCACCTC | 2700 |
| | GAGAACCAAC | CCAGATGCAG | CAACGCAAGG | CAGGCGGATC | CAGTTCACTC | AGAATCAGAA | 2760 |
| 40 | GAAAGAAGAT | TCTAAACGCT | CCACCTCGGT | CACCACTGTC | AACCAAGCCA | GCACATCCCG | 2820 |
| | CCTGGAGGGC | CTACAGTCAG | AAAACCATCG | CCTGCGAATG | AAGATCAGAG | AGCTGGATAA | 2880 |
| | AGACTTGGAA | GAGGTCAACCA | TGCAGCTGCA | GGACACACCA | GAAAGACCA | CCTACATTAA | 2940 |
| | ACAGAACCA | TACCAAGAGC | TCAATGACAT | CCTCAACCTG | GGAACTTCA | CTGAGAGCAC | 3000 |
| | AGATGGAGGA | AAGGCCATTT | TAAAAAATCA | CCTCGATCAA | AATCCCCAGC | TACAGTGGAA | 3060 |
| 45 | CACAACAGAG | CCCTCTCGAA | CATGCAAAAG | TCCTATAGAA | GATATAAACT | CTCCAGAAAC | 3120 |
| | CATCCAGCGT | CGGCTGTCCC | TCCAGCTCCC | CATCCTCCAC | CACGCTTACC | TCCCATCCAT | 3180 |
| | CGGAGGCGTG | GACGCCAGCT | GTGTCAGCCC | CTGCGTCAGC | CCCAACGCCA | GCCCCCGCCA | 3240 |
| | CAGACATGTG | CCACCTCTCT | TCCGAGTCAT | GGTCTCGGGC | CTGTAAGGGT | GGGAGGCGCT | 3300 |
| | CGCCCGGGGG | CTCCCGCGTG | ACAGAACCA | ACTGGGCAGA | GGGCTCTGCT | GCAGAAACAC | 3360 |
| 50 | TGTGCGCTCT | GGCTGCGGAG | AAGCTGGGCA | CCATGGCTGG | CCTCTCAGGA | CCACTCGGAT | 3420 |
| | GGCACTCAGG | TGGACAGGAC | GGGGCAGGGG | GAGACTTGGC | ACCTGACCTC | GAGCCTTATT | 3480 |
| | TGTGAAGTCC | TTATTTCTTC | ACAAAGAAAG | GGAAACGAAA | TGGGACGTCT | TCCTTAACAT | 3540 |
| | CTGCAAAACA | GGAGGCGCTG | GGATATCAAA | CTTGCAAAAA | AAAAAAGAAA | AGAGTGGCTC | 3600 |
| | CAAAAGAACT | AGACAAGGAG | AGAGGCACTA | GAACTCCAGC | TGGAAGTCA | AGAGTGGCTC | 3660 |
| 55 | GAGCAGCCTT | GGGAAGAGGC | AAGGAGCTTC | TGAAGAAACT | GCCTCTGCAC | ACACATCACT | 3720 |
| | GGCTGTGACC | CCTCAGGCTA | GCCTTCTCCC | ACTCTGGGGG | AGGAGGTGGG | AAGGGCCACC | 3780 |
| | AGGCCCCCAG | CTGCGAGGCC | AGCTGACCCC | AGCCTTCTCT | GAACAGGGAG | TCTGCAGGAG | 3840 |
| | CGCAGACAGG | CACAGCCCTG | GAGCAGGCGG | GCCGAGGGCT | GCGGCACTCG | AGCAGGCTGA | 3900 |
| | CTTACATGCT | CCACATGGGA | CCTGTGTGAC | CCAATGAGAT | GTGTTTACT | CTGGTAAATG | 3960 |
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| | CCTTGGGATC | ACTGGGGTGA | TCAGTCAGCA | GATTGATTCT | CATTATAAG | ATCATTCTCT | 4440 |
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| | TTGTTTGTCTC | TTATTTTCAA | CCAGGGGAGCT | ATCTGGCACC | TTTTGTGCTC | CTGGCTTTTT | 4680 |
| | TCAATCATAG | CACATATTGCA | TCTCTAGCT | ATTTCTTTTG | CCCAGCAGGG | TAATATTGAG | 4740 |
| | TCCCATTGCA | AGTATGGACA | AGGCCTCTGG | TTCTCTCTAC | CACCCACCTT | TTAGGCCATA | 4800 |
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| 20 | GTGCTGCGCG | TGCTCTCTCC | TCTCTCGCGG | CCGCGCGCGC | CGCGCGCGCC | TCTCTCGGCT | 180 |
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 35 ACTGCTCGTG GCGCGGGGCG TGGCGGCGCG TGCGCTCTTG CTGGTCCAGC TGCGCGCGCG 1560
 TGGCACTCC CAGGATGCTG GGTCTGCTT GCTGGCTGGG ACCCGGAGC GGTCACTGCA 1620
 CGCACTCCCG GATGCACTCA ACAACCTAAG GACGAGAGG GGTTCGGGG ATGGTCCGAG 1680
 CTGTCCTGTA GATTGGAATC GCCCTGAAGA TGTAACCCCT CAAGGGATTG ATGTGATATC 1740
 TGCTCTCTCC ATCTACGCTG GGGAGGTAGC GACGCCCTT TCCCCCGCG TACACACTGG 1800
 40 GCGCGCTGGG CAGAGGCAAC ACTGCTTTT TCCCTACCTT TCCTCGATTG TGTCCGTGAA 1860
 ATGAATTGGG TAGAGTCTCT GGAAGGTTT AAGCCCATTT TCAGTTCTAA CTTACTTTCA 1920

Seq ID NO: 134 DNA Sequence
 Nucleic Acid Accession #: FGENESH prediction
 Coding sequence: 1..411

1 11 21 31 41 51
 | | | | |
 45 ATGTGTCAGG CTTTCTCTG GGTGCTAGGG ACACTGTGGC TTCTCAAAAA TGCCCGTTGT 60
 CTGCAGCCAT ACCCACTGTA ACATGCCCAA TCTTGCTGTA TCTCAGAAGC TAAAGCAGGT 120
 CAGGCCCATG TACCCTTGG ATGGGTGAAG TGGCCCTTGC ACTTGAGGAG CTCACGTCC 180
 50 AAAAGGTTGG AAAGGAAGTA CCCAGCCTA TTGAATGGGG AAATTGAAGC ACAGATATGT 240
 AAAACATCTT CTCTAGAGTT ACCCAGCTGT GATCTGGTGA CAGCTGATGG TTCCACTGAA 300
 GTAACTATCT CGGAAATCTC CCTGCTGTT GGATTCCATA TCTGTCAACA GCAGGACTCT 360
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Seq ID NO: 135 DNA Sequence
 Nucleic Acid Accession #: NM_024812.1
 Coding sequence: 184..621

1 11 21 31 41 51
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 60 GAGAGGGCCC GGACTAGGGG CGGCGGGCAC CGCAGGAGCT CGCGCGGCT GCAGCGCGGG 60
 CGGGAGCGGG GACGCGATGT GCGCGCGCGC GCCTCCTTGC GGGCGCGGGC TGCGCTCCG 120
 GGGCTGAGCC GCGCGCAGAG CCGACAGCCG AGCAGCGGCT GGGCGCTCCC GCGCGCAGG 180
 AGGATGGGCT GCGCGGGGAG CCGGGCGGAT GCCATCGAGC CCCGCTACTA CGAGAGCTGG 240
 65 ACCCGGGAGA CAGAATCCAC CTGGCTCACC TACCCGACT CGGACGCGCC GCCCAGCGCC 300
 GCGCGCCCGG ACAGCGGCCG CGAAGCGGGC GGCCTGCACT CGGCGATGCT GGAAGATGGA 360
 CTGCCCTCCA ATGGTGTGCC CCGATCTACA GCCCAGGTG GAATACCCAA CCCAGAGAAG 420
 AAGACGAATC GTGAGACCCA GTGCCCAAAT CCCCAGAGCC TCAGCTCAGG CCCTCTGACC 480
 CAGAAACAGA ATGGCCTTCA GACCACAGAG GCTAAAAGAG ATGCTAAGAG AATGCCTGCA 540
 70 AAAGAAGTCA CCATTAATGT AACAGATAGC ATCCAACAGA TGGACAGAAG TCGAAGAATC 600
 ACAAGAATC GTGTCAACTA GCAGAGAGTC CAAGCAGAAG GGCAGATGGA CTTCTTCAGT 660
 GTCCTTCAGC GCACTGGATC CCATCAAAGA ACCTTGAAGA AGTGGCTGCC CCTTGCTGGA 720
 CCTGAATTTCT ACTGAGTCCC TGGCAAGACC GTCTTACCTG GCACGAAATC GCTGCTGAT 780
 TTGTGGGAC CTTCTGAGCC TTCTACTTAT CATGTAAATG TATTGGCACA GTGCTTACAT 840
 75 ATGTTAATAA ACTGCAATGT TGCAGTTCAG TTGTCTCTT TGCAACTCCT GTAATACGGT 900
 CTGGTGTAAA AGTAGTGAGT TAAAGCTACA GGTGAGTTTA TGAACAGAA AAGTAGGAAT 960
 GCATTTTCTG GGTGAAAGAG TCACACCTTA GTGCTATAAC TCTCCTGCCC ATGATAGTGT 1020
 ATTCTGTTTC AGGCAAGCTT ATTCTTTCCT TCCTTCATT TAAATATTGT CATTACAAAT 1080
 CTTACCAAGT TCACTTAAAA GCTGGCTTTC ATCCAACCTC AAACCCACAT ATTGAAAAAA 1140
 80 TCAAGGTACA CGAAACTCC TTGTTATCCT TGTTCCTTA GCTTGGTATG AGACAGATCG 1200
 GATCCAGTTT CCCATGCACC AACCCACTGC CCATGGCATG TCTTTGGGAG GTGCTGTGTA 1260
 AGCAGTCATA CCTGCTCCTC ATCTGCTTGG AAGTCTCTCC TATTCCAGTG TCCATGTTGG 1320
 CCTCCAGTCT TTAATGTCAAC CATGCTTGTG GCCAATGCAT CCAATAAAGG ATACCCCTCA 1380
 GGGCTCAGCT AGACATTGCA ATTTTGCTA GCTTTCAGT TCCCTTTGCT TGTCTCTGT 1440
 ACTGCTTCC CTCTCTACCG GGGTCACTTG CAATTGTATA TCAAGATTG AACACTGCGT 1500

| | | |
|----|---|------|
| 5 | AGGAGAGGGA GATGATCCAG AGACATGTGG CAGCAGGCAT GGCTTCCCCT TGGCCTCTCT | 1560 |
| | GTACACTGCC CCAGGACTGT CATTTTGGCA TCTGCAAGG AATCACTTTA GAAAGCCAGC | 1620 |
| | ACCTGGTTGA TGTGTATTCA TACTGACATT AGATTGATGT GCACATGATT AGAAATGAGG | 1680 |
| | TAGCTGACAC AGAAAAAGGA TGTTTTGATA GGAATAATTT TCTAGTATGT CTTGAAACAT | 1740 |
| | GTTTCATCTGG AAGTATTTTC TCCAAAGTA ATGTAGCATG ATTTTTCAGG GATTGTAAAC | 1800 |
| | ATGCGTGGGA TTGGGAAAGA TAGGACTAAA GTTGTGCCAA ACTATATCAA TAAATTTCCAT | 1860 |
| | GTTTAGCAGA AATAGGCAGC CTATTGGTGT TATGTTTATG TAACATAGTC CAGAGAACTG | 1920 |
| | ACATGCAGGT CAAAGTCAG ATACGCAACC TCCTTATCTG CTAACCTGTG TATTTCTCAA | 1980 |
| | ACACAAGTGG GTAGTGTCTAT TTTTCTTCC TTCCTTCCAT TGGCAGATTG TATATTTATT | 2040 |
| 10 | CACAAAACAT TAAATGTCCA TCCTGTGCCA GGTACTATGC AGATGTTGAG GGATTGGGG | 2100 |
| | TCTGGTTAGT CGTGACTATC TATCCTGAAT CTAACAGTGA CTTCAATACT AGGAGACTGA | 2160 |
| | ATTAGACCCCT TAAGGTATAG TGTGTGTTGC AAATCACTCT GCAATGGAAA CTTTATATTT | 2220 |
| | CAGGTAGGT TGTGTCTTA AACTAGGTGT TCTAATCAAT GTACAAGACT TTACCATACA | 2280 |
| | CGCAACTATA GTTTTCTTAA ACCTTCATCA TTTTGTGATT CTTTGAGAAA GGGCTTTTAG | 2340 |
| 15 | GAACCTTATG TTCTAAAAA TGTTTTAAAC AATAATAAGA TAAAAAGAAA ACCTGTGATT | 2400 |
| | CATATGTCCC CACTGGCATT ACTCAGCAGG AGCCCCAGC TGCCAAAGGT TGGCAGTGAT | 2460 |
| | CCTGCAAGTT CAAGGCTCTT TTCTCCCTGG GGATGTGCTT TGTGGCTTCT CTTTACAGCT | 2520 |
| | TGTGTTCTGC ATCAGTTTCA TGTGTGATGT TGTGGAAT TTATCACCTT AAGAAAGTGT | 2580 |
| 20 | CTCTGTTTAA TATAGAAACA CTTTCTCACT TACAGGGGAG AAGGAAATGC AGGGCAGATG | 2640 |
| | ATCTGGCCCT CCCAGAAACA ATCTGGATT CACGGAGACA GCAACCAGAA GTTAAACCTA | 2700 |
| | GTGACTAAAA ATGCATCTGG CTACTTTTC ATGTATGTAT GAGACAGAAA CTAATCCTTA | 2760 |
| | ATATCCTATT AGGATACCAC TTTTCATTGC AAGTTTGTG TCAATAAAGT CATTAAATTT | 2820 |
| | AAACAT | 2826 |
| 25 | Seq ID NO: 136 DNA Sequence Nucleic Acid Accession #: XM_040550.1 Coding sequence: 82..4158 | |
| | 1 11 21 31 41 51 | |
| 30 | CCTTGGTTTC CGTTGCAGAT TCCCACAAC CTATGCTGTG TGTGTCAGGC TGGTCTGAA | 60 |
| | CCCAGATCTC TGGCTGAGAG GATGGGGGCA GATGGGGAAA CAGTGGTTCT GAAGAATCATG | 120 |
| | CTCATTGGCA TCAACCTGAT CCTTCTGGGC TCCATGATCA AGCCTTCAGA GTGTGAGCTG | 180 |
| | GAGGTCAACA CAGAAAGGTT CCAGAGACAG TCAGTGGAGG AGGAGGGAGG CATTGCCAAC | 240 |
| | TACAACACAT CCAGCAAGA GCAGCCTGTG GTCTTCAACC ACGTGTACAA CATTAACTGT | 300 |
| 35 | CCCTTGGACA ACCTCTGTCT CTCAGGGCTA GAGGCTCTG CTGAGCAGGA GGTGAGTGCA | 360 |
| | GAAGAGGAGA CTCTGGCAGA GTACATGGGC CAGACCTCAG ACCACGAGAG CCAGGTCAAC | 420 |
| | TTTACACACA GGATCAACTT CCCCAGAAAG GCCTGTCCAT GTGCCAGTTC AGCCAGAGTG | 480 |
| | CTGCAGGAGC TGCTGAGCCG GATCGAGATG CTGAGAGGGG AGGTGTGCGT GCTGCGAGAC | 540 |
| 40 | CAGTGCACAG CCAACTGCTG CCAAGAAAGT GCTGCCACAG GACAACTGGA CTATATCCCT | 600 |
| | CAGTGCAGTG GCCACGGCAA CTTTAGCTTT GAGTCTGTG GCTGCATCTG CAACGAAGGC | 660 |
| | TGTTTGGGCA AGAATTGCTC GGAGCCCTAC TGCCCGCTGG GTTGCTCCAG CCGGGGGTG | 720 |
| | TGTTGAGATG GCCAGTGCAT CTCTGCGTGG ACCTGCTCCG GGGATGACTG TTCCGAATCT | 780 |
| | CGGTGCCCAA CAGACTGCAG CTCCCGGGGG CTCTGCGTGG ACCTGCTCCG GGGATGACTG | 840 |
| 45 | GAGCCCTACA CTGCGGAGGA CTGCAGGGAA CTGAGGTGCC CTGCGGAGTG TTCCGGGAAG | 900 |
| | GGGAGATGTG CCAACGGTAC CTGTTTATGC GAGGAGGCTC ACCTTGGTGA GGAAGTGGGC | 960 |
| | CAGCGGCAGT GTCTGAATGC CTGCGTGGGG TGAGGAGGCT GTGAGGAGGG GCTCTGCGTC | 1020 |
| | TGTGAAGAGG GCTACAGGCG CTCTGAGTGC TCAGCAGTTG CCCCCTCAGA GGAAGTGGGC | 1080 |
| | GTGGCTGGTA TCAGCGACAG GTCCATTGAG CTGGAATGGG ACCTGCGGAT GGCAGTGCAG | 1140 |
| | GAATATGTGA TCTCTTACCA GCCGACGGCC CTGCGGGGCC TCCAGCTCCA GCAGCGGGTG | 1200 |
| 50 | CCTGGAGATT GGAGTGGTGT CACCATCAGC GAGCTGGAGC CAGGTCTCAC CTACAACATC | 1260 |
| | AGGCTCTACG CTGTCAATTG CAACATCTCT AGCCTTCCCA TCACTGCCAA GGTGGCCACC | 1320 |
| | CATCTCTCCA CTCTCAAGG GCTACAATT TCCCTTCGAT GGTGGGAAA TCCAAAGAAC | 1380 |
| | CAGTGGGAGC CCTTCTCATT TTCTTCTGAT GGTGGGAAA TCAAGTCTAT TCCAAAGAAC | 1440 |
| 55 | AATGAAGGGG GAGTATTGTC TCAGGTCCCC AGCGATGTTA CGTCTTTTAA CCAGACAGGA | 1500 |
| | CTAAGCCCTG GGGAGGAATA CATTGTCAAT GTGGTGGCTC TGAAGAAACA GGCCCGCAGC | 1560 |
| | CCCTCTACCT CGCCAGCGGT CTCCACAGTC ATTTGACGGC CACGCGAGAT CCGTGTGCG | 1620 |
| | GATGTCTCGG ACACTGTGGC TTTTGTGGAG TGGATTCCCC CTGAGCCAA AGTGTGATTC | 1680 |
| | ATTCTTTTGA AATATGGCCT GGTGGGCGGG GAAGGTGGGA GGACCACTT CCGGCTGCAG | 1740 |
| | CCTTCCCTGA GCCAATACCT AGTGAGGGCC CTGCGGCTCG GCTCCCGATA CGAGGTGTCA | 1800 |
| 60 | GTCAAGTCCG TCCGAGGGAC CAACGAGAGC GATTCTGCCA CCACTCAGTT CACAACAGAG | 1860 |
| | ATCGATGCCC CCAAGAACTT GCGAGTTGTT TCTGCGACAG CAACCAAGCT TGACCTCGAG | 1920 |
| | TGGGATAACA GTGAAGCCGA AGTTGAGGAG TACAAGTTG TGTACAGCAC CCGGCGGGT | 1980 |
| | GAGCAATATC ATGAGGTACT GGTCCCCAGG GGCATTGGTC CAACCAAGCT TGACCTCGAG | 2040 |
| 65 | ACAGATCTGG TACTGGCAC TGAGTATGGA GTTGAATAT CTGCGTCTAT GAACCTCAG | 2100 |
| | CAAGCGGTGC CAGCCCACTT GAATGCCAGG ACTGAATTTG ACAGTCCCCG AGACCTCATG | 2160 |
| | GTGACAGCCT CCTCGGAGAC CTCCATCTCC CTCTCTGGA CCAAGGCCAG TGGCCCATTT | 2220 |
| | GACCACTACC GAATTACCTT TACCCCATCC TCTGGGATTG CCTCAGAGT CACCGTACCC | 2280 |
| | AAGGACAGGA CCTCATACAC ACTAACAGAT CTAGAGCCTG GGGCAGAGTA CATCATTTCC | 2340 |
| 70 | GTCAGTCTG AGAGGGGTGC GCAGCAGAGC TTGAGTCCA CTGTGGATGC TTTTCAAGGC | 2400 |
| | TTCCGTCCCA TCTCTCATCT GCATTTTCT CATGTGACCT CCTCCAGTGT GAACATCACT | 2460 |
| | TGGAGTGATC CATCTCCCC AGCAGACAGA CTCTTTCTTA ACTACAGCCC CAGGGATGAG | 2520 |
| | GAGGAAGAGA TGATGGAGGT CTCCTGGAT GCCACCAAGA GGCATGCTGT CCTGATGGGC | 2580 |
| | CTGCAACCCG CCACAGAGTA TATTGTGAAC CTTGTGGCTG TCCATGGCAC AGTGACCTCT | 2640 |
| | GAGCCCATTT TGGGCTCCAT CACCACAGGA ATTGATCCCC CAAAAGACAT CACAATTAGC | 2700 |
| 75 | AATGTGACCA AGGACTCAGT GATGGTCTCC TGGAGCCCTC CTGTTGCATC TTTGATTTAC | 2760 |
| | TACCGAGTAT CATATCGACC CACCAAGTGC GAGCAGTAG ACAGCTCAGT GGTGCCCAAC | 2820 |
| | ACTGTGACAG AATTCAACAT CACCAAGTGC AACCAGCTA CCGAATACGA AATCAGCCTC | 2880 |
| | AACAGCGTGC GGGGAGGAGA GGAAAGCGAG CGCATCTGTA CTCTTGTGCA CACAGCCATG | 2940 |
| | GACAAACCTG TGGATCTGAT TGCTACCAAT ATCACTCCAA CAGAAGCCCT GCTGAGTGG | 3000 |
| 80 | AAGGCACCAG TGGGTGAGGT GGAGAACTAC GTCAATGTTT TTACACACTT TGCAGTCTCT | 3060 |
| | GGAGAGACCA TCCTGTTTGA CGGAGTCACT GAGGAATTTT GCTTGTGGA CCGTCTCTCT | 3120 |
| | AGCACCCACT ATACTGCCAC CATGTATGCC ACCAATGGAC CTCTCACCAG TGGCACCATC | 3180 |
| | AGCACCAACT TTTCTACTCT CTTGGACCTT CCGGCAACC TGACAGCCAG TGAAGTCACC | 3240 |
| | AGACAAAGTG CCTGATCTC CTGCGAGCCT CCGAGGGCAG AGATTGAAAA TTATGTCTTG | 3300 |

| | | | | | | | |
|----|------------|------------|-------------|-------------|------------|-------------|------|
| | ACCTACAAAT | CCACCGATGG | AAGCCGCAAG | GAGCTGATTG | TGGATGCAGA | AGACACCTGG | 3360 |
| | ATTGACTTGG | AGGGGCTGTT | GGAGAACACA | GACTACACGG | TGCTCCTGCA | GGCAGCACAG | 3420 |
| | GACACCAAGT | GGAGCAGCAT | CACCTCCACC | GCTTTTCAACA | CAGGAGGCCG | GGTGTTCCTT | 3480 |
| | CATCCCAAG | ACTGTGCCCA | GCAATTGATG | AATGGAGACA | CTTGTAGTGG | GGTTTACCCC | 3540 |
| 5 | ATCTTCTCTA | ATGGGGAGCT | GAGCCAGAAA | TTACAAGTGT | ACTGTGATAT | GACCCCGGAC | 3600 |
| | GGGGGCGGCT | GGATTGTATT | CCAGAGGCGG | CAGAATGGCC | AAACTGATTT | TTTCCGAAAA | 3660 |
| | TGGGCTGATT | ACCGTGTGG | CTTCGGGAAC | GTGGAGGATG | AGTTCTGGCT | GGGGCTGGAG | 3720 |
| | AATATACACA | GGATCACATC | CCAGGGCCGC | TATGAGCTGC | GCGTGGACAT | GCGGGATGGC | 3780 |
| | CAAGAGGCGG | CCTTCGCTTC | CTACGACAGG | TTCTCTGTGG | AGGACAGCAG | AAACCTGTAC | 3840 |
| 10 | AAACTCCGCA | TAGGAAGCTA | CAACGGCACT | GCGGGGAGCT | CCCTCAGCTA | TCATCAAGGA | 3900 |
| | CGCCCTTTCT | CCACAGAGGA | TAGAGACAAT | GATGTTGCAG | TGACTAATCT | TGCCATGTGG | 3960 |
| | TACAAGGGAG | CATGTGTGTA | TAAGAACTGC | CACCGGACCA | ACCTCAATGG | GAAGTACGGG | 4020 |
| | GAGTCCAGGC | ACAGTCAGGG | CATCAACTGG | TACCAATTGA | AAGGCCATGA | GTTCTCCATC | 4080 |
| | CCCTTTGTGG | AAATGAAGAT | GCGCCCTTAC | AACCAACGTC | TCATGGCAGG | GAGAAAAAGG | 4140 |
| 15 | CAGTCTTAC | AGTTCTGAGC | AGTGGGCGGC | TGCAAGCCAA | CCAATATTTT | CTGTCAATTTG | 4200 |
| | TTTGTATTTT | ATAATATGAA | ACAAGGGGGG | AGGGTAATAG | CAATGTGTTT | TGCAACATAT | 4260 |
| | TAAGATGAT | TGAAGGAAGC | AGGGATGTGG | CAGGAATCCG | CTGGCTAACA | TCTGCTTTTG | 4320 |
| | GTCTTCTGCT | CCCTGGAGCC | TGACCCCTCAG | TCTCCATTCT | CCCTCCTACC | CAGGCTCCTT | 4380 |
| | CAACCTTAC | CTCCTTTCCC | ACCAAGGAGG | AGAAGTAGGA | AGTTTCTTGA | AAGGGCCAAT | 4440 |
| 20 | TCAAAGCCAA | GTGCTGGGTG | GCAGATTGTT | ATGGTGACAG | GCACACACAT | TTTTCTACCC | 4500 |
| | TTCTTCTGAG | ATGTCTCTGT | CCTTCCAGGT | ATTGTGATT | TTGTACACAG | CTGACATGGC | 4560 |
| | CAGGTTCTCA | CATCTGCCCA | GAGAAAAAGG | CCTCAGCAAG | AGAGTTTGGC | CAACAATTCC | 4620 |
| | CCTTAAAGG | AAACAGATCA | ACTACACCGC | ATCCCAACAA | CCCAGTTCT | TTTCTCTCT | 4680 |
| 25 | TCCTTCTTCT | CTCCCTTCT | TCTTCTCTGC | CTTCCC | | | 4716 |

Seq ID NO: 137 DNA Sequence

Nucleic Acid Accession #: NM_005883.1

Coding sequence: 1714..8625

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| 30 | | | | | | | |
| | GGGTTTGGGG | AGCAGGAGGC | AGACATGTGT | TGCTTTGCAC | GTCTATCTGGT | CCTTCCACCT | 60 |
| | GGCTGGGCAT | GGATGGTGA | CCTCAGCTGG | AACATGGGGC | TGGAGCCAGA | CCTCAGGGTC | 120 |
| | TCCTGCGGTG | TAGCCCCCAA | CCCCAAGCCT | GATCCCCACC | GGAGACCTGA | ACAGCCTTGG | 180 |
| | ACATCATCGG | ATCAGGGTGG | GAGGTGCCAG | CCTCTGCCAE | CTGACTTCCA | GTCCCTGTGC | 240 |
| 35 | CCCTCCACCC | CTGCCCTTGG | GCACTCCTGC | CCTGCAGGTT | CCTCAGAGGG | GCAACCCAAA | 300 |
| | GCCAGAGAGG | GGCGGGTCTT | GTCCGGCCTC | CAGCCTGGAC | TTCCAGCCCC | CTCTGGGGCA | 360 |
| | GCATCTGGGT | CCAGACCTTC | GGTTCTTAGG | GCCTCGTTTC | TCCTCTGGGG | AACAGCCAAA | 420 |
| | TGGTGTCTCC | TGAGACTCAG | GACAGACCAA | GAAGAAGCCG | GATGACATGG | CAAGCCACAC | 480 |
| 40 | ACTGCTCTCC | CTGAGCAGGA | CGGACAGGCC | CGACTCCATC | CTCCACCTGT | CGACTGAGCC | 540 |
| | CCCACCCCTA | CTCTGTCTCC | AGCCGTGCCC | CTGTGACAT | TTGGGTGGGA | GGGAGGGGGA | 600 |
| | TGAGGGGGCA | CCTGGGGGTC | AGAGAACAAA | TGAGGGGTGA | ATACATGTGT | GTGGCCAGGT | 660 |
| | GGAGGAGGGA | GGGAGGAGGC | AGGTGGGCTG | GACAGGGCCG | GTGTGAGGAA | GGGGCTCAGG | 720 |
| | CTGGCAGGGG | GAGGTGGCAA | GAGGGATGGG | CTGCCATTGG | TGGTCTGAGA | CAAAAGCCGA | 780 |
| 45 | GGGAGGAGGC | GAGCGCTGAT | GGGAAAGGAA | CAAAGAGGGA | AGGGGGGCGT | GAAGGGGGTT | 840 |
| | CCGGCGGGAG | GGCGAGCCCG | AGGGAGGAGG | CGCCGGCCAG | CTGGACAGAG | GGAGGAGGCC | 900 |
| | AGGCCAGAGC | CAGAAGACCG | CCAGAGGCAC | AAAGAAGCCA | GCGCGCTGGC | GGAGTCAAGG | 960 |
| | GATGGGGCAG | AGACTCCCGG | GGCCAGCAGG | GACCAGCTGA | AGGCTGCCGA | GGGGGTCCGG | 1020 |
| | GCCACACAGG | TAGCCACCTT | GAGCTCAGCC | ACCGATGGAG | GGTCTGTTGG | CTGCTGCGGT | 1080 |
| 50 | GATGGCGGTG | GGCTTGGGTC | CATCTGTCTT | GCGGTTTCTG | CACAGCTTAG | GTGTCAACCA | 1140 |
| | CTGGCCTTGG | TGGTGTTTTC | ATTGTCCATC | GGCAGGGACA | GCTGGTGGTC | TGTCTGCCCC | 1200 |
| | CCCTGTCTGG | CTGTGAGCCT | CTGGGCAGGC | TGTCTTTTAT | GGGGGAGGGT | CCTGTCTGTG | 1260 |
| | TGTCTGTGCG | CCTCTCTGCG | TGTGAGCCTG | GGGGTGCTGG | GCTGGCCAGT | CGGCTTGGCT | 1320 |
| | GGTTAGGCTG | TCCAGCTGTG | CTGAGTGTTC | GTCGCGCTGT | CAGGATGTGT | CCTGGGGGCT | 1380 |
| 55 | GGGAAGGAGA | GGCCGACCCA | TNGTCTGTCT | GTCGACTGGT | CAGTTGGAGC | TTGAGCTGTC | 1440 |
| | TGTACGTCTG | TCTGTGTGCC | CATCTGTCTC | CCCTGGGGGC | CACCTCTCAC | TCCACCTGCC | 1500 |
| | CCTCTGCGCC | CCGGATTGCC | TGGCCAGCAC | CACGTGGGCC | TGTACTTGTC | CACACCAAGT | 1560 |
| | ACTCTGCTCG | GAGACCCCGC | CCCAACCCAG | GATCAGGCAG | GACGGCTGGG | GCTTAGGTCA | 1620 |
| | GGGGCGGTCT | GTCGGGAAGG | CATCACCGCG | CCCTCCCCAG | ACCATCAGCT | GAACCTCTG | 1680 |
| 60 | ACCCTGTGAT | CCCAGACCGT | GCAGGAGCTG | AAGATGGCGA | GCTCCGTGGC | GCCCTACGAG | 1740 |
| | CAGCTGGTGA | GGCAGGTGGA | GGCCTTGAAG | GCTGAGAAAC | GCCACCTGAG | GCAGGAGCTA | 1800 |
| | AGGGACAAC | CCAGCCACCT | GTCCAAAGCT | GAGACAGAGA | CGTCCGGCAT | GAAGGAGGTC | 1860 |
| | CTGAAGCACC | TACAGGGAAG | ACTGGAGCAG | GAGGCCCGAG | TGCTGGTGTG | CTCGGGGCGG | 1920 |
| | ACGGAGGTGC | TGGAGCAGCT | GAAGGCCCTA | CAGATGGACA | TCACCAAGCT | GTACCAACCT | 1980 |
| 65 | AAGTTCACAG | CGCCCAACCT | GGGCCCCGAG | CCTGCCCGCC | GGACCCCGCA | GGGCAACCCA | 2040 |
| | GTACACGGCT | CGGGGCCCTC | CAAGGACAGC | TTTGGGGAGC | TGAGCCGGGC | CACCATCCGG | 2100 |
| | CTGCTGGAGG | AAGTGGACCG | GGAACGGTGT | TTCTGTCTGA | ATGAGATTGA | GAAGGAGGAG | 2160 |
| | AAGGAGAAGC | TCTGGTACTA | CTCTCAGCTG | CAGGGCCTGT | CCAAGCGCCT | GGACGAGCTG | 2220 |
| | CCGCAAGTGG | AGAGCAGATT | CTCGATGCAG | ATGGACCTGA | TCCGGCAGCA | GCTTGAAGTT | 2280 |
| 70 | GAGGCCAGC | ACATCCGCTC | GCTGATGGAG | GAGCGCTTGG | GCACCTCGGA | CGAGATGGTG | 2340 |
| | CAGCGGGCAC | AGATCCGCGC | CTCGCGCCTG | GAGCAGATTG | ACAAGGAGCT | GCTGGAGGCG | 2400 |
| | CAGGACCGAG | TGCAGCAGAC | GGAGCCCCAG | GCCTTGCTGG | CGGTGAAGTC | GGTGGCCGGT | 2460 |
| | GAGGAGGACC | CCGAGACAGA | GGTCCCCACA | CACCTGAGG | ATGGCAACCC | TCAGCCGGGC | 2520 |
| | AACAGCAAGG | TGGAGGTGGT | CTTCTGGCTG | TTGTCCATGT | TGGCGACGCG | CGACCAAGGAG | 2580 |
| | GATACAGCGC | GCACGTGTCT | GGCCATGTCC | AGCTCGCCCG | AGAGCTGCGT | GGCCTAGCGC | 2640 |
| 75 | CGCTCGGGCT | GTCTGGCTCT | GCTGTGCAAA | ATCCTCCACG | GCACGAGGCG | CGCGCCCGGG | 2700 |
| | GGTGGCGCGG | GGGCCCCAGG | GGCACCGGGC | GCCAAGGACG | CACGATGCGG | CGCCCAACGG | 2760 |
| | GCGCTGCACA | ACATCGTCTT | CTCGCAGCGG | GACCAGGGCC | TGGGCGCAAA | GAGAGATGCG | 2820 |
| | GTCTGTGACG | TGCTGGAGCA | GATCCGGGCC | TACTGCGAGA | CCTGTGCGGA | CTGGCTGCAG | 2880 |
| 80 | GCCCGAGAGC | GCGGGCCCGA | GGGAGGTGGC | GCGGCGAGCG | CCCCGATCCC | CATCGAGCCG | 2940 |
| | CAGATCTGCC | AGGCCACCTG | TGCTGTTATG | AAGCTGTCTT | TTGATGAGGA | GTACGCGCGT | 3000 |
| | GCCATGAACG | AGCTAGGTGG | GCTGCAGGCC | GTGGCAGAGC | TGCTGCAGGT | TGACTATGAG | 3060 |
| | ATGCACAAGG | TGACCCGGGA | CCCGCTGAAC | CTGGCGCTGC | GCGGCTACGC | GGGCATGACC | 3120 |
| | CTCACCAACC | TCACCTTTGG | GGAGTTGGCC | AACAAGGCCA | CCCTGTGTGC | GCGCGCGGCG | 3180 |
| | TGCATGGAGG | CCATCTGTGG | CCAGCTGGCC | TCCGACAGTG | AGGAGCTCCA | CCAGGTGGTG | 3240 |

| | | | | | | | |
|----|-------------|------------|------------|------------|-------------|------------|------|
| | TCCAGCATCC | TTCCGAACTT | GTCTGGAGG | GCCGACATCA | ACAGCAAGAA | GGTCTGAGG | 3300 |
| | GAGGCGGGCA | GGGTGACTGC | CCTGGTGACG | TGTGTCTGTC | GGGCCACCAA | GGAGTCCACC | 3360 |
| | CTGAAGAGCG | TGCTGAGCGC | CCTGTGGAAT | CTGTCTGCAC | ACAGCACAGA | GAACAAGGGG | 3420 |
| | GCCTATCTGCC | AGGTGGATGG | CGCCTGGGC | TTCTGTGTGA | GCACCTGAC | CTACAAGTGT | 3480 |
| 5 | CAGAGCAACT | CGCTGGCCAT | CATCGAGAGC | GGCGGCGCA | TCCTCCGCAA | TGTGTCCAGC | 3540 |
| | CTCGTGCACA | CCCGTGAGGA | CTACAGGCAG | GTGCTCCGGG | ATCACAACCTG | TCTGCAGAGC | 3600 |
| | CTGCTGCAGC | ATCTGACTTC | GCACAGCCTG | ACCATCGTGA | GCAACGCGTG | CGGCACGCTC | 3660 |
| | TGGAACCTGT | CGGCCCGCAG | CGCCCGTGC | CAGGAGCTGC | TGTGGGACCT | GGGCGCGGTG | 3720 |
| | GGCATGTGTC | GTAATCTGGT | GCACTCCAAG | CACAAGATGA | TGCCATGGG | CAGCGCCGCC | 3780 |
| 10 | GCCCTGGCCA | ACCTGCTGGC | CCATCGGCC | GCCAAGCACC | AGGCGGCGCG | CACCGCGGTG | 3840 |
| | TCCCGAGGCA | GCTGCGTGCC | CAGCCTGTAC | GTGCGCAAGC | AGCGGCGCGT | GGAGGCGGAG | 3900 |
| | CTGGAGCGAC | GGCAGCTGCG | GCAGGCGCTG | GAGCACCTGG | AGAAGCAGGG | CCCGCGGCA | 3960 |
| | GCGAGGCGCG | CCACTAAGAA | GCGCGTGCG | CCCTGCGAC | ACCTGGACGG | CCTGGCCCAA | 4020 |
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| 15 | GCCGCGGCA | CCGCGGAGCC | AGCCAGCCCT | GCCGCGCTGT | CCCTCTTCT | GGGAGGCCCC | 4140 |
| | TTCTCTGAGG | GGCAGGCGCT | GGCTCGCACC | CCGCCCAACC | GCCGAGGCGG | CAAGGAGGCA | 4200 |
| | GAGAAGGACA | CCAGTGAGGA | GGCAGCGGTG | GCGGCCAAGG | CCAAGGCCAA | GCTGGCGCTT | 4260 |
| | GCAGTGGCGC | GCATCGACCA | GCTGGTGAG | GACATCTCG | CCCTGCACAC | CTCGTCCGAC | 4320 |
| | GATAGCTTCA | GCCTCAGCTC | TGGAGACCG | GGACAGGAG | CGCCACGGGA | GGGCGCGCC | 4380 |
| 20 | CAGTCTGTCT | CGCCATGCGG | CGGCCCGGAG | GGCGGCGGCG | GAGAGGCAGG | AAGCGGCGG | 4440 |
| | CACCGCGTGC | TGCGGCTCAA | GGCGGCCAC | GCCAGCCTCT | CCAACGACAG | CCTCAACAGC | 4500 |
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| | CTGGCTTGC | GCGCGAGGA | CCCGAGGTGT | GGGAGCCTCT | GGCCAGCGCG | GCTTGACCTT | 4620 |
| | GACCTGCGCG | GCTGCCAGGC | CGAGCCCGCG | GCCCGGAGG | CCACCTCGCG | CGAGCGCGCG | 4680 |
| 25 | GTGCGACCA | TCAAGCTGTG | GCCTACCTAT | CAGCACTGTC | CACCTGTGTA | GGGTGCTTCA | 4740 |
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| 30 | CTGGATGACA | CTGACTCTCT | CCTGGAAGGG | CTGGAGGAGG | CGGCGCCAG | CGAGGCTGAC | 5040 |
| | CTGGACAGCA | CGTGGCGGCG | GCCCGGGGCC | ACCTCGCTGC | GAAGACGCCA | CGGTGGTGAC | 5100 |
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| 35 | AGCGGCACCA | TCAAGCTTAG | CGAGCTGCCC | GACAGCCCCG | GACAGACCAT | GCCTCCGACG | 5340 |
| | CGGAGCAAGA | CGCCACCGCT | GGCGCCCGCG | CCACAGGGTC | CCCGGAGGC | CACCCAGTTC | 5400 |
| | AGCCTGCACT | GGGAGAGCTA | CGTGAAGCGC | TTCTTGAGCA | TCCGCGACTG | CCGCGAGCGC | 5460 |
| | TGCGGCTGTC | CATCTGAGCT | GGAGCGAGGC | AGCGTGCGCT | TTACCGTGGA | GAAGCCAGAC | 5520 |
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| | GGCGCGGCGC | TCCATTTTGC | AGGGCACCGG | CGCGGAGGAG | AGGGCGCGCG | GCCACGCGGT | 5700 |
| | TCTCGGCTCT | GCGGCGCGCG | GGACCAAGAG | CTGGAATCTG | TGCGGAGTGC | CCTGGAGGCG | 5760 |
| | GCGGTGCTGT | CCCGGCTGCG | CAAGGTGGCC | TCCGCGCTGG | TGCCAGGTGC | CGCGGCACTC | 5820 |
| 45 | CCCGTGCCCG | CTCTAGTTT | GGTGCCCGCC | CGGCGCCCGG | CCCAGGAGGA | CGACTCTTGC | 5880 |
| | ACTGACTCTG | CGGAGGACAC | GCGGCTCAAC | TTCTCTAGCG | CGGCTCGCT | CAGCGACGAG | 5940 |
| | ACCGTGCAGG | GACCCCCCAG | GGACCAAGCC | GGGGAACAG | CGGCGAGGCA | AAGACCCACC | 6000 |
| | GGCGGCGCCA | CCTCTGCGAG | ACAGGCCATG | GGGACCGGCG | ACAAGGCGGG | AGGCGCGCGG | 6060 |
| | CGCAGCGCGG | AGCAGTCTCG | GGGCGCGGCG | AAGAACCAGG | CAGGCTGGA | GCTGCCCTGT | 6120 |
| 50 | GGCGGCGGCG | CGAGCGGCCC | CGCAGACAG | GACGCGTCAA | AGCCCGGCGG | GACCTCGCGG | 6180 |
| | GACGCGGCGG | TCCAGTCTCG | GTGCTCTCAG | ACGCGCACTG | AGGAGGCGGT | GTAAGTCTTC | 6240 |
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| | ACATCGGCCA | TCCCTCGCGC | TTTTAGCGCG | GAGCGTCCCG | AGGCGCGGAA | GGAGGCCCTT | 6360 |
| | GCCCGCTGCA | AGGCTGCACC | AGCTGCCCCG | CCGCGCGCCC | GGACCCAGCC | CAGCCTCTAT | 6420 |
| 55 | GCTGACGAGA | CCCGGCGCTG | CTACTCCCTG | AGCTCTCTCG | CCAGCTCCCT | CAGCGAGCCC | 6480 |
| | GAGCCCTCGG | AGCGCGCGGC | CGTCCATCCA | CGAGGCGCGG | AGCCCGCGGT | CACCAAGGAC | 6540 |
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| 60 | GAGGAGGAC | CGGGCTGGGA | CCGGGCTCC | GACCTGGATA | GCGTGGAGTG | GCGCGGATC | 6780 |
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| 65 | GGCCCCGAGA | AGCCACGTGG | CACACAGAAG | ACCACGCGCG | GGGTGCCAGC | AGGGACCCCC | 7080 |
| | GGACGAACAG | TGATCTACGT | CCCGAGCCCG | GCAACCCGCG | CCGACGCCAA | AGGGACCCCC | 7140 |
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| 70 | AAGACCCCTC | CCTCCAGCTC | CTCCAGACCC | TGCGCGGCT | CCGAGCCCCC | GCCCAGAAAG | 7380 |
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| | ATCCCGTTCA | TGCAGAGGCT | GGCCCGGCGT | GGGCGCGCAC | CGCTGGCTCG | GGCAGTCCCG | 7560 |
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| | CCCGCGGAGG | GCGCGGCCCC | GGCCCGGCGG | CGGCCCCCGG | GCGCGCGGAC | CAGCCTTGGC | 7920 |
| 80 | GAGCGGCTTG | CCGCGGCGAC | CACCTCCGAG | AGCCCGTCCC | GCTTGCCTGT | GCGCGGCGCC | 7980 |
| | GCGCGGCGCG | CGGAGCTGTG | CAAGCGCTAC | GCGTGCCTGC | CGCACATCAG | CGTGGCGCGC | 8040 |
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| | GAGGGGCCCC | CAGCTCCTCC | GGGGGACGCA | GCAGCTCGGG | CCCCAAGGGG | AACGGGCTCA | 180 |
| | TCCCCAGTCC | GGCGCACAGT | GCCCACTGCA | GCTTCTACCG | CACGCGGACC | CTGCAGGCCC | 240 |
| | TCAGCTCGGA | GAAGAAGGCC | AAGAAGGCGC | GCTTCTACCG | GAACGGGGAC | CGCTACTTCA | 300 |
| | AGGGCTCGGT | GTTTGCCATC | TCCAGCGACC | GCTTCCGGTC | CTTCGATGCG | CTCCTCATAG | 360 |
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| 10 | TGTGTGCATC | CAATGAACCA | TTTGTAAAG | TGATTACAC | CAAAAATATT | AATCCAACCT | 540 |
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| 15 | TCTGCACCTT | GSATGGAAG | CAGGTTACTT | GTCTGCAAGA | CTTTTTTGGT | GATGACGATG | 840 |
| | TTTTTATTGC | ATGTGGACCA | GA AAAATTTC | GTATGCCCCA | AGATGACTTT | GTCTGGATC | 900 |
| | ATAGTGAATG | TGCTGTCCGT | AACTCATCTT | ATTCTCGATC | CTCAGCTGTT | AAGTATTCTG | 960 |
| | GATCCAAAG | CCCTGGGCCC | TCTCGACGCA | GCAAACTACC | AGCTTCAGTT | AATGGAATC | 1020 |
| | CCAGCAGCCA | ACTTCTACT | CCTAAATCTA | CGAAATCTCT | CAGTTCTCTT | CCAACCTAGT | 1080 |
| 20 | CAGGAAGTTT | CAGAGATTAT | AAGATTCTG | CTCATGGCAG | ATCTTCTTCC | AATGTAACG | 1140 |
| | GTGGACCTGA | TCTTTCAGGT | TGCATAAGTC | CTGAAGGTGT | GAATGGAAC | AGATGCTCTG | 1200 |
| | AATCATCAAC | TCTTCTTGA | AAATACAAA | TTGGAAGGT | GTTTGGCCTA | AAGATTATAG | 1260 |
| | CAGTAGTCAA | AGAGGTGATA | GACAGGTCCA | CTGGAAGGGA | GTTTGGCCTA | AAGATTATAG | 1320 |
| | ACAAAGCCAA | ATGTTGTGGA | AAGGAACACC | TGATTGAGAA | TGAAGTGTCA | ATACTGCGCC | 1380 |
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| | AGTACACTGA | GAGAGATGGC | AGTGCCATGG | TGTACAACTT | AGCCAAATG | CTCAGGTATC | 1560 |
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| | TGGCTGGGAA | CTGGAGTTT | CCGGCCCCCT | ACTGGGATAA | CATCACGGAC | TCTGCCAAGG | 1920 |
| | AATTAATCAG | TCAATGCTT | CAGGTAAATG | TTGAAGCTCG | GTGTACCGCG | GGACAAATCC | 1980 |
| 35 | TGAGTCAACC | CTGGGTGTCA | GATGATGCTT | CCCAGGAGAA | TAACATGCAA | GCTGAGGTGA | 2040 |
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| 40 | CTCTCCAGTT | CTCCCTCAG | TGGAGGAGAT | CCCTGTGCTT | GGGGAAGCAG | TCCCGGCCCC | 2340 |
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| | CTTACCGGCC | TGCGCTGAG | TTGCGGGGTC | CTCCGACGCG | CGCTTGGGAA | CGGAGCCCTG | 2580 |
| 45 | GGGTGCGGCG | CGCTGGCCTG | GTGCTCTGGG | CTCTGCTTTC | TGGTTCTTGG | AGGCATCAAA | 2640 |
| | GGCTGCATCC | GTCTGCTCAA | CAGCTGTTCC | GAGAGACTCG | TTCCAGATCA | TCCGCTCATT | 2700 |
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| 50 | TACGAAGAGC | TTAGAATTGC | ATTGTCTCTT | TTGTGGGTGT | CCTGTGAGAG | GTGATATGGG | 2940 |
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Seq ID NO: 140 DNA Sequence
Nucleic Acid Accession #: NM_015163.2
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| 70 | GCAAGCAAGA | AGCAAGCAA | GAAAGAAAAC | AAAGAAAGAA | AGAAAGAAAG | AAAGAAAGAA | 180 |
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| 75 | ACCTGAGGTT | GGAGTGGGA | GACCAAGCTG | ACCAACATGG | AAAAACACCG | TCTCTACTAA | 480 |
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| | TGAGGCAGGA | GAATCGCTTG | AACCTGGGAG | GCGGAGGGTG | CGGTGAGCCG | AGATGCAACC | 600 |
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| | AGTAATAAAG | AAAGAAGAA | AGAAAGGCA | AGGCAAGGCA | AGTCCAGGCA | AGGCAAAATCT | 780 |
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| 70 | AAAAAAAAG | AGTGACCAGA | GGGCAAGGA | CCCATTCTCA | GTAATGGGAG | ATCTTGAGTT | 5160 |
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Seq ID NO: 141 DNA Sequence
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Seq ID NO: GAD8 DNA Sequence
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Seq ID NO: 142 DNA Sequence
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Coding sequence: 1..1641

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CAAAGCCGAA  GTCTGGCGCG  GCTCTTCGAC  TCGCTGCGCC  ACGTCCCGCG  GGGTGGCGAG  900
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GGCGGGTGTG  GCCGTGCGGG  CGCGGACGTG  AGCTTGGGCG  ACCTGGAGAA  GGGCGGGAG  1140
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Seq ID NO: 143 DNA Sequence
Nucleic Acid Accession #: NM_022123.1
Coding sequence: 76..2781

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| 15 | GCAGTGAGCG CAGCTAGCTG GACGAGATG CCGCGCGCA ACGTGTTCAC CACGCGCGAG 2700 |
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| 20 | ATTCTTTCGT GTAAAGATAT GTTTATTTT TGCTTCTAGA GGTGACAGC ACCAGTTGCC 3000 |
| | TGCGGTTTGT TCTTCTCTA AGGTGTGTGT TGGGTTGTT TGCTTTCTT TGCTCTTTA 3060 |
| | TTAAGATGTC TTTCACTGTG ATATGCTCT GGCATAGAAT ACTCAGTCT GTGGTCAAGA 3120 |
| | GAGTTCTCAA GTGACACCA TTGGGTTTC TTCAATAAGA TCTGTATAG ATCAAGATGG 3180 |
| | AAAGAGACAA GCATAACAA TTGTCCCTGT TGTACTAAGT CAAATGAAT AGGGTGGTTT 3240 |
| 25 | TTGTTTCTGT TCCTAATTCC TTTAAAAAT AGGGGAATA GTATTTAGA ATTTATGCA 3300 |
| | GAATTTAATT CTCTTTTAC GGTAAAGAT TTAAGATTT CTACTTGCA CATAAAAAAT 3360 |
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| | CCTCGTGC |
| 30 | Seq ID NO: 144 DNA Sequence Nucleic Acid Accession #: NM_005806.1 Coding sequence: 105..1076 |
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| 40 | CTGGGGACAA GCTAGGAGCG AGTGGCTTCA AGTCGCTCT GTCCAGCACC TCGTCTCTA 360 |
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| | TTTCCAGAT CGCCACGCTG CTGCTGGCGC GCAACTACAT CCTCATGCTC ACCAATCGC 600 |
| 45 | TGGAGGAGAT GAAGCGACTG GTGAGCGAGA TCTACGGGG CCACCAAGCT GGTCTCAACC 660 |
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| | CAGCAGCAGC GCACGCGCA CATACCCCG CGGTGCACCA CCCCCTCTG CCGCCCGCG 780 |
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| 50 | CTGCGCGCG CGCCCGCTG GGGGGCGGG GCGCGGCGAG TGGGGGAGC GGGGGCTTC 960 |
| | AGCACTGGGG CGGCATGCC TGCCTCTGCA GCATGTGCCA CTCCAGCGCC AAGTGAGCG 1020 |
| | AGTGTGCGG TATGGGCGCC GGCAGCCTGC CGCGCTCAC CTCCAGCGCC AAGTGAGCG 1080 |
| | ACTGGCGCG GCGGCTCTG GCGAGCGGG AGCCAGGGG CGCGGGGAAG CGAGGACTGG 1140 |
| | CCTGCGCTG GCTCGGAGC TCTGTGCGA GGAGGGGCG AGGACCATG ACTGGGGTG 1200 |
| 55 | GGGCATGGT GGGATTCAG CATCTCGAA CCCAAGCAAT GGGGGCGCC ACAGAGCAGT 1260 |
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| 60 | AGGGGGACAC ATTGGGCGCT TGCTCCTCT CTCTCTTCT TGGCGGTGG GAGACTCCGG 1560 |
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| 65 | AGTATGAGCA AGTTTATAGA CATTGAGAGT AGAACCATT GTGGATTGGA ATAACCCAAA 1860 |
| | ACTGCGGATT TCAGGGGCGG GTGCATTGTA GTTATTATT TAAATAGAA ACTACCCAC 1920 |
| | CGACTCATCT TTCCTTCTCT AAGCACAAAG TGATTGGTT ATTTGGTAC CTGAGAACGT 1980 |
| | AACAGAAATTA AAGGCGATT GCTGTGGAAG CAGTTTGGGT TATTTGGGG TTCTGTTGGC 2040 |
| | TTTTTAAAT TTTCTTTTT GGATGTGTAA ATTTATCAAT GATGAGGTAA GTGCGCAATG 2100 |
| 70 | CTAAGCTGTT TGCTCAGTG ACTGCCAGCC CCATCGAGT CTAAGCCGGC TTCTCTCTAT 2160 |
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| | TGTAAAAACA AAGTGCTAAA TAATATTTAT TACTTGTGTT GTTGCAAAAA CGGAATAAAT 2400 |
| 75 | GACTGAGTGT TGAGATTTTA AATAAAATTT AAGT 2435 |
| 80 | Seq ID NO: 145 DNA Sequence Nucleic Acid Accession #: XM_045127.3 Coding sequence: 21..4469 |
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| | CAAGGGCCCT | TCACCTTCAT | GTCTGAAATG | GAACCTTGGC | TTTTCTAGTG | GAAGAAATAG | 5160 |
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5264

Seq ID NO: 146 DNA Sequence
Nucleic Acid Accession #: AK096568.1
Coding sequence: 63..797

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1 11 21 31 41 51

ATCTTCGGCG GCGGAGTGG CTGGCCTGT GCAACCCGCA CCTGCGTCCC TGGCCCGGCC 60
CGATGGCGCC GCGGCGCGTG GGCCTCTTGG TGCTGGCGCT CGGCGGCGCC GCGGCGGTGC 120
TGGGCTCGGT GCTCTTCATC CTCTGGAAGA CCTACTTCGG CCGCGGCGGA GAGCGCGGCT 180
GGGACCGGG AGAGGCTGG TGGGCGCGG AGGCTGCCCG CCTCCCGAG TGGGAGGAGT 240
GGGACCCGA GAGCGAGGAG GACGAGGAGC CGGCGCTGGA GGAGCTGGAA CAGCGCGAGG 300
TGCTGGTGCT GGGCTGGAT GCGCAGGCA AGAGCACGTT CCTCGCGTG TTGTGGGGA 360
AGCCACCGCT GGAAGGCCAC ATCCCCACT GGGCTTCAA CTCGCTGGT CTGCCACCA 420
AGGACTTTGA GTTGAACCTG CTAGAAATTG GGGCAGCCA GAACCTGGC TTCTACTGGA 480
AGGAGTTTGT GAGCGAGGTG GATGTGCTGG TGTGTGGT GGACTCGGT GACCTGCTGC 540
GGCTGGCCCT GGGCGGAGAG GAGCTGCACA AGCTGCTGGA CAAGGACCT GACCTGCTGC 600
TGCTGGTGCT GGGCAACAG CAGGACCTGA GCGAGGCCAT GAGTATGGG GAGCTGCAGC 660
GGGAGCTGGG TCTACAGGCT ATCGATAACC AGCGGAGGT TTTCTCTTG GCAGCCAGCA 720
TTGCCCTCG AGGACCCACC TTTGAAGAGC CTGGCACGCT GCACATCTGG AAACCTGCTCT 780
TGGAGCTCCT CTCTTAGGCT GGAGCTCTCC TGCTTGCCAC CTGCTGTCA AGACCATAGT 840
TGTAAGTCTG CTGCTTCAAT GCCAGACTGG GCCTGGGGCA AGAGCCACAT GGCAGCATTT 900
CCCTTTTCCC CTCTTTGCC TTTCAAGAGC AGGCGCTGG CAAGGCCAAG AACCATGCAG 960
AAGCTTCTCT GGTGAGGTGG CCGTGAAGCC GAAGCAGGGA GGTGGGTGAG ACAGAGGGTG 1020
GGGAGGATAG TGTCTGGCT ATTCCAGGCT GGAATGTGGA TCCAGCTTTC CCTTCTCTTA 1080
CTGTACAGT GAGATGCTCA GTGGGCTCAA TCCTCCACTA CAGGTCCCGG TACCTGAGGA 1140
ACCAAGTGTG GTGTCAGAA TACTCTAGA GCCTCAAGGT CTCCAGTCC AGAAACAGTC 1200
TGGTGACGTG TGTCCCTTCT CATGTGGCA GCCTCTGAGT GGTGACACAG CAAGCCTTTG 1260
TTCTGTCTCT GCATTGTCCA GCGCCAGCTC CACTTAAGTG ACTTGTGGCC TTGTGCAATC 1320
TCTGCTCTC TGACCCGAGG GCCATTATTT TTAAGGGAG GTGGTTTCTT AATTGGAGA 1380
TGCTTTTCCC AGCCATGGGA GTGTGAAGTG CTAGGATGAA CCTGGCCATC CTAGCAAGGA 1440
GCTTTCTGAA GACCTCCCTG CCTTCCCTG AGCCAGGCC TGGCCCGCCA GCCTCTCTTG 1500
ACTACAGAA TACTGATATT CACCCACCAA ACAGAAAAG TGAAGGCTGG GTTTTCCCC 1560
TCTAATCTGG AGGCAAGCTG CTGCTCTCT ACTAATCTGT CCACTGCCCA TGTTTACAGA 1620
AGTCAGGGGA AGGAAGGAGC CTGTGCTCT GGGACGACAG TCAACTGGAG CTAGGTGTTG 1680
ACCTCAGAAC TGCAATTTAT TTATTAATTT ATAAGCAGAA CAGGCCAGAG TTCTAGGCTC 1740
TGTTTCTAGG TGCTGTTTTC AAAACCCAG ATGACAGTCA TAGAAAATT GGAACCTAGG 1800
AAAAATCAGT GAATCATGAA TGACAATGAG ATAACATACA GATGTCAGT GAGACAAAGT 1860
TGTGGGTTCC TCCTCCACC TGGCTTTGAG GCTGTCTGCT ATATCATAGT ACTTTACATG 1920
GATTACATG AACTGAAACG CCACCACTTG GCCCAGGATG TTGAAAGGT GCAATTTCTT 1980
TCTGGGTAGA TAAGAAATGA CTCTGGGAGA GGATTTCCCT TATGTGAATC TAGGTAAAAA 2040
GATGAAAAAA AATTGTATTA TGTGATCTTA AGGACAGGAA TAGCAGACCA GCCAACGGGA 2100
TGGCTTGGG TACATCACTC AGCCTTCTG GACCCAATTT TTCCCAAGT AAAGCCAAAGT 2160
TGAAGCTAAT TTCTGGAGT CTCTGAGTG CACATTCCAT AGTTCTCCAG TGCTTGGCGA 2220
TCAGCCCAAT TGAAGGACTG GCTCTGTACT GACACTTATT ATCGGTACAG GCAAGAGGA 2280
GCCTGTGTG TGTAGGGAC CACTAAATCA ACAACCACAA ATGGATTTT TTTTAAAGAG 2340
GAGCTGTGCA CCTCAATTG CTGTCTAGT GAGAAATAG ATTGTGTGCC TTCAATTCAT 2400
TTTCATTGCT TTGTAGTATT TTATGTATG CATGTACCAT AATTATTTA TCCAGTTGGA 2460
ATTTATCCTG GCAAGATTT AGTGAGTAAT CCGTCTTTT TCCACTAATG TAAATGCCAC 2520
CAGTTGCACC AACAAATTT AGTGAATAT TGTGTCTCT TCCAGACTT GCTCTTCTG 2580
TTTTATTATT TATTAAATGA CCTTAAATAT TGTGTCTCT TCCAGACTT GCTCTTCTG 2640
TCCATTATC TTTCTATTTC TGAATTTGCA ATGAACAGT TATTATTGTC ACTTATAAT 2700
ACACTTTAAG ATCTGGCAGA GTTGTCTCC GCATTCTCT TTTCTTTTC AGAATCTTTC 2760
TTGATTTCCC TGCAATGATC TTGGAATCAG CTGTCAAGA TCCAAAATAA TCCTGTGTGT 2820
ATGTTTGTCT GTATCCCAT AAAATTATAG ATGAAAAG 2858

Seq ID NO: 147 DNA Sequence
Nucleic Acid Accession #: NM_021077.1
Coding sequence: 37..402

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CGCGCGCCCG AACGAAGCG CGGCCCCGGC ACAGCCATGG CCGGCGGGC GGGGGGCGCT 60
CGGATGTTG GCGGCTCTCT GCTCTTCGCC CTGCTCGCTG CCGGCGTGC CCGCTCAGC 120
TGGGATCTCC CGGAGCCCG CAGCCGAGCC AGCAAGATCC GAGTGCACTC GCGAGGCAAC 180
CTCTGGGCA CCGTCACTT CATGGGCAAG AAGAGTCTGG AGCCTTCCAG CCCATCCCAT 240
TGGGGACAGC TCCCCACACC TCCCTGAGG GACCAGCGAC TGCAGCTGAG TCATGATCTG 300
CTCGGAATCC TCCTGCTAAA GAAGGCTCTG GCGGTGAGCC TCAGCGGCC CGCACCCCAA 360
ATCCAGTACA GAGGCTGCT GGTACAAAAT CTGCAGAAAT GACACCAATA ATAGGGGAG 420
ACACAACAGC GTGGCTTGA TTGTGCCAC CCAGGGAAGG TGCTGAATGG GACCTGTTG 480
ATGGCCCCAT CTGGATGTA ATCTGAGCT CAAATCTCTG TTAATCTATT ACTGTATT 540
CTGGCTGGGT CACCAAGAA ATCGTGAATG CAGACACAGA TTATGTTCT GCTGTATTTC 600
CTGCTTCCCT GTTGAATTG TGAATAAAC CTGCTCTT 639

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80

Seq ID NO: 148 DNA Sequence
Nucleic Acid Accession #: NM_002055.1
Coding sequence: 15..1313

1 11 21 31 41 51

AGAGCCAGAG CAGGATGGAG AGGAGACGCA TCACCTCGCG TGCTCGCGC TCCTACGTCT 60
CCTCAGGGGA GATGATGGTG GGGGCGCTGG CTCTGGCGG CCGTCTGGT CCTGGCACCC 120
GCCTCTCCCT GGCTCGAATG CCGCTCCAC TCCCGACCG GGTGGATTTC TCCTGGCTG 180
GGGCATCTAA TGCTGGCTTC AAGGAGACCC GGGCCAGTGA CCGGCGAGAG ATGATGGAGC 240
TCAATGACCG CTTTGCAGC TACATCGAGA AGGTTGCTT CTGGAACAG CAAACCAAGG 300
CGCTGGCTGC TGAGCTGAAC CAGCTGCGGG CCAAGGAGCC CACCAAGCTG GCAGACGTCT 360

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|----|------------|-------------|------------|------------|------------|-------------|------|
| | ACCAGGCTGA | GCTGCGAGAG | CTGCGGCTGC | GGCTCGATCA | ACTCACCGCC | AACAGCGCCC | 420 |
| | GGCTGGAGGT | TGAGAGGGAC | AATCTGGCAC | AGGACCTGGC | CACTGTGAGG | CAGAAGCTCC | 480 |
| | AGGATGAAAC | CAACCTGAGG | CTGGAAGCCG | AGAACAACTT | GGCTGCTTAT | AGACAGGAAG | 540 |
| | CAGATGAAGC | CACCCTGGCC | CGTCTGGATC | TGGAGAGGAA | GATTGAGTCG | CTGGAGGAGG | 600 |
| 5 | AGATCCGGTT | CTTGAGGAAG | ATCCACGAGG | AGGAGGTTCC | GGAACTCCAG | GAGCAGCTGG | 660 |
| | CCGACAGACA | GGTCCATGTG | GAGCTTGAGC | TGGCCAAGCC | AGACCTCACC | GCAGCCCTGA | 720 |
| | AAGAGATCCG | CACGCAAGAT | GAGGCAATGG | CGTCCAGCAA | CATGCATGAA | GCCGAAGAGT | 780 |
| | GGTACCGCTC | CAAGTTTGCA | GACCTGACAG | ACGCTGTGTC | CCGCAACGCG | GAGCTGCTCC | 840 |
| | GCCAGGCCAA | GCACGAAGCC | AACGACTACC | GGCGCCAGTT | GCAGTCTTTG | ACCTGCGACC | 900 |
| 10 | TGGAGTCTCT | GCGCGGCAAG | AACGAGTCCC | TGGAGAGGCA | GATGCGCGAG | CAGGAGGAGC | 960 |
| | GGCAGCTGGC | GGAGGCGGCC | AGTTATCAGG | AGGCGCTGGC | GCGGCTGGAG | GAAGAGGGGC | 1020 |
| | AGAGCCTCAA | GGACGAGATG | GCCCGCCACT | TGCAGGAGTA | CCAGGACCTG | CTCAATGTCA | 1080 |
| | AGCTGGCCCT | GGACATCGAG | ATGCCCACTT | ACAGGAAGCT | GCTAGAGGGC | GAGGAGAAAC | 1140 |
| | GGATCAACAT | TCCCGTGCAG | ACCTTCTCCA | ACCTGCAGAT | TCGAGAAACC | AGCCTGGACA | 1200 |
| 15 | CCAAGTCTGT | GTGAGAAGGC | CACCTCAAGA | GGAAACATCG | GGTGAAGACC | GTGGAGATGC | 1260 |
| | GGGATGGAGA | GGTCATTAAAG | GAGTCCAAGC | AGGAGCACAA | GGATGTGATG | TGAGGCAGGA | 1320 |
| | CCCACTCTGT | GGCTCTGTGC | CCGTCTCATG | AAGGGCCCGA | GCAGAAGCAG | GATAGTTGCT | 1380 |
| | CCGCTCTGTC | TGGCACAATT | CCCCAGACCT | GAGCTCCCCA | CCACCCACAG | TGCTCCCTCT | 1440 |
| | CCTCTCTGT | CCCTAGGTCA | GCTTGTGTC | CTAGGCTCCG | TCAGTATCAG | GCCTGCCAGA | 1500 |
| 20 | CGGCACCCAC | CCAGCACCCA | GCAACTCCAA | CTAACAGAA | ACTCACCCCC | AAGGGCAGTC | 1560 |
| | TGGAGGGGCA | TGGCCAGCAG | CTTGCGTTAG | AATGAGGAGG | AAGGAGAGAA | GGGGAGGAGG | 1620 |
| | GCGGGGGGCA | CCTACTACAT | CGCCCTCCAC | ATCCCTGATT | CCTGTTGTTA | TGGAAACTGT | 1680 |
| | TGCCAGAGAT | GGAGGTTCTC | TGGAGTATC | TGGGAACTGT | GCCTTTGAGT | TTCTCAGGCG | 1740 |
| | TGCTGGAGGA | AACTGAGAC | TCAGACAGGA | AAGGGAAGGC | CCACAGACA | AGGTAGCCCT | 1800 |
| 25 | GGCCAGAGGC | TGTGTTTGTG | TTTTGGTTTT | TATGAGGTGG | GATATCCCTA | TGCTGCCTAG | 1860 |
| | GCTGACCTTG | AATCTCTGGG | CTCAAGCAGT | CTACCCACCT | CAGCCTCCTG | TGTAGCTGGG | 1920 |
| | ATTATAGATT | GGAGGCCACCA | TGCCAGCTC | AGAGGGTTGT | TCTCTAGAGC | TGACCCCTGAT | 1980 |
| | CAGTCTAAGA | TGGGTGGGGA | CGTCTGCCA | CCTGGGGCAG | TCACCTGCCC | AGATCCCGAG | 2040 |
| | AGGACCTCCT | GAGCGATGAC | TCAAGTGTCT | CAGTCCACCT | GAGCTGCCAT | CCAGGGATGC | 2100 |
| 30 | CATCTGTGGG | CACGCTGTGG | GCAGGTGGGA | GCTTGATTCT | CAGCACTTGG | GGGATCTGTT | 2160 |
| | GTGTAGCTGG | AGAGGGATGA | GGTGCTGGGA | GGGATAGAGG | GGGGCTGCCT | GGCCCCCAGC | 2220 |
| | TGTGGGTACA | GAGAGGTCAA | CCCCAGGAGG | ACTGCCCCGT | GCAGACTGGA | GGGGAACGCTG | 2280 |
| | GTAGAGATGG | AGGAGGAGGC | AATTGGGATG | GCACATAGGA | TACAAGTAGG | GGTTGTGGGT | 2340 |
| | GACCAGTTGC | ACTTGCCCTC | TGSATTGTGG | GAATTAAGGA | AGTGACTCAT | CCTCTTGAAG | 2400 |
| 35 | ATGCTGAAAC | AGGAGAGAAA | GGGGATGTAT | CCATGGGGGC | AGGGCATGAC | TTTGTCCCAT | 2460 |
| | TTCTAAAGGC | CTCTCTCTTG | CTGTGTCTAT | CCAGGCCGCC | CCAGCCTCTG | AGCCCTCTGG | 2520 |
| | ACTGCTGCTT | CTTAACCCCA | GTAAGCCACT | GCCACAGCTC | TGACCCCTCT | CACCCCATAG | 2580 |
| | TGACCGGCTG | CTTTTCCCTA | AGCCAAAGGC | TCTTGCGGTC | CCTTCTTACT | CACACACAAA | 2640 |
| | ATGTACCCAG | TATTTAGAGT | AGTGCCCTAT | TTTACAATTG | TAAAACTGAG | GCACGAGCAA | 2700 |
| 40 | AGTGAAGACA | CTGGCTCATA | TTCTTGACAG | CTGGAGGCGG | GGTGCTCAGG | GCTGACACGT | 2760 |
| | CCACCCCACT | GCACCCACTC | TGCTTTGACT | GAGCAGACTG | GTGAGCAGAC | TGGTGGGATC | 2820 |
| | TGTGCCACGA | GATGGGACTG | GGAGGGCCCA | CTTCAGGGTT | CTCCTCTCCC | CTCTAAAGGC | 2880 |
| | GAAGAAGGGT | CCTTCCCTCT | CCCCAAGACT | TGTTGTCTCT | TCCCTCCACT | TCTTCTGCTC | 2940 |
| | ACCTGCTGCT | GCTGCTGCTG | CTAATCTTCA | GGGCACTGCT | GCTGCCCTTA | GTCGCTGAGG | 3000 |
| 45 | AAAAATAAAG | ACAAATGCTG | CGCCCTTAAA | AAA | | | 3033 |

Seq ID NO: 149 DNA Sequence
Nucleic Acid Accession #: L29126.1
Coding sequence: 445..1845

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| 50 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| | GAATTCGCCC | TCACAGTGGC | CAGGTCCTGT | GCCAGATTGT | CCCTCTCAAC | CTCCAGCCGG | 60 |
| | GCGCTGTTGG | CGTGAGTTGA | TGAGGCCGCA | GCGCGAGCTC | TGCGAGTCA | GCCTGGTAGA | 120 |
| | CGTCTGCCAG | CTTGGTGGGC | TCCTTGCCCC | GCAGCTGGTT | CAGCCTCAGC | AGCCAGCCGC | 180 |
| 55 | TTGTTTTGCT | GTTCAGAGAA | GCGAACCTTC | TGATGTAGC | TGGCAAGCG | GATTGTAGCT | 240 |
| | CCATCATCTC | TGCCCGCTCA | CTGGCCCGGG | TCTCCTTGAA | GCCAGCATTG | AGTGCCCGAG | 300 |
| | CCAGGGAGAA | ATCCACCCGG | GTCCGAGTGG | AGGGGGCATT | CGAGCCAGGG | AGAGGCGGGT | 360 |
| | GCAGGACCCA | GACGCGCGCC | AGGAGCCAGG | CCCCCACCA | TCATCTCCCC | TGAGGAGACG | 420 |
| | TAGGAGCGCG | GAGCAGCGGA | GGTGATGCGT | CTCTCTTCCA | GCCTGTCCGG | CTCGTGGGTG | 480 |
| 60 | TGCTCCGATG | CTGAAGAATA | CCAGCCTCCT | ATATGGAAAT | CATACCTATA | TCAGTTACAG | 540 |
| | CAAGAGGCAC | CTCGTCCCAA | GAGAATCAAT | TGTCTCGGG | AGGTGGAAAA | CAGACCAAAA | 600 |
| | TATTATGGAA | GAGAGTTTCA | TGGGATCATC | TCTCGGGAGC | AGGCGGATGA | GCTTCTTGGA | 660 |
| | GGCGTGGAGG | GTGCTACAT | CCTTAGAGAA | AGCCAGCGGC | AACCAGGATG | CTACACGCTG | 720 |
| | GCTCTCAGGT | TTGGAACCA | GACCTTAAAC | TACAGGCTCT | TCCAGCAGCG | GAACACATTT | 780 |
| 65 | GTGGGTGAGA | AGAGGTTTGA | GTGATTTCAT | GATCTGGTGA | CAGATGGCTT | GATAACACTG | 840 |
| | TACATAGAAA | CAAAAGCTGC | CGAGTACATT | TCAAAAATGA | CAACTAACCC | CATCTATGAA | 900 |
| | CACATTGGAT | ATGCCACCCT | ACTCAGAGAA | AAAGTATCCA | GAAGGCTGAG | CAGGTCTAAA | 960 |
| | AATGAACCAA | GA AAAACAAA | CGTCACACAT | GAAGAACACA | CAGCGGTGGA | AAAGATCTCC | 1020 |
| | TCCCTGGTTC | GAAGGGCTGC | CCTCACACAC | AACGACAACC | ACTTCAATTA | TGAGAAGACA | 1080 |
| 70 | CACAACCTTA | AGGTCCACAC | GTTCGAGGC | CCACACTGGT | GTGAATATTG | TGCCAATTTT | 1140 |
| | ATGTGGGGCC | TCATCGCCCA | AGGGGTCCGG | TGCTCAGACT | GTGGATTGAA | CGTACACAAA | 1200 |
| | CAGTGTTCGA | AGCAGCTTCC | CAATGACTGC | CAACCTGATC | TCAAGAGGAT | CAAGAAAGTG | 1260 |
| | TACTGTGTGT | ACCTCACAAC | ACTTGTGAAG | GCTCACAACA | CTCAGAGACC | CATGTTGGTA | 1320 |
| | GACATATGCA | TTGCGGAAAT | TGAAGCAAGA | GGATTAAAT | CGGAAGGCCT | TTACAGAGTC | 1380 |
| 75 | TCTGGGTTCA | GTGAACACAT | TGAAGATGTC | AAAAATGGCAT | TTGACAGAGA | TGGTGAAAAG | 1440 |
| | GCCGATATAT | CTGCCAATGT | CTATCCAGAC | ATAAACATCA | TCACTGGAGC | CCTTAAACTG | 1500 |
| | TATTTACAG | ACTTACCCAT | CCCTGTCTAT | ACATATGATA | CCTATTCCAA | ATTATATAGT | 1560 |
| | GCAGCAAAAA | TCTCCAATGC | AGATGAGAGG | CTGGAAGCCG | TCCATGAAGT | GCTGATGCTG | 1620 |
| | CTGCCTCCTG | CCCACTATGA | AACCCCTCCG | TACCTAATGA | TCCACCTCAA | AAAGGTTACT | 1680 |
| 80 | ATGAATGAAA | AAGACAATTT | CATGAATGCA | GA AAAATCTGG | GGATCGTGTG | TGGGCCCACT | 1740 |
| | CTGATGAGGC | CCCCTGAGGA | CAGCACCCCTG | ACCACCCCTG | ATGATATGCG | GTACCAAAAAG | 1800 |
| | CTGATTGTGC | AGATTTTAAAT | AGAAAACGAA | GACGTTTTAT | TCTAATCCAT | CAGGGAAATG | 1860 |
| | AGCTGAATGG | CCAGCACCA | TCAAGTTGAC | ACAGCTAAGG | ATAAAACATT | TCTTACCACCT | 1920 |
| | TGATTTGTTT | TCCAAGCAAG | TGCTAGAATT | TGCTGGACTG | CAGAGGATCG | CTGAGTGGGG | 1980 |

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Seq ID NO: 150 DNA Sequence
Nucleic Acid Accession #: XM_113553.1
Coding sequence: 25..939

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| 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | |
| CCCAGGAACC | CCCAGGGAGC | CAGCATGAAG | CGAGCTCACC | CCGAGTACAG | CTCCTCGGAC | 60 |
| AGCGAGCTGG | ACGAGACCAT | CGAGGTGGAG | AAGGAGAGTG | CGGACGAGAA | TGGAAACTTG | 120 |
| AGTTCGGCTC | TAGGTTCCAT | GTCCCCAACT | ACATCTTCCC | AGATTTTGGC | CAGAAAAAGA | 180 |
| CGGAGAGGAA | TAATTGAGAA | GCGCCGACGA | GACCGGATCA | ATAACAGTTT | GTCTGAGCTG | 240 |
| AGAAGGCTGG | TACCCAGTGC | TTTTGAGAA | CAGGGATCTG | CTAAGCTAGA | AAAAGCCGAG | 300 |
| ATCCTGCAGA | TGACCGTGA | TCACCTGAAA | ATGCTGCATA | CGGCAGGAGG | GAAAGGTTAC | 360 |
| TTTGACGCGC | ACGCCCTTGC | TATGGACTAT | CGGAGTTTGG | GATTTGCGGA | ATGCCTGGCA | 420 |
| GAAGTTGCCG | GTTATCTGAG | CATCATTGAA | GGACTAGATG | CCTCTGACCC | GCTTCGAGTT | 480 |
| CGACTGGTTT | CGCATCTCAA | CAACTACGCT | TCCAGCGGGG | AAGCCGCGAG | CGGCGCCAC | 540 |
| GCGGGCTCTG | GACACATTCC | CTGGGGGACC | GTCTTCGGAC | ATCACCCGCA | CATCGCGCAC | 600 |
| CCGCTGTTGC | TGCCCCAGAA | CGGCCACGGG | AACGCGGGCA | CCACGGCCTC | ACCCACGGAA | 660 |
| CGCACCAACC | AGGGCAGGCT | GGGCTCGGCA | CATCCGGAGG | CGCCTGCTTT | GCGAGCGCCC | 720 |
| CCTAGCGGCA | GCCTCGGACC | GGTGCTCCCT | GTGGTCACCT | CCGCTCCCAA | ACTGTGCGCG | 780 |
| CCCTCTGCTC | CCTCAGTGCG | CTCCCTGTGG | GCCTTCCCCC | TCTCTTTGGG | CTCCTTCCAC | 840 |
| TTACTGTCTC | CCAAATGCAAT | GAGCCCTTCA | GCACCCACGC | AGGCTGCAAA | CCTTGGCAAG | 900 |
| CCCTATAGAC | CTTGGGGGAC | GGAGATCGGA | GCTTTTAA | GAACTGATGT | AGAATGAGGG | 960 |
| AGGGGAAAGT | TAAAAATCCC | AGCTGGGCTG | GACTGTTGCC | AACATCACCT | TAAAGTCGTC | 1020 |
| AGTAAAGTA | AAAAGGAAAA | AGGTACACTT | TCAGATAATT | TTTTTTTAA | AGACTAAAGG | 1080 |
| TTTGTGGT | TACTTTTATC | TTTTTTAATG | TTTTTTTCA | CATGTCATGT | ATTAGCAGTT | 1140 |
| TTTAAAACT | AGTTGTAA | TTTTGTCAA | GACATTAAT | TGAAATAGTG | AGTATAAGCC | 1200 |
| AACACTTTGT | GATAGGTTTG | TACTGTGCCT | AATTTACTTT | GTAACCCAGA | ATGATTCGGT | 1260 |
| TTTTGCCTCA | AAATTTGGGG | AATCTTAACA | TTTAGTATTT | TTGGTCTGTT | TTTCTCCTTG | 1320 |
| TATAGTTATG | GTCTGTTTTT | AGAAATTAAT | TTCCAAACCA | CTATGCTTAA | TGTTAACATG | 1380 |
| ATTCTGTTTG | TTAATATTTT | GACAGATTAA | GGTGTGTAT | AAATAATATT | CTTTTGGGGG | 1440 |
| GAGGGGAAC | ATATTGAATT | TTATATTTCT | GAGCAAAAGG | TTGACAAATC | AGATGATCAG | 1500 |
| CTTTATCCAA | GAAAGAAAGC | TAGTAAATTG | TCTGCCTCCT | ATAGCAGAAA | GGTGAATGTA | 1560 |
| CAAACTGTTG | GTGGCCCTGA | ATCCATCTGA | CCAGCTGCTG | GTATCTGCCA | GGACTGGCAG | 1620 |
| TTCTGATTTA | GTTAGGAGAG | AGCCGCTGAT | AGGTTAGGTC | TCATTGAGAG | TGTTGGTGGG | 1680 |
| AAGGAAACTG | AAGGTAATTG | AATAGAAATC | GCCTGCATT | ACCAGCCCCA | GCAACACAAA | 1740 |
| GAATTTTTTA | TCACACGGAT | CTCAAATTCA | CAAATGTTAA | CATGGATAAG | TGATCATGGT | 1800 |
| GTGCGAGTGG | TCAATTGAGT | AGTACAGTGG | AAACTGTAA | ATGCATAACC | TAATTTTCCT | 1860 |
| GGGACTGCCA | TATTTTCTTT | TAACTGGAAA | TTTTTATGTG | AGTTTTCCCT | TTGGTGATG | 1920 |
| GAACTGTGGT | TGCCAAGGTA | TTTAAAGGG | CTTCTCTGCC | TCCTCTCTCT | TGATTTATTT | 1980 |
| AATTTGATT | GGGCTATAAA | ATATCATTTT | TCAGGTTTAT | TCTTTAGCA | GGTGTAGTTA | 2040 |
| AACGACCTCC | ACTGAACCTG | GTTTGACCTC | TGTTGACTG | ATGTTGTTG | ACTAAATAAA | 2100 |
| AAA | | | | | | 2103 |

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Seq ID NO: 151 DNA Sequence
Nucleic Acid Accession #: NM_001936.2
Coding sequence: 178..2589

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| 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | |
| AGCAAACTCG | TCTTGTCTAC | CCACCCCTCCC | TCCCCCATCC | TCCCCAAAT | AGCCTTGTA | 60 |
| TTTCGGAAAGT | ATGGACTAAA | ATCACACTCC | TCTTACCTT | ACCGCTTGGG | CTCTGGTGGC | 120 |
| TCCCAACTCG | CCGTGAGACC | CCACCTGCCC | CGGTGGTGGG | AAGCGCCTGG | ACAGACCATG | 180 |
| ACCAAGAGCA | AGGAGCCAG | CGCTTCGGGG | AAATCCGTGC | AGCAGCAGGA | ACAGGAGCTG | 240 |
| GTGGGGAGTA | ACCCTCCGCA | GAGGAATTGG | AAAGGAATAG | CAATTGCAC | GCTTGTCAAT | 300 |
| CTGGTCATCT | GCTCCTTGAT | CGTCACCTCG | GTCATACTTC | TGACACCAGC | GGAAGATAAT | 360 |
| AGTCTGTCTC | AAAAGAAGAA | GGTCACTGTA | GAAGATCTCT | TCAGTGAAGA | CTTCAAAATT | 420 |
| CATGACCCCG | AGGCTAAGTG | GATAAGTGAT | ACAGAAATCA | TCTACAGAGA | ACAGAAAGGA | 480 |
| ACAGTGAGAC | TGTGAAATGT | TGAAACAAAT | ACTTCTACTG | TCTTAATAGA | AGGCAAAAAA | 540 |
| ATTGAATCAT | TAAGAGCCAT | CAGATATGAA | ATATCTCCAG | ATAGAGAGTA | TGCATTTTTT | 600 |
| TCATACAAATG | TGGAACCCAT | ATATCAACAC | TGCTATACTG | GATATTACGT | CCTGAGCAAA | 660 |
| ATTCCTCATG | GGGATCCTCA | AACTCTGGAC | CCACAGAAAG | TCAGCAATGC | AAAGCTTCAG | 720 |
| TATGCAAGAT | GGGGCCCTAA | AGGCCAACAG | CTGATATTTA | TTTTTGAAAA | CAATATCTAC | 780 |
| TACTGTGCAC | ATGTCCGGAA | ACAGGCCATC | CGTGTGGTCT | CCACTGGCAA | GGAAGGTGTG | 840 |
| ATTTACAATG | GCCTCAGTGA | CTGGCTGTAT | GAAGAGGAGA | TTTTGAAGAC | ACACATCGCA | 900 |
| CACTGGTGGT | CTCCGGATGG | CACGAGACTC | GCCTACGCGG | CCATCAATGA | TTCCGCTGTC | 960 |
| CCCATCATGG | AGCTCCCAAC | TTACACCGGC | TCCATCTACC | CCACCGTGAA | GCCCTACCAC | 1020 |
| TATCCCAAGG | CTGGAAGTGA | GAACCCACG | ATTCCCTAC | ACGTTATTGG | CTTAAATGGA | 1080 |
| CCCAACCATG | ATCTGGAGAT | GATGCCGCTC | GATGATCCAC | GGATGAGGGA | GTAACATATC | 1140 |
| ACCATGGTGA | AGTGGGCCAC | CAGCACCAAG | GTCCCGTGA | CCTGGCTGAA | CCGGGCGCAG | 1200 |
| AACGTGTCCA | TCTTCAACCT | CTGCGACGCC | ACCAAGGGGG | TCTGCACGAA | GAAACACGAG | 1260 |
| GATGAAAGTG | AGGCCTGGCT | CCACAGACAG | AATGAAGAAC | CTGTGTTCTC | CAAGGATGGC | 1320 |
| CGAAAGTTTT | TCTTCATCAG | AGCCATCCCC | CAGGAGGAGC | GAGGGAAATT | CTATCACATC | 1380 |
| ACGGTGTCTC | CGTCCACGCC | CAACAGCAGC | AACGACAACA | TCCAGTCCAT | CACCTCCGGG | 1440 |
| GACTGGGACG | TGACCAAGAT | CCTAGCCTAC | GATGAGAAGG | GGAATAAGAT | CTACTTCTCG | 1500 |
| AGCACGGAGG | ACCTGCCTCG | GAGACGACAA | CTCTACAGTG | CCAACACGGT | GGGCAACTTC | 1560 |
| AACAGGCAGT | GCCTCTCCTG | TGACCTGGTT | GAGAACTGCA | CCTACTTCAG | CGCTTCTCTC | 1620 |
| AGCCATAGCA | TGGACTTCTT | CCTGCTCAAG | TGCGAAGGTC | CTGGTGTTC | TATGGTGAAG | 1680 |

5 GTGCACAACA CAACAGATAA GAAAAAATG TTTGACCTAG AAACAAATGA ACATGTCAAG 1740
 AAGGCCATAA ATGACCCGACA GATGCCATAA GTGGAATACA GGGACATTGA GATTGATGAT 1800
 TACAACCTGC CCATGCGAGT ACTGAAGCCA GCAACCTTCA CCGACACCAC CCACTACCCT 1860
 CTGCTCTCGG TGGTGGATGG CACCCCGGGC AGCCAGAGTG TAGCTGAGAA GTTCGAGGTG 1920
 AGCTGGGAGA CGGTGATGGT GAGCAGCCAC GCGCGGTGG TGGTAAAGTG TGACGGCCGT 1980
 GGCACGGGCT TCCAAAGGAC CAAGCTCCTG CACGAAGTGA GCGCGCGCTG GGGCTTGCTG 2040
 GAGGAGAAGG ACCAGATGGA GGCGGTGCGG ACGATGCTGA AGGAGCAGTA CATTGACAGG 2100
 AGCGCGGTGG CCGTGTCTGG GAAGGATTAC GGTGGCTACC TGAGCACCCTA CATCTCCCA 2160
 10 GCAAAGGGAG AAAATCAAGG CCAGACATTG ACCTGCGGCT CTGCTCTCTC TCCAATAACA 2220
 GACTTCAAAC TCTATGCCCT TGCGTTTTCG GAGAGGTACT TGGGCTTCCA TGGACTTGAC 2280
 AACAGAGCAT ACGAGATGAC CAAGGTAGCC CATCGAGTCT CCGCGCTGGA AGAACAGCAG 2340
 TTCCTGATCA TTCATCCACC TGCCGATGAA AAAATTCAAT TCCAGCACAC AGCAGAACTC 2400
 ATTACACAAC TAATTAGGGG AAAGGCTAAT TACAGCTTAC AGATTTACCC GGACGAAAGC 2460
 15 CATTACTTTA CCAGTCCAGC CCTCAAAACG CATCTGTACC GGTCCATCAT CAACTTCTTC 2520
 GTGGAATGCT TCCAGTCCCA GGACAAACTG CCGACAGTCA CAGCGAAAGA GGACGAGGAG 2580
 GAGGACTAAG CTCAGGTGCG TCTAAGCACA AACGTGGCTC TTTCTACAAC CAGATGCAAC 2640
 CGAGGGAATT CCTCGCCCTC CCTCTTCCCT CGGAGGGGCG GGGCGGGGCG GGGCGGGTGG 2700
 TTCCATAGCA TGTGTGCTCT GGATGCGGAA GGCAGTTTGG CTTGGGAAAC AAGCTCCTTC 2760
 20 CCGCGGGTGA TCACTCAGCG CCTCCATGGC ACCAGGGACA ACGCTGTCCC CGCAGCAGCG 2820
 CCTCTCCCG GCGCCCGAGA GACCGGCACG CCAACGGCCC TCCCGCAAGG AACAGAGCAA 2880
 AGGATGGTGG CCGCAGGCC CACGCGAGCC CACAGGACAC CGGCCCTTAG ATTCCAGCCA 2940
 CCAAGCGGAA GCATGAGACC GCGCCCACT AGCCTCTGTG TTCCGTTAG GGACATCA 3000
 CCTGTCTCA CGTCGCGAGT CCATGGACGC AGCAGTTACA GCACCATGTG TTTAGCAGTG 3060
 25 CGTGTTCATA TATGGGCTTG CTACTTCTGT TAATGAGGAC GTTCAACATG GTGAGGGGCT 3120
 ACAAGAAACG GCTTTTCTGT ACAGAGTCTT ACTGTAGCTA CGTAAATGGT TAACCTGATA 3180
 GAATTAACCT GTATTTTTCT ATGGTTTAA CTTGATGCTC CACTGTCTCC GTCATGGGGT 3240
 TGTTTTGTG TTTGGGGTGG GGCTTTGTTT CCTTTTCTT TCTCCAGTCC ACGTGTAGAC 3300
 TTTGGGCTTG ATGAAGAAGC AGATCGGAAG TAACTGCTCC CTCCTCAAGG TTGTCTTCAG 3360
 30 ACGTCTTGGG GAGCTTCTTA AACACTGAGG GGAAGACAG CCAATAGCAC CCATTAAAGC 3420
 AAATACCTAA ATAAACCTC TCTCCCACTC AGCTATGCTA GGGCTTGGCT GTAGGTGTGC 3480
 ACTGTCTATT TACATCCGTC CTTACAACCA TCCTTGTCTT CCTTGTACCC GTATCAAGCT 3540
 CTTTCCCATG ACATTGTGTT 3560

35 Seq ID NO: 152 DNA Sequence
 Nucleic Acid Accession #: XM_087461.1
 Coding sequence: 236..1138

1 11 21 31 41 51
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 40 CCGCGCGCGG GGGCGGCGGG GAACCCCAAA CGCAACCGGG TCTGGAGGGA TCCCGCGCGC 60
 GAGCCAGCCG CCGTCAACGC CTCGCGCGCG CCCCTGCGGG CTTGGCAGGC GCCCGGCGCG 120
 CCGCAGCTGC GCCCGGCGCG CGGCTCCGCG GGTCCACCGG TGAGCTCGCC GGGCGGTGCG 180
 CCGCTCGCCA TGCAACCGCC GCGCGCTCG CGCGCGTAGG CGCCCGCGCG AGGCCATGCT 240
 GCGCTGCTGC GCGCGCTGCG TGCGCGCGCG CTGCGCGCTG CCGCGCGTCC GCGCGGCGGC 300
 45 GCGGAGCGCG CCGCGCTTCC TCGGGGTGCC TCCAATGCT TCAGTCAACG CGTCTCTCGC 360
 GCGGAGCCCA TCGCGCGCGG GCTGCTGGCC TCGCGCGCCC CGGGGCCCCC CGAGCGCCCG 420
 GCGCGGAGGG AGCGCGCGCG GCGCGCGCGG CCTGTGCAAC ATCAGCGTGC AGCGGCAGAT 480
 GCTGAGCTCG CTGCTGCTGC GCTGGGGCGG CCGCGCGGGC TTCCAGTGGG ACCTACTGCT 540
 CTTCTCCACC AACCGCGCAG GCGCGCTTTT CTTCGCGCGC GCCTTCCACC GCGTGGGGCC 600
 50 GCGCGTCTGC ATCGAGCACC TGGGGCTGGG GCGCGCGCGC GCGCAGCAGG ACCTGCGGCT 660
 CTGGTGGGCG TGGCGCTGCG TGCGCGGTGC CGCACCGGCG CGCTCCGCGC CCGCGCGCGC 720
 CCGCAGCGCC GCGCGCGCCA CCGCGCGGGC GCGCACCGCG CTGCCAGCCT ACCCGCGGCG 780
 CGAGCGCGCC GGGCGGCTGT GGCTGCAGGG CGAGCGCGTG CATTTCTGCT GCCTAGACTT 840
 CAGCTTGAAG GCGCTGAGG GCGAGCGCGG CTGGCGGCTG AACGTAAGC CCATTGAGTC 900
 55 CACGCTGGTG GCGTGTCTCA TGACCTGGT CATCGTGGTG TGGAGCGTGG CCGCCCTCAT 960
 CTGGCGGGTG CCGCATGCG CGGCTTCTT GCCCAACGGC ATGGAACAGC GCGGAGCCAC 1020
 CGCGAGCACC ACCGAGCCCA CCGCGCGCGG AGTGGCCGCA GGGACCAACG CAGCGCGCGC 1080
 GCGCGCGCGG GCTGCGCGCG CCGCGCGGGC CGTCACTTGG GGGGTGGCGA CCAAGTGACC 1140
 CGCTCGCTCC CTCTCTGTG TCGCGCGCGG CGGTGCGCTT TCCGCGCGGA 1200
 60 GACTCGGCGG GTGTGCTTGG TGCTGTAGTT ATCGTTAGTT CCTCTTCCCG AGATGGGGCC 1260
 GCGGAGAGAG CCGAGCGGCT TTGAAAGACA AGGTTTGTGC TGCGCTTCCA GTTCCGAAAA 1320
 GCAGATGTTT AAGCCCTTGG ACTGAGGGTG GSATCGCAGC TCCGAAGACG GAGAGGAGGG 1380
 AAATGGGGCC CTTTCCCTTC TATTGCATCC CCTGCGCGGA CTCCTTCCCC GCACCCACGT 1440
 GCGCTAGATT CATGGCAGAA AATGACCAAA TCCTGTGTAT TTGTTTATA TATTTAATAA 1500
 65 CTGTTTAAAG TGAAGTTTAT AGTAAAGAAA ATACAAAACA AAAAGATTAA ATTGCTATTG 1560
 CTGTAGTAAG AGAAGCTCTT TGTATCTGAA CATAGTTGTA TTTGAAATTT GTGGTTTTTT 1620
 AATTTATTTA AAATTTGGGG GAGGGCATGG GAAGSATTTA ACACCGATAT ATTGTTACCG 1680
 CTGAAATGAC ACTTATAGAA CCTTTTCCAA GTTGATCTAT CCAGTGACGT GGCCTGGTGG 1740
 GCGTTTCTTC TTGTACTTAT GTGGTTTTTT GCGTTTTAAT ACAGACATT TCTTCC 1796

70 Seq ID NO: 153 DNA Sequence
 Nucleic Acid Accession #: NM_012261.1
 Coding sequence: 1-843

1 11 21 31 41 51
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 75 ATGGATCTCC AAGGAAGAGG GGTCCCCAGC ATCGACAGAC TTCGAGTTCT CCTGATGTTG 60
 TTCCATACAA TGGCTCAAAT CATGGCAGAA CAAGAAGTGG AAAATCTCTC AGGCCCTTCC 120
 ACTAACCTCG AAAAAGATAT ATTTGTGGTG CGGGAATATG GGAAGAGTGT TCTCATGGCA 180
 GAGTTTGCAG CCAAAATTTAT TGTACCTTAT GATGTGTGGG CCAGCAACTA CGTAGATCTG 240
 80 ATCAGAAAC AGGCCATATG GCATTGAGC CGGGGAGCTG AGGTGAAGGG CCGCTGTGGC 300
 CACAGCCAGT CGGAGCTGCA AGTGTCTGCG GTGGATCGCG CATATGCACT CAAATGCTC 360
 TTTGTAAAGG AAAGCCACAA CATGTCCAAG GGACCTGAGG CGACTTGGAG GCTGAGCAAA 420
 GTGCAGTTTG TCTACGACTC CTCGGAGAAA ACCCACTTCA AAGACGCAGT CAGTGCTGGG 480
 AAGCACACAG CCAACTCGCA CCACTCTCTC GCCTTGGTCA CCGCGCTGCG GAAGTCTCTAT 540
 GAGTGTCAAG CTCACAAAC CATTTCACTG GCCTCTAGTG ATCCGAGAAA GACGCTCACC 600

5
 ATGATCCTGT CTGCGGTCCA CATCCAACTT TTTGACATTA TCTCAGATTT TGTCTTCAGT 660
 GAAGAGCATA AATGCCAGT GGTGAGCGG GAGCACTGG AAGAAACCTT GCCCTGATT 720
 TTGGGGCTCA TCTTGGGCTT CGTCATCATG GTAACTCTG CGATTACCA CGTCCACCAC 780
 AAAATGACTG CCAACCAGGT GCAGATCCCT CGGGACAGAT CCCAGTATAA GCACATGGGC 840
 TAG 843

Seq ID NO: 154 DNA Sequence
 Nucleic Acid Accession #: NM_144586
 Coding sequence: 261..686

10
 1 11 21 31 41 51
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 GGCACGAGGC CGGAGGCGCG GTGCTCGGCC CGGAGCGCG AGCGGGAGGA GCAGAGACCC 60
 GCAGCCGGGA GCCCGAGCGC GGGCGATGCA GGCTCCGCGA GCGGCACCTG CGCTCTCTCT 120
 AAGCTAAGAC CGTGTCTCTC GCGGCAGCAG CGCGGGCCCC AGCAGCCTCG GCAGCCACAG 180
 15 CCGCTGCAGC CGGGGACGCC TCCGCTGCTG TCGCTCTCTT TGATGCGCTT GCCCTCTCCC 240
 GGCCCGGGGA CTCGCGGAGA ATGTGGGTCC TAGGCATCGC GGCACCTTTT TCGCGATTGT 300
 TCTTGCTTCC AGGCTTTGCG CTGCAAAATCC AGTGCTACCA GTGTGAAGAA TTCCAGCTGA 360
 ACAACGACTG TCCTCCCCCG GAGTTCATTG TGAATTGCAC GGTGAACGTT CAAGACATGT 420
 20 GTCAGAAAGA AGTCATGGAG CAAAGTGCAG GGATCATGTA CGCAAGTCC GTGTCATCAT 480
 CAGCGCGCTG TCTCATCGCC TCTGCGGGGT ACCAGTCTCT CTGCTCCCCA GGGAAACTGA 540
 ACTCAGTTTG CATCAGCTGC TGCAACACCC CTCTTTGTAA CGGGCCCAAG CCCAAGAAAA 600
 GGGGAAGTTC TGCTCCGGCC CTCAGGCCAG GGCTCCGCAC CACCATCTCT TTCTCTCAAT 660
 TAGCCCTCTT CTGCGCACAC TGCTGAAGCT GAAGGAGATG CCACCCCTCT CTGCATTGTT 720
 25 CTTCCAGCCC CTGCCCCCAA CCCCCACCT CCTGAGTGA GTTTCTTCTG GGTGCTCTTT 780
 TATTCTGGGT AGGGAGCGGG AGTCGCTGTT CTCTTTGTTT CCGTGTGAAA TAATGAAAGA 840
 GCTCGGTTAA GCATTCTGAA TAAATTGAG CTGACTGAA TTTTCAGTATG TACTTGAAGG 900
 AAGGAGGTGG AGTGAAGATT CACCCCAAAA AAAAAA 946

Seq ID NO: 155 DNA Sequence
 Nucleic Acid Accession #: NM_004694
 Coding sequence: 166..1737

30
 1 11 21 31 41 51
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 TTGGGGGTTT ATTCTCTTCC CTCTAACTT GACAGGGTCT TGCTCTGTCA TTCAGGCAAG 60
 35 AGTGCACTAG TGTGATCACT TCTTACTGCC GCCTCAAGCT TCCAGCCTCA ACTCAAGCAA 120
 TCCTCCACC TCAGCCACCC AAGTGGCTGG GACTACAGAT TAAGAATGAC CCAAAATAAA 180
 TTAAAGCTTT GTTCCAAAGC CAATGTGTAT ACTGAAGTGC CTGATGGAGG ATGGGGCTGG 240
 GCGGTAGCTG TTTCAATTTT CTTCGTTGAA GTCTTCACTT ACGGCATCAT CAAGACATT 300
 40 GGTGTCTTCT TTAATGACTT AATGGACAGT TTTAATGAAT CCAATAGCAG GATCTCATGG 360
 ATAATCTCAA TCTGTGTGTT TGTCTTAACA TTTTCAGCTC CCTCGCCAC AGTCTCTGAGC 420
 AATCGTTTCG GACACCGTCT GGTAGTGATG TTGGGGGGGC TACTTGTCAG CACCGGATG 480
 GTGGCCGCTT CCTTCTCACA AGAGGTTTCT CATATGTACG TCGCCATCGG CATCATCTCT 540
 GGTCTGGGAT ACTGCTTTAG TTTTCTCCCA ACTGTAACCA TCCTATCACA ATATTTTGGC 600
 45 AAAAGAGCTT CCATAGTCAC TGCAAGTGTG TCCACAGGAG AATGTTTTCG TGTGTTTGCT 660
 TTCGACCCAG CAATCATGGC TCTGAAGGAG CGCATTGGCT GGAGATACAG CCTCCTCTTC 720
 GTGGGCTTAC TACAGTTAAA CATTGTATC TTGGAGCAC TGCTCAGACC CATCATTATC 780
 AGAGGACCAG CGTCACCGAA AATAGTCATC CAGGAAAATC GGAAGAAGC GCAGTATATG 840
 CTTGAAATAG AGAAAACAGC AACCTCAATA GACTCCATTG ACTCAGGAGT AGAACTAACT 900
 50 ACCTCACTTA AATAATGTGCC TACTCACACT AACCTGGAAC TGGAGCCGAA GGCCGACATG 960
 CAGCAGGTCC TGGTGAAGAC CAGCCCCAGG CCAAGCGAAA AGAAAGCCCC GCTATTAGAC 1020
 TTCTCCATT TGAAGAGCAA AGTTTATT TGTATGCAT TATTTGGTCT CTTTGCAACA 1080
 CTGGGATTCT TTGCACCTTC CTGTACATC ATTCCTCTGG GCATTAGTCT GGGCATTGAC 1140
 CAGGACCGCG CTGCTTTTTT ATTATCTACG ATGGCCATTG CAGAAGTTT CGGAAGGATC 1200
 55 GGAGCTGGTT TTGTCTCAA CAGGGAGCCC AITCGTAAGA TTTACATTGA GCTCATCTGC 1260
 GTCATCTTAT TGACTGTGTC TCTGTTTGCC TTTACTTTTG CTAAGTAAAT CTGGGGCTCA 1320
 ATGTCAATGA GCATATTTT TGGGTTATG GTTGAACAA TAGGAGGACT CACATTCCAC 1380
 TGCTTGCTGA AGATGATGTC GTGGGCATTG CAGAAGATGT CTTCTGCAGC TGGGGTCTAC 1440
 ATCTTCAATC AGAGCATAGC AGGACTGGCT GGACCGCCCC TTGCAGGTTT GTTGGTGGAC 1500
 60 CAAAGTAAGA TCTACAGCAG GGCTTCTAC TCTGCGCAG CTGGCATGGC CCTGGCTGCT 1560
 GTGTGCTCG CCTCGGTGAG ACCGTGTAAG ATGGGACTGT GCCAGCGTCA TCACTCAGGT 1620
 GAAACAAAGG TAGTGAGCCA TCGTGGGAG ACTTTACAGG ACATACCTGA AGACTTTCTG 1680
 GAAATGGATC TTGCAAAAAA TGAGCACAGA GTTCACGTGC AAATGGAGCC GGTATGACAC 1740
 ACTTTCTTAC AACCAACGCC ACTGTGTTGG CTGGAGAGGG ATGGGGTGGG CCCAAGGGG 1800
 65 ACACAAGGAG GCAGAGGAGC TAACCCCTCT ACTCCACTTT CAAAACCTACA TTTTAAAGGG 1860
 AATGTGTATG TGAAGAGCAC TACCAACATC GCTTTTGTGT TGTTTTGTGT TGTTTTAAAG 1920
 TTTTGTGTGT TGCTTGTGTT TAAAGCCAAA ACAAAAAACA ACCAAGCACT CTTCCATATA 1980
 TAAATCTGGC TGTATTCACT AGCAATACAA GAGATATGTA GAAAGACTCT TTGGTTTACA 2040
 70 TTCCGATATT AAAATAGTGA CATGAACCTG CAAAGTGGTT TTTAAAGCTT TCAGTGGGA 2100
 TAAATGATTT TCTTTTCTT TTTTCTTCT TCTATGGTC TTGTCTGAAT AAACCTACTCT 2160
 CCTGAATAAA ACAACATCCA ACCCAGGTCA TTGAATGAA ATTGGCCAGT C. 2212

Seq ID NO: 156 DNA Sequence
 Nucleic Acid Accession #: NM_004833.1
 Coding sequence: 246..1277

75
 1 11 21 31 41 51
 | | | | |
 TCAGCCAATT AGAGCTCCAG TTGTCACTCC TACCCACACT GGGCCTGGGG GTGAAGGGAA 60
 GTGTTTATTA GGGGTACATG TGAAGCCGTC CAGAAGTGTG AGAGTCTTTG TAGCTTTGAA 120
 80 AGTCACCTAG GTTATTGGG CATGCTCTCC TGAGTCTCTT GCTAGTTAAG CTCTCTGAAA 180
 AGAAGGTGGC AGACCGGTT TGCTGATCGC CCCAGGGATC AGGAGGCTGA TCCCAAGTT 240
 GTCAGATGGA GAGTAATAC AAGGAGATAC TCTTGCTAAC AGGCTTGGAT AACATCACTG 300
 ATGAGGAATC GGATAGGTTT AAGTTCTTTC TTTTACAGCA GTTTAATATT GCCACAGGCA 360
 AACTACATAC TGCAACACGA ATACAAGTAG CTACCTTGAT GATTCAAAT GCTGGGGCGG 420
 TGTCTGCAGT GATGAAGACC ATTGTAATTT TFCAGAAATT GAATTATATG CTTTGGCAA 480

AACGTCTTCA GGAGGAGAAG GAGAAAAGTTG ATAAGCAATA CAAATCGGTA ACAAACCAA 540
 AGCCACTAAG TCAAGCTGAA ATGAGTCTCTG CTGCATCTGC AGCCATCAGA AATGATGTCG 600
 CAAAGCAACG TGCTGCACCA AAGTCTCTCT CTGATGTTAA GCCTGAACAG AACAGATGG 660
 TGGCCAGCA GGAATCTATC AGAGAAGGGT TTCAGAAGCG CTGTTTGCCA GTTATGGTAC 720
 5 TGAAGACAAA GAAGCCCTTC ACGTTTGAGA CCAAGAAGG CAAGCAGGAG ATGTTTCATG 780
 CTACAGTGGC TACAGAAAAG GAATTTCTCT TGTAAAAGT TTTAATACA CTGCTGAAAG 840
 ATAAATTCAT TCCAAGAGA ATAATTATA TAGCAAGATA TTATCGGCAC AGTGGTTTCT 900
 TAGAGGTAAA TAGCGCTCA CGTGTGTAG ATGCTGAATC TGACCAAAAG GTTAATGTCC 960
 CGCTGAACAT TATCAGAAA GCTGGTGAAA CCCCAGGAT CAACACGCTT CAACTCAGC 1020
 10 CCCTTGAAC AATTGTGAAT GGTGTGTTG TAGTCCAGAA GGTAACAGAA AAGAAGAAAA 1080
 ACATATTATT TGACCTAAGT GACAACACTG GAAAAATGGA AGTACTGGGG GTTAGAAACG 1140
 AGGACACAAT GAAATGTAA GAAAGAGATA AGTTTCGACT TACATTCTTC ACCTGTCAA 1200
 AAAATGGAGA AAACTACAG CTGACATCTG GAGTTCATAG CACCATAAAG GTTATTAAGG 1260
 CCAAAAAAA AACATAGAGA AGTAAAAAG ACCAATTCAA GCCAACTGGT CTAAGCAGCA 1320
 15 TTTAATTGAA GAATATGTGA TACAGCCTCT TCAATCAGAT TGTAAAGTAC CTGAAAGCTG 1380
 CAGTTCCAGG GCTCTCTCT CCAACCAATT AGGATAGAAT AATTGCTGGA TAAACAAATT 1440
 CAGAATATCA ACAGATGATC ACAATAAACA TCTGTTCTC ATTCC 1485

Seq ID NO: 157 DNA Sequence
 Nucleic Acid Accession #: NM_005409.3
 Coding sequence: 94..378

1 11 21 31 41 51
 | | | | |
 25 TTCCTTTTAT GTTCAGCATT TCTACTCCTT CCAAGAAGAG CAGCAAAGCT GAAGTAGCAG 60
 CRACAGCACC AGCAGCAACA GCAAAAAACA AACATGAGTG TGAAGGGCAT GCTATAGGCC 120
 TTGGCTGTGA TATTGTGTGC TACAGTTGTT CAAGGCTTCC CCATGTTCAA AAGAGGACGC 180
 TGTCTTTTGA TAGGCCCTGG GGTAAAAGCA GTGAAAGTGG CAGATATTGA GAAAGCCTCC 240
 ATAAATGACC CAAGTAACAA CTGTGACAAA ATAGAAGTGA TTATTACCCT GAAAGAAAAT 300
 30 AAAGGACAA ACATGCTAAA TCCCAATCG AAGCAAGCAA GGCTTATAAT CAAAAAAGTT 360
 GAAAGAAAGA ATTTTAAAA ATATCAAAAC ATATGAAGTC CTGAAAAGG GCATCTGAAA 420
 AACCTAGAAC AAGTTTAACT GTGACTACTG AAATGACAAG AATTCTACAG TAGGAAACTG 480
 AGACTTTTCT ATGGTTTGTG GACTTTCAAC TTTGTACAG TTATGTGAAG GATGAAAGGT 540
 GGGTGAAGG ACCAAAAACA GAAATACAGT CTTCTGAAAT GAATGACAAT CAGAATTCCA 600
 35 CTGCCCAAAG GAGTCCAGCA ATTAATGGA TTTCTAGGAA AAGCTACCTT AAGAAGGCT 660
 GGTACCATC GGAGTTTACA AAGTGCTTTC ACGTCTTAC TTGTGTATT ATACATTCAAT 720
 GCATTTCTAG GCTAGAGAAC CTTCTAGATT TGATGCTTAC AACTATTCTG TTGTGACTAT 780
 GAGAACAATT CTGTCTCTAG AAGTTATCTG TCTGTATTGA TCTTTATGCT ATATTACTAT 840
 CTGTGTTTAC AGTGGAGACA TTGACATTAT TACTGGAGTC AAGCCCTTAT AAGTCAAAG 900
 40 CATCTATGTC TCGTAAAGCA TTCTCAAAC ATTTTTCAT GCAAAATACAC ACTCTTTTCC 960
 CCAAAATATCA TGTAGCACAT CAATATGTAG GGAACATTC TTATGCATCA TTTGGTTTGT 1020
 TTTATAACCA ATTCATTAAA TGTAATTCAT AAAATGTACT ATGAAAAAAA TTATACGCTA 1080
 TGGGATACCT GCAACAGTGC ACATATTCCA TAACCAAATT AGCAGCACCG GTCTTAAATT 1140
 GATGTTTTTC AACTTTTATT CATTGAGATG TTTTGAAGCA ATTAGGATAT GTGTGTTTAC 1200
 45 TGTACTTTTT GTTTTGATCC GTTTGTATAA ATGATAGCAA TATCTTGAC ACATTTGAAA 1260
 TACAAAATGT TTTTGTCTAC CAAGAAAAA TGTGAAAAA TAAGCAAAAT TATACCTAGC 1320
 AATCATTCTT ACTTTTGTGA ATTCTGTCTC TTAGAAAAAT ACATAATCTA ATCAATTCTC 1380
 TTGTTATGTC CTATATACTG TAAAAATTAG GTATACTCAA GACTAGTTTA AAGAAATCAA 1440
 GTCATTTTTT TCTCTAATAA ACTACCACAA CCTTCTTTTT TAAAAAAA AAA 1493

Seq ID NO: DNA Sequence 158
 Nucleic Acid Accession #: NM_002562.1
 Coding sequence: 27..1814

1 11 21 31 41 51
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 55 AAAACGCAGG GAGGAGGGCT GTCACCATGC CGGCCTGCTG CAGCTGCAGT GATGTTTTTC 60
 AGTATGAGAC GAACAAGTCT ACTCGGATCC AGAGCATGAA TTATGGCACC ATTAAGTGGT 120
 TCTTCCAGCT GATCATCTTT TCCTACGTTT GCTTTGCTCT GGTGAGTGAC AAGCTGTACC 180
 AGCGGAAAGA GCCTGTCTATC AGTTCTGTGC ACACCAAGGT GAAGGGGATA GCAGAGGTGA 240
 60 AAGAGGAGAT CGTGGAGAA GTGAGTGAAGA AGTTGGTGCA CAGTGTCTTT GACACCCGAG 300
 ACTACACCTT CCCTTTGCGA GGGAACTCTT TCTTCGTGAT GACAAACTTT CTCAAAAACG 360
 AAGGCCAAGA GCAGCGGTTG TGTCCCGAGT ATCCCAACCG CAGGACGCTC TGTTCCTCTG 420
 ACCGAGGTTG TAAAAAGGGA TGGATGGACC CGCAGAGCAA AGGAATTACG ACCGGAAGGT 480
 GTGTAGTGCA TGAAGGGAAC CAGAAGACCT GTGAAGTCTC TGCCGTGTGC CCCATCGAGG 540
 65 CAGTGGAAAG GGCCCCCGG CCTGCTCTCT TGAACAGTGC CGAAAACCTC ACTGTGCTCA 600
 TCAAGAACAA TATCGACTTC CCGGCCACCA ACTACACCAC GAGAAACATC CTGCCAGGTT 660
 TAAACATCAC TTGTACCTTC CACAAGACTC AGAATCCACA GTGTCCCAT TCCGAGTAGT 720
 GAGACATCTT CCGAGAAACA GCGGATAATT TTTAGATGT GGCAATTACG GCGGAATAA 780
 TGGGCATTGA GATCTACTGG GACTGCAACC TAGACCGTTG GTTCCATCAC TGCCATCCCA 840
 AATACAGTTT CCGTCCGCTT GACGACAAGA CCACCAACGT GTCCTTGATC CCTGGCTACA 900
 70 ACTTCAGATA CGCCAAGTAC TACAAGGAAA ACAATGTTGA GAAACGGACT CTGATAAAAG 960
 TCTTCGGGAT CCGTTTGTAC ATCTGTGTTT TTGGCACCGG AGGAAAAATT GACATTATCC 1020
 AGCTGGTTGT GTACATCGGC TCAACCTCTC CTAATCTGG TCTGGCCGCT GTGTTCTACG 1080
 ACTTCTCAT CGACACTTAC TCCAGTAACT GCTGTGCTC CCATATTAT CCCTGGTGCA 1140
 AGTGCTGTCA GCCCTGTGTG GTCAACGAAT ACTACTACAG GAAGAAGTGC GAGTCCATTG 1200
 75 TGGAGCCAAA GCGACATTA AAGTATGTGT CCTTTGTGGA TGAATCCCACT ATTAGGATGG 1260
 TGAACAGCA GCTACTAGGG AGAAGTCTGC AAGATGTCAA GGGCCAAGAA GTCCCAAGAC 1320
 CTGCGATGGA CTTACAGAT TGTCCAGGC TGCCCTTGGC CTTCCATGAC ACACCCCGA 1380
 TTCTGGGACA ACCAGAGGAG ATACAGCTGC TTAGAAAGGA GGCGACTCCT AGATCCAGGG 1440
 ATAGCCCCGT CTGCTGCCAG TGTGGAAGCT GCCTCCCATC TCAACTCCCT GAGAGCCACA 1500
 80 GGTGCTTGA GCGAGCTGTG TGCCGGAATA AGCCGGGGGC CTGCATCACC ACCTCAGAGC 1560
 TGTTCAGGAA GCTGCTCTG TCCAGACACG TCCTGCAGTT CCTCTGCTC TACCAGGAGC 1620
 CCTTGTGCGC GCTGGATGTG GATTCCACCA ACAGCCGCTC GCGGCACTGT GCCTACAGGT 1680
 GCTAOCGCAC CTGGCGCTTC GGCTCCAGG ACATGGCTGA CTTTGCCATC CTGCCAGCT 1740
 GCTGCCGCTG GAGGATCCGG AAAGAGTTTC CGAAGAGTGA AGGGCAGTAC AGTGGCTTCA 1800

AGAGTCCTTA CTGAAGCCAG GCACCGTGGC TCACGTCTGT AATCCCACT TTT 1853

Seq ID NO: 159 DNA Sequence

Nucleic Acid Accession #: NM_001793.2

Coding sequence: 54-2543

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15
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1 11 21 31 41 51
| | | | |
AAAGGGGCAA GAGCTGAGCG GAACACCGGC CGCGCGTCCG GGCAGCTGCT TCACCCCTCT 60
CTCTGCGACC ATGGGGCTCC CTGCTGGACC TCTCGCGTCT CTCCTCCTTC TCCAGGTTTG 120
CTGGCTGCGAG TGCGGGCGCT CCGAGCCGTG CCGGGCGGTC TTCAGGGAGG CTGAAGTGAC 180
CTTGAGGCGG GGAGGCGCGG AGCAGGAGCC CGGCCAGGCG CTGGGGAAAG TATTCATGGG 240
CTGCCCTGGG CAGAGGCCAG CTCTGTTTAG CACTGATAAT GATGACTTCA CTGTGCGGAA 300
TGGCGAGACA GTCCAGGAAA GAAGGTCACT GAAGGAAAGG AATCCATTGA AGATCTTCCC 360
ATCCAAACGT ATCTTACGAA GACACAAGAG AGATTGGGTG GTTGCTCCAA TATCTGTCCC 420
TGAAAAATGGC AAGGGTCCCT TCCCCCAGAG ACTGAATCAG CTCAGTCTCA ATAAAGATAG 480
AGACACCAAG ATTTTCTACA GCATCACGGG GCGGGGGGCA GACAGCCCCC CTGAGGGTGT 540
CTTCGTGTA GAGAAAGGAGA CAGGCTGGTT GTTGTGAAT AAGCCACTGG ACCGGGAGGA 600
GATTGCCAAG TATGAGCTCT TTGGCCACGC TGTGTCAGAG AATGGTGCCCT CAGTGGAGGA 660
CCCCATGAAC ATCTCCATCA TCGTGACCGA CCAGAATGAC CACAAGCCCA AGTTTACCCA 720
GGACACCTTC CGAGGGAGTG TCTTAGAGGG AGTCTACCA GGTACTTCTG TGATCGAGGT 780
GACAGCCCAAG GATGAGGATG ATGCCATCTA CACTACAAT GGGGTGGTTG GTTACTCCAT 840
CCATAGCCAA GAACCAAGG ACCCACAGA CTCTATGTTT ACCATTACCC GGAGCACAGG 900
CACCATCAGC GTCTATCTCA GTGGCCTGGA CCGGAAAAAA GTCCCTGAGT ACACACTGAC 960
CATCCAGGCC ACAGACATGG ATGGGGACGG CTCACCAACC ACGGCAGTGG CAGTAGTGGG 1020
GATCCCTGAT GCCAATGACA ATGCTCCCAT GTTTGACCCC CAGAAGTACG AGGCCCATAT 1080
GCCTGAGAAT GCAGTGGGCC ATGAGGTGCA GAGGCTGACG GTCACTGATC TGAGCGCCCT 1140
CAACTCACC GCGTGGCGTG CCACCTACCT TATCATGGGC GGTGACGACG GGGACCATTT 1200
TACCATCACC ACCCACCTGT AGAGCAACCA GGGCATCTGT ACAACCCAGG AGGGTTTGGG 1260
TTTTGAGGCC AAAAACCCAGC ACACCTGTGA CGTTGAAGTG ACCAACGAGG CCCCTTTTGT 1320
GCTGAAGCTC CCAACCTCCA CAGCCACCAT AGTGGTCCAC GTGGAGGATG TGAATGAGGC 1380
ACCTGTGTTT GTCCACCCCT CCAAAGTCGT TGAGGTCCAG GAGGGCATCC CCATCTGCGA 1440
GCCTGTGTGT GTCTACACTG CAGAAGACCC TGACAAGGAG AATCAAAAGA TCAGTACCG 1500
CATCTGAGA GACCCAGCAG GGTGGCTAGC CATGGACCCA GACAGTGGGC AGGTACAGC 1560
TGTGGGCACC CTGACCGGTG AGGATGAGCA GTTTGTGAGG AACAACTCT ATGAAGTCAT 1620
GGTCTTGGCC ATGGAACAAT GAAGCCCTCC CACCACTGGC ACGGGAACCC TTCTGTAA 1680
ACTGATTGAT GTCAATGACC ATGGCCAGT CCCTGAGCCC CGTCAGATCA CCATCTGCAA 1740
CCAAAGCCCT GTGGGCCAGG TGCTGAACAT CACGGACAAG GACCTGTCTC CCCACACCTC 1800
CCCTTTCCAG GCCCAGCTCA CAGATGACTC AGACATCTAC TGGACGGCAG AGGTCAACGA 1860
GGAAGGTGAC ACAGTGGTCT TGTCCCTGAA GAAGTTCTGT AAGCAGGATA CATATGACGT 1920
GCACCTTTCT CTGCTGACG ATGGCAACAA AGAGCAGCTG ACGGTGATCA GGGCCACTGT 1980
GTGGCACTGC CTAGGCCATG TCGAAACCTG CCCTGGACCC TGGAAAGGAG GTTTCATCCT 2040
CCCTGTGCTG GGGGCTGTCC TGGCTCTGCT GTTCTCTCTG CTGGTGTCTG TTTTGTGGT 2100
GAGAAAGAAG CCGAAGATCA AGGAGCCCTC CTACTCCCA GAAGATGACA CCGGTGACAA 2160
CGTCTTCTAC TATGGCGAAG AGGGGGGTGG CGAAGAGGAC CAGGACTATG ACATCACCCA 2220
GCTCCACCGA GGTCTGGAGG CCAGGCCCGA GGTGGTTCTC CGCAATGAGC TGGCAACCA 2280
CATCATCCG ACACCCATGT ACCGTCTCTG GCCAGCCAAC CCAGATGAAT TCGGCAACTT 2340
TATAATTGAG AACCTGAAGG CGGCTAACAC AGACCCCA CAACCCCGCTC ACGCACCTC 2400
CTTGGTGTCT GACTATGAGG GCAGCGGCTC CGAGCGCGCG TCCCTGAGCT CCCTCACCTC 2460
CTCGGCTTCC GACCAAGACC AAGATTACGA TTATCTGAAC GAGTGGGGCA GCCGCTTCAA 2520
GAAGCTGGCA GACATGTACG GTGGCGGGGA GGACGACTAG GCGGCTGCTC TGCAGGGCTG 2580
GGGACCAAA CTTAGGCCAC AGAGCATCTC CAAGGGGTCT CAGTTCCCCC TTCAGCTGAG 2640
GACTTGGAG CTGTGACGGA AGTGGCCGTA GCAACTTGGC GGAGACAGGC TATGAGTCTG 2700
ACGTTAGAGT GGTGTCTTCC TTAGCCTTTC AGGATGGAGG AATGTGGGCA GTTTGACTTC 2760
AGCACTGAAA ACCTCTCCAC CTGGGCCAGG GTTGCTCTCAG AGGCCAAGTT TCCAGAAAGC 2820
TCTTACCTGC CGTAAATGTC TCAACCTCTG GTCTGGGCC TGGGCTGCT GTGACTGACC 2880
TACAGTGGAC TTCTCTCTG GAATGGAACC TTCTTAGGCC TCCTGGTGCA ACTTAATTTT 2940
TTTTTTTAA TCTATCTTCA AAAAGTTAGT GAAAGTTCTT CAAAAGTGCA GCCCAGAGCT 3000
GCTGGGCCCA CTGGCCGTCC TGCATTCTG GTTTCAGAC CCCAATGCCT CCCATTCCGA 3060
TGGATCTCTG CGTTTATTATA CTGAGTGTGC CTAGGTTGCC CCTTATTTT TATTTTCCCT 3120
GTGCGTTCG TATAGATGAA GGGTGAGGAC AATCGTGAT ATGTACTAGA ACTTTTTTAT 3180
TAAAGAACT TTTCCAGAA AAAAA 3205

Seq ID NO: 160 DNA Sequence

Nucleic Acid Accession #: NM_002571.1

Coding sequence: 99..587

65
70
75
80

1 11 21 31 41 51
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CATCCCTCTG GCTCCAGAGC TCAGAGCCAC CCACAGCCGC AGCCATGCTG TGCCTCCTGC 60
TCACCCCTGG CGTGGCCCTG GTCTGTGGTG TCCCGGCCAT GGACATCCCC CAGACCAAGC 120
AGGACCTGGA GCTCCCAAAG TTGGCAGGGA CCTGGCACTC CATGGCCATG GCGACCAACA 180
ACATCTCCCT CATGGCGACA CTGAAGGCC CTCTGAGGGT CCACATCACC TCACTGTTGC 240
CCACCCCGGA GGACAACTG GAGATCGTTC TGACAGATG GGAGAAACAAC AGCTGTGTTG 300
AGAAGAAGGT CCTTGGAGAG AAGACTGGGA ATCCAAAGAA GTTCAAGATC AACTATACGG 360
TGGCGAACGA GGGCAGCGTG CTGATACTG ACTACGACAA TTCTCTGTTT CTCTGCTAC 420
AGGACACCA CACCCCATC CAGAGCATGA TGTGCCAGTA CCTGGCCAGA GTCTGGTGG 480
AGGACGATGA GATCATGCAG GGATTATCA GGGCTTTCAG GCCCTGCCC AGGCACCTAT 540
GGTACTTGCT GGACTTGAAG CAGATGGAAG AGCCGTGCCG TTTCTAGCTC ACCTCCGCT 600
CCAGGAAGAC CAGACTCCCA CCCTTCACA CTCCAGAGC AGTGGGACTT CCTCTGCC 660
TTTCAAGAA TAACCACAGC TCAGAAGAGC ATGACGTGGT CATCTGTGTC GCCATCCCT 720
TCCTGCTGCA CACTGCACC ATTGCCATGG GAGGGCTGCT CCCTGGGGGC AGAGTCTCTG 780
GCAGAGGTTA TTAATAAAC CTTGAGCAT G 811

Seq ID NO: 161 DNA Sequence

Nucleic Acid Accession #: NM_001327.1

Coding sequence: 89..631

| | | | | | | | |
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| | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| 5 | AGCAGGGGGC | GCTGTGTGTA | CCGAGAATAC | GAGAATACCT | CGTGGGCCCT | GACCTTCTCT | 60 |
| | CTGAGAGCCG | GGCAGAGGCT | CCGAGGCCAT | GCAGGCCGAA | GGCCGGGGCA | CAGGGGGTTC | 120 |
| | GACGGGCGAT | GCTGATGGCC | CAGGAGGCCC | TGGCATTCTCT | GATGGCCCTAG | GGGGCAATGC | 180 |
| | TGGCGGCCCA | GGAGAGGGCG | GTGCCACGGG | CGGCAGAGGT | CCCGGGGGCG | CAGGGGCAGC | 240 |
| | AAGGGCTCTG | GGGCCGGGAG | GAGGCGCCCC | GCGGGGTCCG | CATGGCGGGG | CGGCTTCAGG | 300 |
| | GCTGAATGGA | TGCTGCAGAT | GCGGGGCCAG | GGGCCGGGAG | AGCCGCCCTGC | TTGAGTTCTA | 360 |
| 10 | CCTCGCCATG | CCTTTCCGGA | CACCCATGGA | AGCAGAGCTG | GCCCCGAGGA | GCCTGGCCCA | 420 |
| | GGATGCCCCA | CCGCTTCCCG | TGCCAGGGGT | GCTTCTGAAG | GAGTTCACTG | TGTCGGGCAA | 480 |
| | CATACTGACT | ATCCGACTGA | CTGCTGCAGA | CCACGCCCAA | CTGCAGCTCT | CCATCAGCTC | 540 |
| | CTGTCTCCAG | CAGCTTTCCC | TGTTGATGTG | GATCACGCAG | TGCTTCTCTG | CGGTGTTTTT | 600 |
| | GGCTCAGCCT | CCCTCAGGGC | AGAGGCGCTA | AGCCAGCCTT | GGCGCCCTTT | CCTAGGTCAAT | 660 |
| 15 | GCCTCTCCC | CTAGGAATG | GTCCAGCAC | GAGTGGCCAG | TTGTTGTGG | GGGCTTGATT | 720 |
| | GTTTGTGCT | GGAGGAGGAC | GGCTTACATG | TTTGTTCCTG | TAGAAAATAA | AACTGAGCTA | 780 |

Seq ID NO: 162 DNA Sequence

Nucleic Acid Accession #: NM_020994

Coding sequence: 53..459

| | | | | | | | |
|----|------------|-------------|------------|------------|------------|------------|-----|
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| 20 | CCTCGTGGGC | CCTGAACCTTC | TCTCTGAGAG | CCGGGCAGAG | GCTCCGGAGC | CATGCAGGCC | 60 |
| | GAAGGCCAAG | GCACAGGGGG | TTCCAGCGGC | GATGCTGATG | GCCCAGGAGG | CCCTGGCATT | 120 |
| 25 | CTGATGGGCC | CAGGGGGCAA | TGCTGGCGGC | CCAGGAGAGG | CGGTTGCCAC | GGGCGGCAGA | 180 |
| | GGTCCCGGGG | GGCAGGGGGC | AGCAAGGGGC | TGGGGGCGGA | GAGGAGGGGC | CCCGCGGGGT | 240 |
| | CCGATAGGCG | GTGCGGCTTC | TGCGCAGGAT | GGAAGGTGCC | CCTGCGGGGC | CAGGAGGGCG | 300 |
| | GACAGCGGCC | TGCTTCAGTT | CCGACTGACT | GCTGCAGACC | ACCGCCAAGT | GCAGCTCTCC | 360 |
| | ATCAGCTCCT | GTCTCCAGCA | GCTTTCCTTG | TTGATGTGGA | TCACGCACTG | CTTTCGCCCC | 420 |
| 30 | GTGTTTTTGG | CTCAGGCTCC | CTCAGGGCAG | AGGCGCTAAG | CCCAGCTTGG | CGCCCTTTC | 480 |
| | TAGGTCAATG | CTCCTCCCTT | AGGGAATGGT | CCCAGCACGA | GTGGCCAGTT | CATTGTGGGG | 540 |
| | GCCTGATTGT | TTGTGCTGG | AGGAGGACGG | CTTACATGTT | TGTTTCTGTA | GAATAATAAG | 600 |
| | CTGAGCTA | | | | | | 608 |

Seq ID NO: 163 DNA Sequence

Nucleic Acid Accession #: NM_006928.2

Coding sequence: 1..1986

| | | | | | | | |
|----|-------------|------------|------------|------------|------------|-------------|------|
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| 40 | ATGGATCTGG | TGCTAAAAAG | ATGCCTTCTT | CATTGGCTG | TGATAGGTGC | TTTGCTGGCT | 60 |
| | GTGGGGGCTA | CAAAAGTACC | CAGAAACCAG | GACTGGCTTG | GTGTCTCAAG | GCAACTCAGA | 120 |
| | ACCAAGGCTT | GGAAACAGGA | CTGTATCCA | GAGTGGACAG | AAGCCAGAG | ACTTGACTGC | 180 |
| | TGGAGAGGTG | GTCAGTGTTC | CCTCAAGGTC | AGTAATGATG | GGCCTACACT | GATTGTGTGA | 240 |
| | AATGCTCCTT | TCTCTATTGC | CTTGAACCTC | CCTGGAAGCC | AAAAGGTATT | GCCAGATGGG | 300 |
| 45 | CAGGTTATCT | GGGTCAACAA | TACCATCATC | AATGGGAGCC | AGGTGTGGGG | AGGACAGCCA | 360 |
| | TGTATATCCC | AGGAAACTGA | CGATGCCTGC | ATCTTCCCTG | ATGGTGGACC | TTGCCCATCT | 420 |
| | GGCTCTTGTT | CTCAGAAGAG | AAGCTTTGTT | TATGTCTGGA | AGACCTGGGG | CAAATACTGG | 480 |
| | CAAGTTCTAG | GGGCCCCAGT | GTCTGGGCTG | AGCATTGGGA | CAGGCAGGGC | AATGCTGGGC | 540 |
| | ACACACACCA | TGGAAGTGAC | TGTCTACCAT | CGCGGGGAT | CCCGAGGCTA | TGTGCCTCTT | 600 |
| 50 | GCTCATTTCCA | GCTCAGCCTT | CACCATTAAT | GACCAAGTGC | CTTCTCCCTG | GAGCGTGTCC | 660 |
| | CAGTTGCGGG | CCTTGGATGG | AGGGAACAAG | CACCTTCTGA | GAAATCAGCC | TCTGACCTTT | 720 |
| | GCCTCTCAG | TCATGACCC | CAGTGGCTAT | CTGGCTGAAG | CTGACCTCTC | CTACACCTGG | 780 |
| | GACTTTGGAG | ACAGTAGTGG | AACCCGTATC | TCTCGGGCAC | TTGTGGTCC | TCATACTTAC | 840 |
| 55 | CTGAGGCTCT | GGCCAGTCC | TGCCAGGCTG | GTCTGTCAGG | CTGCCATTCC | TCTCACTCTC | 900 |
| | TGTGGCTCTT | CCCCAGTTCC | AGGCACACCA | GATGGGCACA | GGCCAACTGC | AGAGGCCCTT | 960 |
| | AAACACACAG | CTGGCCAAAT | GCCTACTACA | GAAGTTGTGG | GTAATACACC | TGGTCAGGGC | 1020 |
| | CCAATGTCAG | AGCCCTCTGG | AACCACTACT | GTGCAGGTGC | CAACCACTGA | AGTCATAAGC | 1080 |
| | ACTGCACCTG | TGCAGATGCC | AATGCAGAG | AGCACAGGTA | TGACACCTGA | GAAGGTGCCA | 1140 |
| | GTTCAGAGGG | TGATGGGTAC | CACACTGGCA | GAGATGTCAA | CTCCAGAGGC | TACAGGTATG | 1200 |
| 60 | ACACCTGCAG | AGGTATCAAT | TGTGGTGTCT | TCTGGAACCA | CAGCTGCACA | GGTAACAACCT | 1260 |
| | ACAGAGTGGG | TGGAGACCA | AGCTAGAGAG | CTACCTATCC | CTGAGCCTGA | AGGTCCAGAT | 1320 |
| | GCCAGCTCAA | TCATGTCTAC | GGAAAGTATT | ACAGGTTCCC | TGGGCCCTCT | GCTGGATGGT | 1380 |
| | ACAGCCACCT | TAAGGCTGGT | GAAGAGACAA | GTCCCCCTGG | ATTGTGTCTT | GTATCGATAT | 1440 |
| | GGTTCTTTTT | CCGTACCCCT | GGACATTGTC | CAGGATATTG | AAAGTGCCGA | GATCCTGCAG | 1500 |
| 65 | GCTGTGCCGT | CCGGTGAGGG | GGATGCATTT | GAGCTGACTG | TGTCCTGCCA | AGGCGGGCTG | 1560 |
| | CCCAAGGAAG | CCTGCATGGA | GATCTCATCG | CCAGGGTGCC | AGCCCTCTGC | CCAGCGGCTG | 1620 |
| | TGCCAGCCTG | TGCTACCCAG | CCAGCCTGTC | CAGCTGGTTC | TGCACCATAT | ACTGAAGGGT | 1680 |
| | GGCTCGGGGA | CATACTGCCT | CAATGTGTCT | CTGGCTGATA | CCAACAGCCT | GGCAGTGGTC | 1740 |
| | AGCACCCAGC | TTATCATGCC | TGGTCAAGAA | GCAGGCCTTG | GGCAGGTTCC | GCTGATCGTG | 1800 |
| 70 | GGCATCTTGC | TGGTGTGTAT | GGCTGTGGTC | CTTGCACTCT | TGATATATAG | GCGCAGACTT | 1860 |
| | ATGAAGCAAG | ACTTCTCCGT | ACCCAGTTTG | CCACATAGCA | GCAGTCACTG | GCTGCGTCTA | 1920 |
| | CCCCGCATCT | TCTGCTCTTG | TCCCATTTGG | GAGAATAGCC | CCCTCTCTAG | TGGGCAGCAG | 1980 |
| | GTCTGA | | | | | | 1986 |

Seq ID NO: 164 DNA Sequence

Nucleic Acid Accession #: NM_001922.2

Coding sequence: 415..1974

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|----|------------|------------|------------|------------|------------|------------|-----|
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| 80 | GCAATTAAG | TCAAGAGCTA | AGGAGGGAGG | GAGAGGGTTT | AGAAATACCA | GCATAATAAG | 60 |
| | TAGTATGACT | GGGTGCTCTG | TAAATTAAT | CAATTAGACA | AAGCCTGACT | TAACGGGGGA | 120 |
| | AGATGGTGAG | AAGCGCTACC | CTCATTAAT | TTGGTTGTTA | GAGGCGCTTC | TAAGGAAATT | 180 |
| | AAGTCTGTGA | TTGTGTTGAA | TCACATAAAA | TTGTGTGTGC | ACGTTTATGT | ACACATGTGC | 240 |
| | ACACATGTAA | CCTCTGTGAT | TCTTGTGGGT | ATTTTTTTAA | GAAGAAAGGA | ATAGAAAGCA | 300 |

5
 10
 15
 20
 25
 30
 35

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AAGAAAAATA AAAAACTACTG AAAAGAAAAAG ACTGAAAGAG TAGAAGATAA GGAGAAAAAGT 360
ACGACAGAGA CAAGGAAAGT AAGAGAGAGA GAGAGCTCTC CCAATTATAA AGCCATGAGC 420
CCCCTTTGGT GGGGGTTTCT GCTCAGTTGC TTGGGCTGCA AAATCCTGCC AGGAGCCGAG 480
GGTCAGTTCC CCCAGTCTCG CATGACGGTG GACAGCCTAG TGAACAAGGA GTGCTGCCCA 540
CGCCTGGGTG CAGAGTGGCG CAATGTCTGT GCCTCTCAGC AAGGCCGGGG GCAGTGCACA 600
GAGGTGGGAG CGACACAAGG GCCCTGGAGT GGTCCTTACA TCCTACGAAA CCAGGATGAC 660
CGTGAGCTGT GGCCAAGAAA ATTCTTCCAC CGSACCTGCA AGTGACAGG AAATCTTGCC 720
GGCTATAATT GTGGAGACTG CAAGTTTGGC TGGACCGGTC CCAACTGCGA GCGGAAGAAA 780
CCACAGCTGA TTCCGAGAAA CATCCATTCC TTGAGTCTTC AGGAAAAGAG GCAGTTCTTG 840
GGCGCCTTAG ATCTCGCGAA GAAGAGAGTA CACCCGACT ACGTGATCAC CACACAACAC 900
TGGCTGGGCC TGCTTGGGCC CAATGGAACC CAGCCGAGT TTGCCAACTG CAGTGTATTAT 960
GATTTTTTTG TGTGGCTCCA TTATTATTCT GTTAGAGATA CATTATTAGG ACCAGGACGC 1020
CCCTACAGGG CCATAGATTT CTCACATCAA GGACCTGCAT TTGTTACCTG GCACCGGTAC 1080
CATTGTGTGT GTCTGGAAGG AGATCTCCAG CGACTCATTG GCAATGAGTC TTTTGTCTTG 1140
CCCTACTGGA ACTTGGCCAC TGGGAGGAAC GAGTGTGATG TGTGTACAGA CCAGCTGTTT 1200
GGGCGCAGCA GACCAGACA TCCGACTCTG ATTAGTCGGA ACTCAAGATT CTCAGCTGG 1260
GAAACTGTCT GTGATAGCTT GGATGACTAC AACCACCTGG TCACCTTGTG CAATGGAACC 1320
TATGAAGGTT TGCTGAGAAG AAATCAAATG GGAAGAAAAC GCATGAAATT GCCAACCTTA 1380
AAAGACATAC GAGATTGGCT GTCTCTCCAG AAGTTTGACA ATCCTCCCTT CTTCCAGAAC 1440
TCTACCTTCA GTTTCAGGAA TGCTTTGGAA GGGTTTGATA AAGCAGATGG GACTCTGGAT 1500
TCTCAAGTGA TGAGCCTTCA TAATTGGTTT CATTCTCTCC TGAACGGGAC AAACGCTTTG 1560
CCACATTGAG CCGCCAATGA TCCCATTTTT GTGGTTCTTC ATTCTTTTAC TGATGCCATC 1620
TTTGATGAGT GGATGAAAAG ATTTAATCCT CCGTCAGATG CCGTGGCTCA GGAGCTGGCC 1680
CCTATTGGTC ACAATCGGAT GTACAACATG GTTCTTTCT TCCTCCAGT GACTAATGAA 1740
GAACCTTTTT TAACTCTAGA CCAACTGGGC TACAGCTATG CCATGATCTC GCCAGTTTCA 1800
GTTGAAGAAA CTCACGGTTG GCCACAACCT CTCTTAGTAG TCATGGGAAC ACTGGTGGCT 1860
TTGGTTGGTC TTTTGTGCT GTTGGCTTTT CTTCATATA GAAGACTTCG AAAAGGATAT 1920
ACACCCCTAA TGGAGACACA TTAAAGCAGC AAGAGATACA CAGAAGAAGC CTAGGCTGCT 1980
CATGCGCTAC CTAAGAGAAG AGGCTGGCCA AGCCACAGTT CTGACGCTGA CAATAAAGGA 2040
ACTAATCTCT ACTGTTCTCT CTTGAGTTGA AGATCTTTGA CATAGGTTCT TCTATAAGTA 2100
TGATGATCTC ATTCAGAAGA TGCTTAGCTG TAGTTTCCGC TTTGCTTGCT TGTTTAACAA 2160
ACCCAACCTAA AGTGCTTGAG GCTACCTCTA CCTTCAAATA AAGATAGACC TGACAATTG 2220
TGATATCTAA TAATAACCCC CCCCCAATA TTGATTAAGC CTCTCCTTT TCTGAAAGCA 2280
TTTAAAAAAA A
  
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Seq ID NO: 165 DNA Sequence
 Nucleic Acid Accession #: XM_059422.3
 Coding sequence: 207..1400

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 65
 70
 75

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1 11 21 31 41 51
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TGTGGGGCTG CCCGGGCTGC GCGGCGTCTG CAGGCGCCAC CGCTGCCTCT TCCGCGCTGT 60
GACCTCTCTC GCGCGCGCGG CTTGGCTGCG TCCTCGACT CCCCGCGCG CCGAGACCAG 120
GCTCCCGCTC CGGTGCGGCG CGCACCGCCC TCCGCGGCGG CCCCCTGGGG ATCCAGCGAG 180
CGCGGTGCTC CTTGGTGGAA GGAACCATGA ACTGGCATCT CCCCCTCTC CTCTTGGCGT 240
CTGTGACGCT GCCTTCCATC TGCTCCCACT TCAATCCTCT GTCTCTCGAG GAACTAGGCT 300
CCAACACGCG GATCCAGGTT TTCAATCAGA TTGTGAAGTC GAGGCTCAT GACAACATCG 360
TGATCTCTCC CCATGGGATT GCGTCGGTCC TGGGGATGCT TCAGTGGGG GCGGACGGCA 420
GGACCAAGAA GCAGCTCGCC ATGGTGATGA GATACGGCGT AAATGGAGTT GGTAAAAATAT 480
TAAAGAAGAT CAACAGGCG ATCGTCTCCA AGAAGAATAA AGACATTGTG ACAGTGGCTA 540
ACGCGGTGTT TGTTAAGAAT GCCTCTGAAA TTGAAGTGCC TTTTGTTACA AGGAACAAAG 600
ATGTGTTCCA GTGTGAGGTC CGGAATGTGA ACTTTGAGGA TCCAGCCTCT GCCTGTGATT 660
CCATCAATGC ATGGGTAAAA AATGAAAACA GGGATATGAT TGACAATCTG CTGTCCCCAG 720
ATCTTATTGA TGGTGTGCTC ACCGACTGG TCCTCGTCAA CGCAGTGTAT TTCAAGGGTC 780
TGTGGAATC ACGGTTCCAA CCGGAGAACA CAAAGAAACG CACTTTCGTG GCAGCGGAGC 840
GGAAATCCTA TCAAGTGCCA ATGCTGGCCC AGCTCTCCGT GTTCCGGTGT GGGTCGACAA 900
GTGCCCCCAA TGATTATTGG TACAACCTCA TTGAACCTGC CTACACGGG GAAAGCATCA 960
GCATGCTGAT TGCACCTGCC ACTGAGAGCT CCACTCCGCT GTCTGCCATC ATCCACACA 1020
TCAGACCAAA GACCATAGAC AGCTGGATGA GCATCATGGT GCCCAAGAGG GTGCAAGTGA 1080
TCTGCCCCAA TCTCAGCTC GTAGCACAAA CAGATTGTGA GGAGCGGCTG AAAGTTCTTG 1140
GCATTACTGA CATGTTTGAT TCATCAAAAG CAAATTTTGC AAAATAACA AGSTCAGAAA 1200
ACCTCCATGT TTCTCATATC TTGCAAAAAG CAAAAATTGA AGTCAGTGAA GATGGAACCA 1260
AAGCTTCAGC AGCAACAAC TCAATTCTCA TTGCAAGATC ATCGCCTCCC TGGTTTATAG 1320
TAGACAGACC TTTTCTGTTT TTCAATCGAC ATAATCCTAC AGGTGCTGTG TTATTCAATG 1380
GGCAGATAAA CAACACCTGA AGAGTATACA AAAGAAACCA TGCAAGCAA CGACTACTTT 1440
GCTACGAAGA AAGACTCCTT TCCTGCATCT TTCATAGTTC TGTTAAATAT TTTGTACAT 1500
CGCTCTTTT TCAAACTAG TTCTTAGGAA CAGACTCGAT GCAAGTGTG CTGTTCTGGG 1560
AGGTATTGGA GGGAAAAAAC AAGCAGGATG GCTGGAACAC TGTACTGAGG AATGAATAGA 1620
AAGGCTTCCA GATGCTCTAA AGATTCTTTA AACTACTGAA CTGTTACCTA GGTTAACAAC 1680
CCTGTTGACT ATTTGCTGTT TGTCAGTTT AGGAATTTT GTTTTGTGTT GTCTATATG 1740
GCGGCTTTTC AGAAGAAATT TAATCAGTGT GACAGAAAAA AAAATGTTTT ATGGTAGCTT 1800
TTACTTTTTA TGAAAAAAAA ATTATTGCTC TTTTAAATTC TTTTCCCCCA TCCCCCTCCA 1860
AAGTCTTGAT AGCAAGCGTT ATTTTGGTGG TAGAAACGGT GAAATCTCTA GCCTCTTTGT 1920
GTTTTGTGTG TTTGTTGTGT TGTGTTTATA TATAATGCAT GTATTCACTA AAATAAAATT 1980
TAAAAAATC CTGCTTGTCT AGACAAGGTT GCTGTTGTGC AGTGTGCTG TCACTACTGG 2040
TCTGTACTCC TTGGATTGTC ATTTTGTGAT TTTGTACAAA GTAAAAATAA ACTGTTATGA 2100
GTAGT
  
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Seq ID NO: 166 DNA Sequence
 Nucleic Acid Accession #: XM_040512.3
 Coding sequence: 382..1302

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1 11 21 31 41 51
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GCGCGCCCTC TTTTGGGCTC CGGACCCCC GGGAGTGGGA GCGGCGAGTC GGGACGCTC 120
  
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| | | | | | | | |
|----|-------------|------------|------------|------------|-------------|-------------|------|
| 5 | AACCTGTTCA | CTCAGGGAAT | CCTGCCCATC | GCCTTCTCCA | GGCGGACTTC | GCAGAACTAC | 180 |
| | TGCTCCCTCG | AGCAGCCAGG | CCAGGGCGGC | AGCACCAGCG | CCTTCGAGCA | GCTGCAGAGG | 240 |
| | TCCGACCGGC | GCCTCATCTC | CCAGAGATCT | TCCTTGGAGA | CCCTGGGAAGA | TATTGAGGAG | 300 |
| | AACGCCCTCT | TCCGGAGATG | TCGAACTCTC | TCAGGTTTCA | CCAGACCAAA | GAATTTTAAG | 360 |
| | AAGATTCATT | TTATCAAGAA | CATGCCGCAA | CACGATACCA | GGAAATGGCAG | AATAGTCCTT | 420 |
| | ATCAGTGGCA | GAAGATCCTT | CTGTAGTATA | TTTTCACTGC | TGCCGTATCG | CGACAGTACC | 480 |
| | CAAGTCGGGG | ACTTGAAGTT | GGACGGAGGA | AGACAATCAA | CTGGTGCACT | GAGTTTGAAA | 540 |
| | GAGATCAITG | GTCTGGAAGG | TGTGGAGCTG | GGTGCTGATG | GGAAAGACTGT | TTCTATATACC | 600 |
| | CAATTTCTGT | TACCCACAAA | TGCCTTTGGA | GCCCGGAGAA | ATACCATAGA | CTCCACCTCC | 660 |
| 10 | TCITTTCTCCC | AGTTCCGTAA | CCTGAGCCAC | CGCAGCCTCT | CCATAGGCCG | GGCAAGCCGC | 720 |
| | ACCCAGGGGA | GCCTCGACAC | AGGTAGTGAC | CTGGGAGACT | TTATGGACTA | TGACCCAAAT | 780 |
| | CTCTTGGATG | ACCCCCAGTG | GCCTTGTGGC | AAACACAAAC | GCGTTCTGAT | CTTCCCTTCC | 840 |
| | TACATGACAA | CAGTGATTGA | CTACGTGAAG | CCCTCGGATC | TCAAGAAAGG | CATGAACGAG | 900 |
| | ACCTTCAAGG | AGAAGTTTCC | TCACATTAA | CTGACACTCA | GCAAAATTAG | GAGTCTGAAA | 960 |
| 15 | CSAGAGATGC | GGAAAGCTTG | GCAGGAGGAC | TGTGGCCTTG | AGGAGCCAC | GGTGGCCATG | 1020 |
| | GCCTTGTCT | ACTTTGAAAA | GCTCGCCCTC | AAGGGGAAAC | TCAACAAACA | GAACCGGAAG | 1080 |
| | CTGTGTGCTG | GGGCATGTGT | GCTGTTAGCA | GCCAAAATTG | GAAGTGACCT | CAAAAAACAC | 1140 |
| | GAAGTCAAGC | ATTTAATTGA | CAAACTGGAA | GAGAAAGTCC | GGCTGAACAG | GCGAGAACTG | 1200 |
| | ATTGCCCTTG | AATTCOCGT | GTTAGTGGCC | TGGAATTGCG | CCCTCCACTT | GCCCGAGCAC | 1260 |
| 20 | GAAGTCATGC | CCCACTACAG | ACGGCTGGTC | CAGAGTTCTT | AGCACTGGCC | CCGAGGACAG | 1320 |
| | CCAAGGGCCA | TTTCTTCTCA | GCTTGGTGA | GCAGCACTTA | CTTACTACTG | GAAATGAAAA | 1380 |
| | AAAGTAGAAC | TCAGAAATCC | AGACTTTTCT | TCCTCTGAC | ATAGTTTGGG | GAGAAGCAGT | 1440 |
| | ACTAGAAACT | TTCCAAGGAG | TCTTGGGTGT | GAGGCCAAGA | GGAGCCATGA | GCTATGGACT | 1500 |
| | CCTCAAGCAC | GGGAAGAGGA | GGTGTGTGCT | GAGAACAGAG | AGGCCCTGCC | CTCTGTCCAC | 1560 |
| 25 | TAGCGAGAAT | CCCTAGCTGC | CCCAGCCGAG | TCTTTCTCCC | CGGCATTAC | AAACTTTGCA | 1620 |
| | AGCGTGGTCC | AGGGCCTTCT | CCAGATCTGT | TCCAACTTGG | AGTGTGAAGG | GCTTGAGCAT | 1680 |
| | ACGGGGGAAG | AGAGTCTGCA | GAAGTTGGGG | GAAAACTTTT | AAAAGATAAC | CTCATTGTGT | 1740 |
| | CAAGAGTGT | GCCAACTAT | TTTTGTATCA | GCATTGGAAG | TGCACCTTCC | CCTGGGCGGT | 1800 |
| 30 | GTGGGTGTGT | GAATGTGCAA | GTGTCTGAGA | GATACTGCAT | CAGCCCTAGA | CCCCAGAGC | 1860 |
| | CAGTCCCGCC | CTTTACAGAG | CAGCCCTTAG | CCTGGGGCCA | TGGTCAAGGC | TGACCTTCAA | 1920 |
| | CAATTATTTT | TAGATGATTT | CTGGATAAGA | ATTGCTCTCT | CGGTACCAGA | CAGTTTGACA | 1980 |
| | TCCTCCACCC | TTAGAAAATG | ACTGACATTG | TTTTGTACT | GCTCCTACCC | ACCAAGGGGA | 2040 |
| | TAAAGAAAGC | GAGTCTGTAG | TGTTGGATGA | GTCAGTCOGG | TGGAAGGAGC | TGGAGCGTGG | 2100 |
| 35 | CGCTCTGTAA | CTTCTGCGC | TCTGCCACCC | CGCCACGTGT | ATTTAACCTT | CGCACTTTCT | 2160 |
| | CCACTGTGGA | GATGGCTGGG | CGCGCGCCCC | ACAGTGTGTA | TTCCTGTCTT | CTATGTTAGA | 2220 |
| | GTGCATCAGA | AGCACATTTA | CTGTGCTATC | TATATCGCTA | TATAAAAGTG | TTTTATAAAA | 2280 |
| | ACCCAGAATA | GGAGCAAGAC | GCATGATTGG | TGTTTGAGGC | GTTTGCCAGC | TGGGACAAAC | 2340 |
| | TGGCTTTGGA | GCTGTGGTTA | AGCTGACTAA | GGAGCGGGTG | GCTCTTCTT | AACATTCCTA | 2400 |
| 40 | CGTGCCCAAG | GCTGTTTCA | CAAGATTTTA | ATGGTGACTT | GTCTGGCTT | ACTGGGACAG | 2460 |
| | TCGTGTATGAG | GCATGTCACC | ACACTGTGCG | CTCATAGCTG | CAAGAGAGAG | GCACCAGCTG | 2520 |
| | AAGTTCCCTT | GACTGAAGAG | AGCCTGTGGC | CATGTAAAAA | GAGAAATAAA | CTCTTGTGTC | 2580 |
| | TTTTTGT | | | | | | 2587 |

| | | | | | | | |
|------------------------------------|------------|-------------|------------|------------|------------|-------------|------|
| Seq ID NO: 167 DNA Sequence | | | | | | | |
| Nucleic Acid Accession #: BC008826 | | | | | | | |
| Coding sequence: 188..2695 | | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
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| 50 | GGCAGGAGGC | TCCGGCCTCT | GGACTAGGAA | CCGACAGCCC | CCCTCCCCGC | GTCCCTCCCT | 60 |
| | CTCTCTCCAG | CCGTTTGGG | GAGGGGCTCT | CCACGCTCCG | GATAGTTCCT | GAGGGTCATC | 120 |
| | CGCGCCGAC | TGCGCTTTCC | GTTTGGCCTT | CACCTGGATA | TAAATTTCCG | GCGAAGCTGC | 180 |
| | CCCCAGGATG | ACCAAGCTGG | CGCGGCTGT | GCCAGGATG | ATGGCGCCGG | GCCCGGGGCA | 240 |
| | GAATACCCG | CGTAGCGGT | TCCGCTGGA | AGTGTCCACT | CCCTCGGCC | AGGGCCGGGT | 300 |
| 55 | CAACGAGCT | GCGCGCTTT | TTATCAACGG | CAGGCGCGTG | CCCAACCA | TCCGCCACAA | 360 |
| | GATGCTGGAG | ATGGCCACCC | ACGGCATCCG | GCCCTGGGTC | ATCTCGCGGC | AGCTGCGGCT | 420 |
| | GTCCCAAGCG | TGCGTCTCCA | AGATCCTGTG | CAGGTACCAG | GAGACTGGCT | CCATACGTCC | 480 |
| | TGGTGCCTC | GCGGGCAGCA | AGCCCAAGGT | GACCAACGCT | GACGTGGAGA | AGAAAATTGA | 540 |
| | GGAATACAAA | AGAGAGAAAC | CGGGCATGTT | CAGCTGGGAA | ATCCGAGACA | AATTAATCAA | 600 |
| 60 | GGAGCGGCT | TGTGATCGAA | ACACCGTGCC | GTCAGTGAGT | TCCATCAGCC | GCATCCTGAG | 660 |
| | AAGTAAATTC | GGGAAAGGTG | AAGAGGAGGA | GCCGCACTTG | GAGAGGAAGG | AGGCAGAGGA | 720 |
| | AAGCGAGAAG | AAGGCCAAAC | ACAGCATCGA | CGGCATCCTG | AGCGAGCGAG | CCTCAGCACC | 780 |
| | CCAATCAGAT | GAAGGCTCTG | ATATTGACTC | TGAACCAAGT | TTACCACTAA | AGAGGAAACA | 840 |
| | GCGCAGAAGC | CGAACCACTT | TCACAGCAGA | ACAGCTGGAG | GAACTGGAGC | GTGCTTTTGA | 900 |
| 65 | GAGAACTCAT | TACCTTGACA | TTTATACTAG | GGAGGAACTG | GCCAGAGGGG | CGAAGCTCAC | 960 |
| | CGAGGCCCGA | GTACAGGTCT | GGTTTAGCAA | CGCGCTGCA | AGATGGAGGA | AGCAAGCTGG | 1020 |
| | GGCCAAATCA | CTGATGGCTT | TCAACCATCT | CATTCCCGGG | GGGTTCCCTC | CCACTGCCAT | 1080 |
| | GCGGACCTTG | CCAACGTACC | AGCTGTGCGA | GACCTCTTAC | CAGCCACAT | CTATTCCACA | 1140 |
| | AGCTGTGTCA | GATCCAGCA | GCACCGTTCA | CAGACCTCAA | CCGCTTCTCT | CAAGCACTGT | 1200 |
| 70 | ACACCAAAGC | ACGATTCCTT | CCAACCCAGA | CAGCAGCTCT | GCCTACTGCC | TCCCAAGCAC | 1260 |
| | CAGGCATGGA | TTTCCAGCT | ATACAGACAG | CTTTGTGCTT | CGTCCGGGGC | CCTCCAACCC | 1320 |
| | CATGAACCCC | ACCATTTGGCA | ATGGCCTCTC | ACCTCAGAA | TCAATTCGTC | ATAATCTGTC | 1380 |
| | CCTACACAGC | AAGTTTCACT | GTGTGCAGAA | TGAAGGAACT | GGAAGAAAGT | CTTGGTGAT | 1440 |
| | GCTCAATCCA | GAGGGTGGCA | AGAGCGGGAA | ATCTCCTAGG | AGAAGAGCTG | CATCCATGGA | 1500 |
| 75 | CAACAAACAG | AAATTTGCTA | AGAGCCGAAG | CCGAGCTGCC | AAGAAGAAAG | CATCTCTCCA | 1560 |
| | GTCTGGCCAG | GAGGGTGGTG | GGGACAGCCC | TGGATCACAG | TTTTCCAAAT | GGCCTGCAAG | 1620 |
| | CCCTGGCTCT | CACAGCAATG | ATGACTTTGA | TAACTGGAGT | ACATTTGCCC | CTCGAACTAG | 1680 |
| | CTCAATGTCT | AGTACTTTA | GTGGGAGACT | CTACCCATT | ATGACCGAAC | AGGATGATCT | 1740 |
| | TGGAGAAGGG | GATGTGCATT | CTATGGTGTA | CCGCAACATG | GCCGCAAGAA | TGGCCTCTAC | 1800 |
| 80 | TTTACCCAGT | CTGTCTGAGA | TAAGCAATCC | CGAAAACATG | GAAAATCTTT | TGGATAATCT | 1860 |
| | CAACCTTCTC | TCATACCAA | CATCATTAA | TGTTTCGACC | CAGTCTCTAC | CTGGCACCAT | 1920 |
| | GATGACGAGC | ACGCGGTGCT | ACTCGTTTGC | GCCACCAAAC | ACCACTTTGA | ATTCAACCCAG | 1980 |
| | CCCAAACTAC | CAAAAATATA | CATATGGCCA | ATCCAGCATG | AGCCCTTTTG | CCCAGATGCC | 2040 |
| | TATACAAACA | CTTCAGGACA | ATAAGTCGAG | TTATGGAGGT | ATGAGTCAGT | ATAACTGTGC | 2100 |
| | GCCTGGACTC | TTGAAGGAGT | TGCTGACTTC | TGACTCTCTT | CCCCATAATG | ACATTATGAC | 2160 |

| | | | | | | | |
|----|---------------------------------------|-------------|-------------|------------|-------------|-------------|------|
| | ACCAGTTGAT | CCTGGGGTAG | CCCAGCCCAA | CAGCCGGGTT | CTGGGCCAGA | ACGTCATGAT | 2220 |
| | GGGCCCTAAT | TGGGTCTATG | CAACCTATGG | CAGCCAGGCA | TCTCATAACA | AAATGATGAA | 2280 |
| | TCCCAGCTCC | CATACCCACC | CTGGACATGC | TCAGCAGACA | TCTGCAGTTA | ACGGGCGTCC | 2340 |
| 5 | CCTGCCCCAC | ACGGTAAGCA | CCATGCCCCA | CACCTCGGGT | ATGAACCGCC | TGACCCCAAGT | 2400 |
| | GAAGACACCT | GTACAAGTGC | CTCTGCCCCA | CCCATGCGAG | ATGAGTGCCC | TGGGGGGCTA | 2460 |
| | CTCCTCGGTG | AGCAGCTGCA | ATGGCTATGG | CAGAAATGGG | CTTCTCCACC | AGGAGAAGCT | 2520 |
| | CCCAAGTGAC | TGGATGGCA | TGTTCAATGA | GCGCTTAGAC | TGTGACATGG | AATCCATCAT | 2580 |
| | TGGGAATGAC | CTCATGGATG | GAGATACATT | GGATTTTAAC | TTTGACAATG | TGTTGCCCAA | 2640 |
| 10 | CCAAAGCTTC | CCACACAGTG | TCAAGACAAC | GACACATAGC | TGGGTGTGAG | GCTGAGGGTT | 2700 |
| | AGTGAGCAGG | TTACACTTAA | AAGTACTTCA | GATTGTCTGA | CAGCAGGAAC | TGAGAGAAGC | 2760 |
| | AGTCCAAAGA | TGCTTTTCAC | CAACTCCCTT | TTAGTTTCTT | TGGTTAAAAA | AAAAAAAAAA | 2820 |
| | AAAAAA | | | | | | 2827 |
| 15 | Seq ID NO: 168 DNA Sequence | | | | | | |
| | Nucleic Acid Accession #: NM_005761.1 | | | | | | |
| | Coding sequence: 250..4956 | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| 20 | GCGAGGAGGA | AACGGTGC | GAGCGCGCAG | GGCTTGCTGC | CGCCACCGCC | GCTGCACAGG | 60 |
| | CTGCGGAGAC | GAGCTTGCCG | CGCGCGCGCC | TCCCCGCTCT | CCTTCTGGG | CGAGCTGCGG | 120 |
| | GGATGGGGCG | GCGCGGGGAG | CCCGAGCGCG | CGCAGGAACC | GCGCGCGCGG | CCGCCCGGCT | 180 |
| | CTCCGTTCGC | GCGCGCTGGA | GCGCGCTGCG | CGCGCGCGCG | CCTTGCCTGG | GGGCGGCGCC | 240 |
| | CCCAGCCCCA | TGGAGTCTCT | CCGAGGGAAG | GCGCGCGCGG | GCCCCCGCGG | CCCCGCGAGG | 300 |
| | CCACTGCCCC | TGCTCGCCTA | TCTGCTGGCA | CTGGCGGCTC | CGCGCGGGGG | CGCGGACGAG | 360 |
| 25 | CCCGTGTGGC | GCTCGGAGCA | AGCCATCGGA | GCCATGCGCG | CGAGCCAGGA | GGACGCGGTG | 420 |
| | TTTGTGGCGA | GCGCGAGCTG | CCTGGACCAAG | CTGGACTACA | GCTTGGAGCA | CAGCCTCTCG | 480 |
| | CGCCTGTACC | GGGACCAAGC | GGGCAACTGC | ACAGAGCGCG | TCTGCTGGCG | CGCCCCCGCG | 540 |
| | CGGCCCCGCG | CCGCGAGCAG | CTTCAGCAAG | CTGCTGCTGC | CCTACCGCGA | GGGGGCGGCG | 600 |
| | GGCCTCGGGG | GGCTGTGCTG | CACCGCTGG | ACCTTCGACC | GGGGCGCTCT | CGAGGTGCGG | 660 |
| 30 | CCCTCGGGCA | ACCTGAGCGC | CAACTCCCTG | CGCAACGGCA | CCGAGGTGGT | GTGCTGCCAC | 720 |
| | CCGCGGGGCT | CGACGCGCGG | CGTGGTGTAC | CGCGCGGGCG | GGAAACAACG | CTGTTACCTG | 780 |
| | GCGGTGGCGG | CCACTACGCT | GCTGCTGAG | CCGAGACCGG | CGAGCCGCTG | CAACCCCGGG | 840 |
| | GCATCCGACC | ACGACACGCG | CATCGCGCTC | AAGGACACCG | AGGGGCGCAG | CCTGGCCACG | 900 |
| | CAGGAGCTGG | GGCGCTCAA | GCTGTGCGAG | GGCGCGGGCA | GCTGCACTT | CGTGGACGCC | 960 |
| 35 | TTTCTCTGGA | ACGGCAGCAT | CTACTTCCCC | TACTACCCCT | ACAATATAC | GAGCGGCGCT | 1020 |
| | GCCACCGGCT | GGCCAGCAT | GGCGCGCATC | GCGCAGAGCA | CCGAGGTGCT | GTTCCAGGGC | 1080 |
| | CAGGACTCCC | TGACTGCGG | CCAAGGCCAC | CCCGACGGCC | GCGCGCTGCT | CCTCTCCTCC | 1140 |
| | AGCCTAGTGG | AGGCCCTGGA | CGTCTGGGCG | GGAGTGTTC | GCGCGGCGCG | TGGAGAGGGC | 1200 |
| 40 | CAGGAGCGGC | GCTCCCCCAC | CACCACGGCG | CTCTGCTCT | TCAGAAATGAG | TGAGATCCAG | 1260 |
| | GCGCGCGCCA | AGAGGGTCAG | CTGGGACTTC | AAGACGGCGG | AGAGCCAATG | CAAGAAAGGG | 1320 |
| | GATCAACCTG | AAAGAGTCCA | ACCAATCGCA | TCATCTACCT | TGATCCATTG | CGACCTGACA | 1380 |
| | TCCGTTTATG | GCACCTGGT | AATGAACAGG | ACTGTTTTAT | TCTTGGGGAC | TGGAGATGGC | 1440 |
| | CAGTTACTTA | AGGTTATCTT | TGGTGAGAAT | TTGACTTCAA | ATTGTCCAGA | GGTTATCTAT | 1500 |
| 45 | GAAATTAAG | AAGAGACACC | TGTTTTCTAC | AAACTCGTTC | CTGATCCTGT | GAAGAAATATC | 1560 |
| | TACATTATTC | TAACAGCTGG | GAAAGAGGTG | AGGAGAATTC | GTGTTGCAAA | CTGCAATAAA | 1620 |
| | CTAATAATCT | GTTCGGAGTG | TTTAACAGCC | ACAGACCCCT | ACTGGGGTGG | GTGCCATTCC | 1680 |
| | GTACAAAGGT | GCACTTTTCA | AGGAGATTGT | GTACATTCAG | AGAACTTAGA | AAACTGGCTG | 1740 |
| | GATATTTCTG | CTGGAGCAAA | AAAGTGCCCT | AAAATTCAGA | TAATTCGAAG | CAGTAAAGAA | 1800 |
| 50 | AAGACTACAG | TGACTATGGT | GGGAAGCTTC | TCTCCAAGAC | ACTCAAAGTG | CATGGTGAAG | 1860 |
| | AATGTGGACT | CTAGCAGGGA | GCTCTGCCAG | AATAAAGTGC | AGCCCAACCG | GACCTGCAAC | 1920 |
| | TGTAGCATCC | CAACAGAGCG | AACCTACAAA | GATGTTTCAG | TTGTCAACGT | GATGTTCTCC | 1980 |
| | TTCCGTTCTT | GGAAATTTAT | AGACAGATTG | AACCTTACCA | ACTGCTCATC | ATTAAAGAAA | 2040 |
| | TGCCAGCAT | CGGTAGAAAC | TGGCTGCGCG | TGGTGTAAAA | GTGCAAGAAAG | GTGTATCCAC | 2100 |
| 55 | CCCTTCACAG | CTTGGGACCC | TTCTGATTAT | GAGAGAAACC | AGGAACAGTG | TCCAGTGGCT | 2160 |
| | GTGAGAAAGA | CATCAGGAGG | AGGAAGACCC | AAGGAGAACA | AGGGGAACAG | AACCAACACG | 2220 |
| | GCTTTACAGG | TCTTCTACAT | TAAGTCCATT | GAGCCACAGA | AAGTATCGAC | ATTAGGGAAA | 2280 |
| | AGCAACGTGA | TAGTAACGGG | AGCAAACTTT | ACCCGGGCAT | CGAACATCAC | AATGATCCTG | 2340 |
| | AAAGGAACCA | GTACCTGTGA | TAAGGATGTG | ATACAGGTTA | GCCATGTGCT | AAATGACACC | 2400 |
| 60 | CACATGAAAT | TCTCTCTCC | ATCAAGCCCG | AAAGAAATGA | AGGATGTGTG | TATCCAGTTT | 2460 |
| | GATGGTGGGA | ACTGCTCTTC | TGTGGGATCC | TTATCTTACA | TTGCTCTGCC | ACATTGTTCC | 2520 |
| | CTTATATTTG | CTGCTACCAAC | CTGGATCAGT | GGTGGTCAAA | ATATAACCAT | GATGGGCGAG | 2580 |
| | AATTTTGATG | TAATTTGACAA | CTTAATCATT | TCACATGAAT | TAAAGGAAA | CATAAATGTC | 2640 |
| | TCTGAATATT | GTGTGGCGAC | TACTGCGGG | TTTTTAGCCC | CCAGTTTAAA | GAGTTCAAAA | 2700 |
| 65 | GTGCGCACGA | ATGTCACTGT | GAAGCTGAGA | GTACAAGACA | CCTACTTGGA | TTGTGGAACC | 2760 |
| | CTGCAGTATC | GGGAGGACCC | CAGATTCAAG | GGGTATCGGG | TGGAATCCGA | GGTGGACACA | 2820 |
| | GAACTGGAAG | TGAAATTTCA | AAAGAAAAAT | GACAACCTCA | ATATTTCCAA | AAAAGACATT | 2880 |
| | GAAATTAATC | TCTTCCATGG | GGAAAAATGG | CAATTAATTT | GCAGTTTGA | AAATATTACT | 2940 |
| | AGAAATCAAG | ATCTTACCAAC | CATCCTTTGC | AAAATTAAG | GCATCAAGAC | TGCAAGCACC | 3000 |
| 70 | ATTGCCAACT | CTTCTAAGAA | AGTTCCGGTC | AAGCTGGGAA | ACCTGGAGCT | CTACGTGCGAG | 3060 |
| | CAGGAGTCAG | TTCCTTCCAC | ATGGTATTTT | CTGATTGTGC | TCCCTGTCTT | GCTAGTGATT | 3120 |
| | GTCATTTTGG | CGGCGGTGGG | GGTGACCAGG | CACAAATCGA | AGGAGCTGAG | TGCGAAACAG | 3180 |
| | AGTCAACAAC | TAGAAATGCT | GGAAAAAGCG | CTCCGGAAGG | AGATACGTGA | CGGCTTTGCT | 3240 |
| | GAGCTGCAGA | TGGATAAATT | GGATGTGGTT | GATAGTTTGG | GAACTGTTC | CTTCTTGAC | 3300 |
| 75 | TACAAACATT | TGCTCTGAG | AACTTTCTTC | CCTGAGTCAG | GTGGCTTCA | CCACATCTTC | 3360 |
| | ACTGAAGATA | TGCATAACAG | AGACGCCAAC | GACAAGAATG | AAAGTCTCAC | AGCTTTGGAT | 3420 |
| | GCCCTAATCT | GTAATAAAG | CTTTCTTGT | ACTGTCTATC | ACACCTTGA | AAAGCAGAA | 3480 |
| | AACTTTCTTG | TGAAGGACAG | GTGCTGTGTT | GCCTCTCTTC | TAACCAATGC | ACTGCAAAAC | 3540 |
| | AAGCTGGTCT | ACCTGACCAG | CATCCTAGAG | GTGCTGACCA | GGGACTTGAT | GGAAACAGTG | 3600 |
| 80 | AGTAACATGC | AGCCGAAACT | CATGCTGAGA | CGCACGGAGT | CGTCTGCGA | AAAACCTCTC | 3660 |
| | ACAAACTGGA | TGTCGCTCTG | CCTTTCTGGA | TTTCTCCGGG | AGACTGTCSG | AGAGCCCTTC | 3720 |
| | TATTTGCTGG | TGACGACTCT | GAACAGAGAA | ATTAACAAGG | GTCCCGTGGG | TGTAATCACT | 3780 |
| | TGCAAAAGCC | TGTACACACT | TAATGAAGAC | TGGCTGTGTT | GGCAGGTTCC | GGAATTCAGT | 3840 |
| | ACTGTGGCAT | TAAAGCTCGT | CTTTGAAAAA | ATCCCGGAAA | ACGAGAGTGC | AGATGTCTGT | 3900 |
| | CGGAATATTT | CAGTCAATGT | TCTCGACTGT | GACACCATTG | GCCAAGCCAA | AGAAAAAGAT | 3960 |

5
 10
 15
 20

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TTCCAAGCAT TCTTAAGCAA AAATGGCTCT CCTTATGGAC TTCAGCTTAA TGAAATTGGT 4020
CTTGAGCTTC AAATGGGCAC ACGACAGAAA GAACCTCTGG ACATCGACAG TTCCTCGTG 4080
ATTCTTGAAG ATGGAATCAC CAAGCTAAAC ACCATTGGCC ACTATGAGAT ATCAATATGGA 4140
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GACCACTGCC ATTTGATTTT ACCAGATTGG GAAGCATTCC AAGATGTGCA AGGAAAGAGA 4260
CATCGAGGGA AGCACAAGTT CAAAGTAAAA GAAATGTATC TGACAAAGCT GCTGTGAGCC 4320
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AGCAGAGCTC CATTTGCTAT AAAATACTTT TTTGACTTTT TGGACGCCCA GGCTGAAAAC 4440
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CAGCAACTAG GGAAGGAAGC ACCAACTAAT AAGCTTCTCT ATGCCAAGGA TATCCCAACC 4680
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AAACTAGAAA GAGAACGAGG GCTGGAAGAA GCTCAGAAAC AACTCTTGCA TGTAAGAGTC 4920
TTATTTGATG AAAAGAAGAA ATGCAAGTGG ATGTAAGCAC TCTGGGGCCT GGCTTAATCT 4980
GGCAAAATTC TTCAACGAC TTGGAGACAA AATGGCTGCT TGAGCTACTC TGTGTGTTA 5040
ATTTGTTGTT TGACATAGG TTCCACTTTG GGCACGTGCT TTTTAAGAGA CCAAGGCACA 5100
TGACAGCTT TTAGAAAGCA A
  
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Seq ID NO: 169 DNA Sequence
Nucleic Acid Accession #: XM_063670.1

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Coding sequence: 1..708
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ACCTGAGTGA AATTATTAAT GTGCTGACAG CGTACTGTTT ATCCCAACAG TGAGAAGTGG 120
CGTGCTCTCT CAGTCCCTTC ATCTTCTCTAT TTTGAGGAGC TGGTGGGCAC CAGCCAGGAA 180
CTGGCTCTCA CTTTCTGGCA TTTACTGTCT ATGTTTGGAT TCTTCATCGT GTCCTATGGC 240
TTTCTCAGAG CATTTGGCAG GACTCTTTTC CACTTGGATC TGCTACAAAC CAACCTTACA 300
CCTTCAGGCT TTGACAAGTA CACTGGTCTC TTCACTATG AAATAGAGGG AGATGGGTTA 360
GATCCATGTT TTCAAAGCAT GGTCCAAGGA ATCCTAGAGG TTTTGTGGAT GTCCAAAGTG 420
GAGAGTGCAT ACCACACTAA TGATGGTGAT ACTGCTGGAG AGGGGGTGGG AAATGGTACC 480
AGTCAAAACC GAGGCGGAGG AGGAGCAGCC CGCAGTCGCT GCCCGAGAT GGAGGAGCCC 540
ACGCCGAGC CCCTCTATGT CGACGTAGAC AAAGGGCTGA CCTTGGCCTG CTTGCTCTTC 600
CTCTGCTCT TCCTGTGCT GATGATCATC CGCTGTGCCA AGGTATCAT GGACCCCTTAC 660
AGGCCCATCC CCACATCCAC CTGGGAGGAG CAGCACCTGG ACGACTGA 708
  
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Seq ID NO: 170 DNA Sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1-936

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GGCCCGGGCT CGCCCGCGCC GTGGGGGGCT CTGACTCCTG CCGAGCCGGG CCTGGGCAGC 180
GCCCCCGGCG CCCCAGGAGC CCGCGCCCCC GTCACCGGGA AACCGCGTAG CCGGCGATCC 240
CGCGTGCACC TGGGCTCGGC GCCGGCCACG CCAGGACCCC GGGAGCGCAC GGGACGGGCC 300
TCGCCAGCCC TCCCAATATA CTCTGACCTC TTGTCCAAGG CATCTGCTAT AGCTACTGGG 360
ACACCACCTC GTGAAGACTC TACCATTGCA AGGTTCTACC TGCCCCCACC TCTCACCCT 420
CACCCGAGC TGGTGGGCAC CAGCCAGGAA CTGGCTCTCA CCTTCTGGCA TTTACTGTCT 480
ATGTTTGGAT TCTTATCGT GTCTATGGC TTTCTCACAG CATTTGGCAG GACTCTTTTC 540
CACTTGGATC TGCTACAACC CAACCTTACA CCTTCACGCT TTGACAAGTA CACTGGCCAG 600
CTCCTGAGC TCCCAATGTA CTCAAAGTAT GTACTGACCA TCCACTGGAG CCAGGGACTG 660
TGCAATTTGT CGTCACATCC CTGTGAAGCA GGGGTGGAAA ATGGTACCAG TCAAAACCGA 720
GGCGGAGGAG GAGCAGCCCG CAGTCGCTGC CGCGAGATGG AGGAGCCAC GCCCGAGCCC 780
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CTTGTGCTGA TGATCATCCG CTGTGCCAAG GTCATCATGG ACCCTTACAG GCCCATCCCC 900
ACATCCACCT GGGAGGAGCA GCACCTGGAC GACTGA 936
  
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Seq ID NO: 171 DNA Sequence
Nucleic Acid Accession #: FGENESH predicted
Coding sequence: 1-2094

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AACAGACAAC CTACAGAAAT GGAGAAAAAT TTTGCAATCT ACTCATCTGA CGAAGGGCTA 180
ATATCCAGAA TCTACATGTA ACCCAACAA ATTTACAAGA AAAAAACAAA CAACCTATC 240
AACAGTGGG CGAAGGATAT GAACAGACAC TTCTCAAAG AAGACATTTA TGCAGCCAAC 300
AGACACATGA AAAATGCTC ATCATCACTG GCCATCAGAG AAATGCAAAAT CAAAACCACA 360
ACGAGATGCC ATCTCACACC AGTTAGAAAT GCGATCATT AAGAGTCAGG AAACAACAGA 420
ACTGCAAGAG AACAGCCAAA ACTGAGAAAG GAAGCAGTTG GATCTATTGA GATATTCGCG 480
TTTGTGATG GACTGGACAT CACACTCATG ATCCTGGGTA TACTGGCATC ACTGGTCAAT 540
GGAGCCTGCC TTCTTTTAA TCCACTGGT TTAGGAGAAA TGAGTGATAA CCTTATTAGT 600
GGATGTCTAG TCCAACTAA CACAACAAAT TATCAGAACT GTACTCAGTC TCAAGAGAAG 660
CTGAATGAAG ATATGACTCT GTTGACCTG TATTATGTTG GAATAGGTGT TGCTGCCCTG 720
ATTTTGGTT ACATACAGAT TTCTTGTGG ATTATACTG CAGCAGGACA GACCAAGAGG 780
ATTGAAAAC AGTTTTTTCA TTCAGTTTG GCACAGGACA TGGGCTGGTT TGATAGCTGT 840
GACATCGGTG AACTTAACAC TCCATGACA GATGACATTG ACAAATCAG TGATGGTATT 900
GGAGATAAGA TTGCTCTGTT GTTTCAAAAC ATGTCTACTT TTTGATTGG CCTGGCAGTT 960
GGTTTGGTGA AGGGCTGAAA ACTCACCTTA GTGACTCTAT CCACGCTCTC TCTTATAATG 1020
GCTTCAGCGG CAGCATGTTT TAGGATGGTC ATCTCATGTA CCAGTAAGGA ATTAAGTGCC 1080
  
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5 TATTCCAAAG CTGGGGCTGT GGCAGAAAGAA GTCTTGTCAT CAATCCGAAC AGTCATAGCC 1140
 TTTAGGCCCC AGGAGAAAGA ACTTCAAAGG TATACACAGA ATCTCAAAGA TGCAAAGGAT 1200
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 10 TTGGTCCGTC TCAATGGCAG TGGGAAGAGT ACGGTAGTCC AGCTTCTGCA GAGGTTATAT 1680
 GATCCGAGTG ATGCGTTTAT CATGGTGGAT GAGAAATGACA TCAGAGCTTT AAATGTGCGG 1740
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 AGGGAAGCAA ATGCGTATGA TTTTATCATG GAGTTTCTTA ATAAATTAA TACATTGGTA 1920
 15 GGGGAAAAAG GAGCTCAAAAT GAGTGGAGGG CAGAAAAGCA GGATCGCAAT TGCTCGTGCC 1980
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 25 CCTAATTCCT CTAATATCTC TCTGTTTCT TTAGTGTAAT CCATAGCAGT TATTGCATTG 60
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 TCCAGGTTAT TGATAGAGAA CCCAGTATAG ATAACCTTTC CACAGCTGGA TATAAACCTG 180
 AATCCATAGA AGGAACCTGT GAATTTAAAA ATGTTTCTTT CAATTATCCA TCAAGACCAT 240
 CTATCAAGAT TCTGAAGGT CTGAATCTCA GAATTAAGTC TGGAGAGACA GTCCGCTTGG 300
 30 TCGGTCTCAA TGGCAGTGGG AAGAGTACGG TAGTCCAGCT TCTGCAGAGC TTATATGATC 360
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 35 AAAAAAGGAG TCAAATGAGT GGAGGGCAGA AACAGAGGAT CGCAATTGCT CGTGCCCTAG 660
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Seq ID NO: 173 DNA Sequence
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 60 GCAACTGAAT TGGCAAAAGA GAATATTAAA TGTTCCTTGA AGGGCTGCGA TCCAAAAGAA 900
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Seq ID NO: 174 DNA Sequence
 Nucleic Acid Accession #: NM_032211.5
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 1 11 21 31 41 51
 70 GGCTGGGGGG CCGCGGCGG GAGGCGGATA AAAAGGCCCC AGGGCGCCCG GGGAGGGAGC 60
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 75 TCTGTTCTCT TCTGCTGCTAG GCCAGCCCCC TCCAGCAGG CCACAGTCAC TGGGCACCA 240
 TAAGCTCCGG CTGGTGGGCC CAGAGAGCAA GCCAGAGGAG GGCGCGCTGG AGGTGCTGCA 300
 CCAGGGCCAG TGGGGCAGCC TGTGTGATGA CAACTTTGCT ATCCAGGAG CCACAGTGCC 360
 TTGCGCCAG CTGGGCTTGG AAGCTGCCTT GACCTGGGCC CACAGTGCCA AGTACGGCCA 420
 AGGGGAGGGA CCCATCTGTC TGGACAATGT GCAGTGTGTG GGCACAGAGA GCTCCTTTGA 480
 80 CCAAGTCCGG TCTAATGGCT GGGAGTTCAG TGACTGCAGT CACTCAGAAG ACGTAGGGGT 540
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 CAGCGAGGTG CCGTGCAGCA GCCACTACTA CAGGAAAGTC TGGGATCTGA AGATGAGGGA 840

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| | GGTGGCGCTG | CGCTCCGGGG | CCCAGGTGGG | CGAGGGCCGG | GTGGAAGTGC | TCATGAACCG | 1140 |
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| | TCAGCTGGGC | TTTGGCTCTG | CTCGGGAGGC | CCTCTTTGGG | GCCCGGCTGG | GCCAAAGGCT | 1260 |
| | AGGGCCCATC | CACCTGAGTG | AGGTGCGCTG | CAGGGGATAT | GAGCGGACCC | TCAGCGACTG | 1320 |
| | CCCTGCCCTG | GAAGGGTCCC | AGAATGGTTG | CCAACATGAG | AATGCTGCTG | CTGTCAAGTG | 1380 |
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| | TGCCATCCAT | GCCTACAAGG | AAACCTGGTT | CTGGTGGGG | ACGCCAAGGG | CCCAGGAGGT | 1620 |
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| 15 | CGGGCCGGTG | CAGTGTCTCC | ACGGTGGCGG | GCCTTCCTG | GCTGGAGTCT | CCTGCATGGA | 1740 |
| | CAGTGCACCA | GACCTGGTGA | TGAACGCCCA | GCTAGTGCAG | GAGACGGCCT | ACTTGGAGGA | 1800 |
| | CGCGCGCTG | AGCCAGCTGT | ATTGTGCCCA | CGAGGAGAAC | TGCTCTTCCA | AGTCTGGGGA | 1860 |
| | TCACATGGA | TGGCCCTACG | GATACCGCCG | CCTATTGGCG | TTCTCCACAC | AGATCTACAA | 1920 |
| | CTTGGGCGGG | ACTGACTTTC | GTCCAAAGAC | TGACGCGAT | AGCTGGGTTT | GGCACCAGTG | 1980 |
| 20 | CCACAGGCAT | TACCACAGCA | TTGAGGTCTT | CACCCACTAC | GACCTCTCTA | CTCTCAATGG | 2040 |
| | CTCCAAGGTG | GCTGAGGGGC | ACAAGGCCAG | CTTCTGTCTG | GAGGACACAA | ACTGCCCCAC | 2100 |
| | AGGACTGAAC | CGGCGCTACG | CATGTGCCAA | CTTTGGAGAA | CAGGGAGTGA | CTGTAGGCTG | 2160 |
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| 25 | CTCCAACAAT | ATGCTGCAGT | GCGCTGCAA | GTATGATGGG | CACCGGGTCT | GGCTGCACAA | 2340 |
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| 30 | CAGATGGTAT | TGCTCCCTCA | GGATGGCTCT | GGGCTTGCCC | CTAAGGGCCT | GTGGCCTATG | 2640 |
| | GAATATGTCC | TCCAGGCTTT | GCTCAGCTGA | GCTCCTCTTC | TGTAAGGAAA | CCCACTCATC | 2700 |
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| | ATTTAGAACT | CACCTCTCAC | ACTCTGTTCT | TAGTGTCTCT | TACCTTTATC | TTACCAACAC | 3000 |
| | CATGGGTGTT | TCTATTATCC | TGGGAAGCAC | AGACCTCGGG | CATCCCTTAA | TTGCCTGATG | 3060 |
| | GGCCAAACAC | AACAGTTACG | GAGTGTCTGA | GAAGGGGCAA | GTTCACAGA | AATGGCCAGA | 3120 |
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| | ACCAAGTGTC | TGAAGTGAAC | TTTGCAATTGA | ATAAATTTT | GCCATGGAAA | GAACATCAAA | 3360 |
| | CAAGCCACTC | ATCTCTACAG | AGATAAGAAA | ACAAGTTTGG | CAGAGCAAGA | GACAGAAGAC | 3420 |
| | CGTGGAGAAA | TCAGAAGGGG | GAACAGTCAG | TTTAGTTAAG | GATGGAACCT | GGGAAAGGGC | 3480 |
| 45 | ACCATTCCTG | CTTGATGGGG | CTCTGATTTC | CTCTTGCTCA | AGTGGAAATA | AACCCATAGG | 3540 |
| | TCTTCTTGAC | ATGATTCTTG | ATCTTTTCTC | CACCTGAGACA | CACCTAAGTG | ATGATCCTTA | 3600 |
| | CAGGACTGAC | ACCCTAATGC | CAATAAAAGT | TGCTCATTAT | GGACTGCTAC | AAAAAAAAAA | 3660 |
| | AAAAA | | | | | | 3665 |
| 50 | Seq ID NO: 175 DNA Sequence | | | | | | |
| | Nucleic Acid Accession #: NM_001798.2 | | | | | | |
| | Coding sequence: 234..1130 | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
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| | TCAGTGTGGC | CAAAATTGACA | AGAGCGAGAG | GTATAGTCTG | TTCCATCCCG | ACCCGGGGCC | 120 |
| | ACGGTACTGG | GCCCTGTGTT | CCCTCTCTCG | CGCCCGGAGA | GCCAGGGTCC | GCTTCTGCA | 180 |
| | GGGTTCACAG | CGCCCGCTC | CAGGGCCGGG | CTGACCCGAC | TCGCTGGCGC | TTCATGGAGA | 240 |
| 60 | ACTTCAAAA | GGTGGAAAG | ATCGGAGAGG | GCAGTACGGG | AGTTGTGTAC | AAAGCCAGAA | 300 |
| | ACAAAGTGAC | GGGAGAGGTG | GTGGCGCTTA | AGAAAATCCG | CCTGGACACT | GAGACTGAGG | 360 |
| | GTGTGCCAG | TACTGCCATC | CGAGAGATCT | CTCTGCTTAA | GGAGCTTAAC | CATCCTAATA | 420 |
| | TTGTCAAGCT | GCTGGATGTC | ATTACACAG | AAAATAAACT | CTACCTGGTT | TTTGAATTTT | 480 |
| | TGCACCAAGA | TCTCAAGAAA | TTTATGGATG | CCTCTGCTCT | CACTGGCATT | CCTCTTCCCC | 540 |
| 65 | TCATCAAGAG | CTATCTGTTT | CAGCTGTCTC | AGGGCCTAGC | TTTCTGCCAT | TCTCATCGGG | 600 |
| | TCCTCCACCG | AGACCTTAAA | CCTCAGAAATC | TGCTTATTAA | CACAGAGGGG | GCCATCAAGC | 660 |
| | TAGCAGACTT | TGGACTAGCC | AGAGCTTTTG | GAGTCCCTGT | TCGTACTTAC | ACCCATGAGG | 720 |
| | TGGTGACCTT | GTGGTACCGA | GCTCCTGAAA | TCCTCCTGGG | CTGCAAAATAT | TATTCCACAG | 780 |
| | CTGTGGACAT | CTGGAGCCTG | GGCTGCATCT | TTGCTGAGAT | GGTACTCGC | CGGGCCCTAT | 840 |
| | TCCTGGGAGA | TTCTGAGATT | GACCACTCT | TCCGGATCTT | TCGGACTCTG | GGGACCCAG | 900 |
| 70 | ATGAGGTGGT | GTGGCCAGGA | GTTACTTCTA | TGCTTGATTA | CAAGCCAAGT | TTCCCAAGT | 960 |
| | GGGCCCCGCA | AGATTTTAGT | AAAGTTGTAT | CTCCCTGGA | TGAAGATGGA | CGGAGCTTGT | 1020 |
| | TATCGCAAT | GCTGCACTAC | GACCTTAACA | AGCGGATTTT | GGCCAAGGCA | GCCCTGGCTC | 1080 |
| | ACCTTTTCTT | CCAGGATGTG | ACCAAGCCAG | TACCCATCT | TCGACTCTGA | TAGCCTTCTT | 1140 |
| | GAAGCCCCCA | GCCCTAATCT | CACCCCTCTC | TCCAGTGTGG | GCTTGACCAG | GCTTGGCCTT | 1200 |
| 75 | GGGCTATTGT | GACTCAGGTG | GGCCCTCTGA | ACTTGCTTAA | AACACTCACC | TTCTAGTCTT | 1260 |
| | GGCCAGCCAA | CTCTGGGAAT | ACAGGGGTGA | AAGGGGGGAA | CCAGTGAATA | TGAAGGAAG | 1320 |
| | TTTCAGTATT | AGATGCACCT | AGTTAGCCT | CCACCACCTT | TTCCCTCTTC | TCTTAGTTAT | 1380 |
| | TGCTGAAGAG | GCTTGGTATA | AAAAATAATT | TAAAAAAGCC | TTCTTACAG | TTAGATTGTC | 1440 |
| 80 | CGTACCAATC | TCTGAATGCC | CCATAATTAT | TATTTCCAGT | GTTTGGGATG | ACCAGGATCC | 1500 |
| | CAAGCCTCCT | GCTGCCACAA | TGTTTATAAA | GGCCAAATGA | TAGCGGGGGC | TAAGTTGGTG | 1560 |
| | CTTTTGAGAA | CCAAGTAAAA | CAAAACCACT | GGGAGGAGTC | TATTTTAAAG | AATTCGGTTG | 1620 |
| | AAAAAATAGA | TCCAATCAGT | TTATACCTTA | GTTAGTGTTT | TGCCTCACCT | AATAGGCTGG | 1680 |
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| | TTGTCCCTTC | TACAGGCATG | AGGAATCTGG | GAGGCCCTGA | GACAGGGATT | GTGCTTCATT | 1800 |

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| CCAATCTATT | GCTTCACCAT | GGCCTTATGA | GGCAGGTGAG | AGATGTTTGA | ATTTTCTCT | 1860 |
| TCCTTTTAGT | ATTCTTAGTT | GTTTCAGTTGC | CAAGGATCCC | TGATCCCAT | TTCTCTGAC | 1920 |
| GTCCACCTCC | TACCCCATAG | GAGTTAGAAG | TTAGGTTTGA | GGCATCATTT | TGAAATGCT | 1980 |
| GACACTTTTT | CAGGCGCTG | ATTGAGTGAG | GGCATGGGTA | AAAATATTTC | TTTAAAGAA | 2040 |
| GGATGAACAA | TTATATTAT | ATTTCAGGTT | ATATCCAATA | GTAGAGTTGG | CTTTTTTTT | 2100 |
| TTTTTTTTTG | GTCAATAGTG | GTGGATTGT | TGCCATGTGC | ACCTTGGGGT | TTTGTAAATGA | 2160 |
| CAGTGCTAAA | AAAAAAAAG | CATTTTTTTT | TATGATTGT | CTCTGCACC | CTTGTCTTG | 2220 |
| AGTGCTCTTG | CTATTAACGT | TATTTGTAAT | TTAGTTTGTGA | GCTCATTAAA | AAAAATGTGCC | 2280 |
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Seq ID NO: 176 DNA Sequence
Nucleic Acid Accession #: NM_052827.1
Coding sequence: 234..1028

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| ACGGTACTCG | GGCCTGTTTC | CCCCCTCTCG | GGCCCCGAGA | GCCAGGGTCC | GCCTTCTGCA | 180 |
| GGGTTCCAG | GGCCCGCTC | CAGGGCGGG | CTGACCCGAC | TGCTGGCGGC | TTTCATGGAGA | 240 |
| ACTTCCAAA | GGTGGAAAAG | ATCGGAGAGG | GCACGTACGG | AGTTGTGTAC | AAAGCCAGAA | 300 |
| ACAAGTTGAC | GGGAGAGGTG | GTGGCGCTTA | AGAAAATCCG | CCTGGACACT | GAGACTGAGG | 360 |
| GTGTGCCAG | TACTGCCATC | CGAGAGATCT | CTCTGCTTAA | GGAGCTTAAC | CATCCTAATA | 420 |
| TTGTCAAGCT | GCTGGATGTC | ATTACACAG | AAAATAAACT | CTACCTGGTT | TTTGAATTTC | 480 |
| TGCACCAAGA | TCTCAAGAAA | TTTCATGGATG | CCTCTGCTCT | CACCTGGCAT | CTCTTCCCC | 540 |
| TCATCAAGAG | CTATCTGTTT | CAGCTGCTCC | AGGGCCTAGC | TTTCTGCCAT | TCTCATCGGG | 600 |
| TCTCCACCG | AGACCTTAAA | CCTCAGAAATC | TGCTTATTA | CACAGAGGGG | GCCATCAAGC | 660 |
| TAGCAGACTT | TGGACTAGCC | AGAGCTTTTG | GAGTCCCTGT | TGCTACTTAC | ACCCATGAGG | 720 |
| TGACTCGCG | GGCCCTATTC | CCTGGAGATT | CTGAGATTGA | CCAGCTCTTC | CGGATCTTTC | 780 |
| GGACTCTGGG | GACCCAGATG | GAGGTGGTGT | GGCCAGGAGT | TACTTCTATG | CCTGATTACA | 840 |
| AGCCAAGTTT | CCCCAAGTGG | GGCCGGCAAG | ATTTTAGTAA | AGTTGTACCT | CCCTCGGATG | 900 |
| AAGATGGACG | GAGCTTGTTA | TGCAAAATGC | TGCACTACGA | CCCTTACAA | AGGATTTCGG | 960 |
| CCAAGGCAGC | CCTGGCTCAC | CCCTTCTTCC | AGGATGTGAC | CAAGCCAGTA | CCCCATCTTC | 1020 |
| GACTCTGATA | GCCTTCTTGA | AGCCCCCAGC | CCTAATCTCA | CCCTCTCTTC | CAGTGTGGGC | 1080 |
| TTGACCAAGG | TTGGCCTTGG | GCTATTGTGA | CTCAGGTGGG | CCCTCTGAAC | TTGCCTTAAA | 1140 |
| CACCTCACCT | CTAGTCTTGG | CCAGCCAATC | CTGGGAATAC | AGGGGTGAAA | GGGGGGAACC | 1200 |
| AGTGAAATG | AAAGCAAGTT | TCAGTATTAG | ATGCACTTAA | GTTAGCCTCC | ACCACTCTTT | 1260 |
| CCCCCTTCTC | TTAGTTATTG | CTGAAGAGGG | TTGGTATAAA | AATAATTTTA | AAAAAGCCTT | 1320 |
| CCTACAGGTT | AGATTGTCGG | TACCAATCTC | TGAATGCCCC | ATAATTATTA | TTTCCAGTGT | 1380 |
| TTGGGATGAC | CAGGATGCCA | AGCCTCCTGC | TGCCACAATG | TTTATAAAGG | CCAAATGATA | 1440 |
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| TTTTAAAGAA | TCGGGTGAA | AAAATAGATC | CAATCAGTTT | ATACCTAGT | TAGTGTTTTG | 1560 |
| CCTCACCTAA | TAGGCTGGGA | GACTGAAGAC | TCAGCCCGGG | TGGGGCTGCA | GAAAAATGAT | 1620 |
| TGGCCCAAGT | CCCCCTGTTT | GTCCCTTCTA | CAGGCAATGAG | GAATCTGGGA | GGCCCTGAGA | 1680 |
| CAGGGATTGT | GCTTCAATCC | AATCTATTGC | TTCACTATGG | CCTTATGAGG | CAGGTGAGAG | 1740 |
| ATGTTTGAAT | TTTTCTCTTC | CTTTAGTAT | TCTTAGTTGT | TCAGTTGCCA | AGGATCCCTG | 1800 |
| ATCCCATTTT | CCTCTGACGT | CCACCTCCTA | CCCCATAGGA | GTTAGAAGTT | AGGGTTTAGG | 1860 |
| CATCATTTTG | AGAATGCTGA | CACTTTTTCA | GGGCTGTGAT | TGAGTGAGGG | CATGGGTAAA | 1920 |
| AATATTTCTT | TAAAGAAAGG | ATGAACAATT | ATATTTATAT | TTCAAGTTAT | ATCCAATAGT | 1980 |
| AGAGTTGGCT | TTTTTTTTTT | TTTTTTTGGT | CATAGTGGGT | GGATTGTGTT | CCATGTGCAC | 2040 |
| CTTGGGGTTT | TGTAATGACA | GTGCTAAAAA | AAAAAAGCA | TTTTTTTTTA | TGATTGTGCT | 2100 |
| CTGTACCCCT | TGTCCTTGAG | TGCTCTTGCT | ATTAACGTTA | TTTGTAAATT | AGTTTGTAGC | 2160 |
| TCATTAATAA | AATGTGCCCTA | GTTTTATAAA | AAAAAAAAG | AAAAAAAAG | AAAAAAAAG | 2220 |
| AAAAA | | | | | | 2226 |

Seq ID NO: 177 DNA Sequence
Nucleic Acid Accession #: NM_032738.1
Coding sequence: 118..1197

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| AAGCTGGGCT | GTGTCTCAT | GGCCTGGGCC | CTCTACCTTT | CCCTTGGTGT | GCTCTGGGTG | 180 |
| GCCCAGATGC | TACTGGCTGC | CAGTTTGTAG | ACGCTGCAGT | GTGAGGGACC | TGTCGTGCACT | 240 |
| GAGGAGAGTG | GCTGCCACAC | GGAGGATGAC | TTGACTGATG | CAAGGGAAGC | TGGCTTCCAG | 300 |
| GTCAAGGCCT | ACACTTTCAG | TGAACCTTTC | CACCTGATTG | TGTCCTATGA | CTGGCTGATC | 360 |
| CTCCAAGGTC | GAGCCAAGCC | AGTTTTTGAA | GGGGACCTGC | TGGTTCTGGC | CTGCCAGGCC | 420 |
| TGGCAAGACT | GGCCACTGAC | TCAGGTGACC | TTCTACCGAG | ATGGCTCAGC | TCTGGGTCCC | 480 |
| CCCGGGCCTA | ACAGGGAATT | CTCCATCACC | GTGGTACAAA | AGGCAGACAG | CGGGCACTAC | 540 |
| CACCTGCAGT | GCATCTTCCA | GAGCCCTGGT | CCTGGGATCC | CAGAAACAGC | ATCTGTTGTG | 600 |
| GCTATCACAG | TCCAAGAACT | GTTTCCAGGG | CCAATTCTCA | GAGCTGTACC | CTCAGCTGAA | 660 |
| CCCCAAGCAG | GAAAGCCCCAT | GACCCCTGAGT | TGTCAGACAA | AGTTGCCCTC | GCAGAGGTCA | 720 |
| GCTGCCCGCC | TCTCTCTCTC | CTTCTACAAG | GATGGAAAGGA | TAGTGCAAAAG | CAGGGGGCTC | 780 |
| TCTCAGAAAT | TCCAGATCCC | CACAGCTTCA | GAAGATCACT | CCGGGTGATA | CTGGTGTGAG | 840 |
| GCAGCCACTG | AGGACAACCA | AGTTTGAAA | CAGAGCCCCC | AGCTAGAGAT | CAGAGTGCAG | 900 |
| GGTGCTTCCA | GCTCTGTGTC | ACCTCCCA | TTGAATCCAG | CTCTCTCAGAA | ATCAGCTGCT | 960 |
| CCAGGAAGCT | CTCCTGAGGA | GGCCCTGGG | CCTCTGCCCTC | GGCCGCCAAC | CCCATCTTCT | 1020 |
| GAGGATCCAG | GCTTTTCTTC | TCTCTGGGG | ATGCCAGATC | CTCATCTGTA | TCACCATGATG | 1080 |
| GGCCTTCTTC | TCAACACAT | GCAGGATGTG | AGAGTCTCTC | TGGGTCACTC | GCTCATGGAG | 1140 |
| TTGAGGGAAT | TATCTGGCCA | CCAGAGCCT | GGGACCACAA | AGGCTACTGC | TGAATAGAAG | 1200 |
| TAAACAGTTC | ATCCATGATC | TCACTTAACC | ACCCCAATAA | ATCTGATTCT | TTATTTTCTC | 1260 |
| TTCTGTCTCT | GCACATATGC | ATAAGTACTT | TTACAAGTTG | TCCAGTGTGT | TTGTTAGAAT | 1320 |
| AATGTAGTTA | GGTGAAGTGA | AATAAATTTA | TATAAAGTGA | GAATTAGAGT | TTAGCTATAA | 1380 |
| TTGTGTATTG | TCTCTTAAAC | CAACAGAAAT | CTGCTGTCTA | GATCAGGAAT | TTCTATCTGT | 1440 |
| TATATCGACC | AGAATGTTGT | GATTTAAAGA | GAATTAATGG | AAGTGGAATG | AATACAGCAG | 1500 |

5 TCTCAACTGG GGGCAATTTT GGGGGGATGGT GGGATGTGTG TGCTACTGGC ATCCAGTAAA 1560
 GTCATTATAC TTGGGGGGTT GGGGGATGGT GGGATGTGTG TGCTACTGGC ATCCAGTAAA 1620
 TAGAAGCCAG GGGTGCCGCT AAACATCCTA TAATGCACAG GGCAGTACCC CACAACGAAA 1680
 AATAATCTGG CCCAAAATGT CAGTTGTACT GAGTTTGAGA AACCCAGGCC TAATGAAACC 1740
 CTAGGTGTGG GGCTCTGGAA TGGGACTTTG TCCCTTCTAA TTATTATCTC TTTCAGCCT 1800
 CATTGAGCTA TTCTTACTGA CATACAGTC TTTAGCTGGT GCTATGGTCT GTTCTTTAGT 1860
 TCTAGTTTGT ATCCCTTCAA AAGCCATTAT GTTGAAATCC TAATCCCCAA GGTGATGGCA 1920
 TTAAGAAGTG GGCCTTTGGG AAGTGATTAG ATCAGGAGTG CAGAGCCCTC ATGATTAGGA 1980
 10 TTAGTGCCCT TATTTAAAAA GGCCCCAGAG AGCTAACTCA CCTTCCACC ATATGAGGAC 2040
 GTGGCAAGAA GATGACATGT ATGAGAACCA AAAAAAGCT GTGCCAAAC ACCGACTCTG 2100
 TCGTTGCTT GATCTGAAC TTCAGCCCTC CAGAACTATG AGAAATAAAA TTCTGTTGTT 2160
 TGTAAAAAAA AAAAAAAA A 2181

Seq ID NO: 178 DNA Sequence

Nucleic Acid Accession #: NM_002346.1

Coding sequence: 136..531

1 11 21 31 41 51
 20 GCTCCGCCCA GCGCGGTCC AGAGCGCGG AGGTTGCGGG AGCTCCGCCA GGCTGCTGGT 60
 ACCTGCGTCC GCGCGGCGAG CAGGACAGGC TGCTTTGGTT TGTGACCTCC AGGCAGGACG 120
 GGCATCTCTT CCAGAAATGAA GATCTTCTTG CCAGTGCTGC TGGCTGCCCT TCTGGGTGTG 180
 GAGCGAGCCA GCTCGCTGAT GTGCTTCTCC TGCTTGAACC AGAAGAGCAA TCTGTACTGC 240
 CTGAAGCCGA CCATCTGCTC CGACCAGGAC AACTACTGCG TGACTGTGTC TGCTAGTGCC 300
 25 GGCATTGGGA ATCTCGTGAC ATTTGCCAC AGCCTGAGCA AGACCTGTTT CCGGCTGTC 360
 CCCATCCGAG AAGGGCTCAA TGTGTGTGTG GCTTCCATGG GCATCAGCTG CTGCCAGAGC 420
 TTTCTGTGCA ATTTCACTGC GGCCTGAGGC GGGCTGCGGG CAAGCGTCA CTTGCTGGGT 480
 GCGCGGCTGC TGCTGAGCCT GCTGCGGCCC CTGCTGCGGT TTGGCCCTTG ACCGCCAGA 540
 CCTGTGCCCC CGATCCCCCA GCTCAGGAAG GAAAGCCAG CCTTTCTGG ATCCACAGT 600
 30 GTATGGGAGC CCTGACTTCC TCACGTGCTT GATCTGTGCC CTTGGTCCCA GGTGAGGCC 660
 ACCCTCTGCA CCTCCACCTG CCCCAGCCCC TGCTCTGCC CAAGTGGGCC AGCTGCCCTC 720
 ACTTCTGGGG TGGATGATGT GACCTTCTTT GGGGGACTGC GGAAGGGAGC AGGGTTCCCT 780
 GGAGTCTTAC GGTCCAACAT CAGACCAAGT CCGATGGACA TGCTGACAGG TCCCCAGGG 840
 AGACCGTGTG AGTAGGGATG TGTGCTGGC TGTGTACGTG GGTGTGAGT GCAGTGTGAG 900
 35 GCACGTGGCG GCTTCTGGGG GGCATGTTTG GGGAGGGAGG TGTGCCAGCA GCGTGAGAG 960
 CCTCAGTCCC TGTAGCCCCC TGCCCTGGCA CAGCTGCATG CACTTCAAGG GCAGCCTTTG 1020
 GGGGTGTGGG TTTCTGCCAC TTCGGGCTT AGGCCCTGCC CAAATCCAGC CAGTCTCTGC 1080
 CCAGCCACC CCCACATTGG AGCCCTCTCT CTGCTTTGGT GCCTCAATA AATACAGATG 1140
 TCCCC 1145

Seq ID NO: 179 DNA Sequence

Nucleic Acid Accession #: XM_113526.2

Coding sequence: 253..2409

1 11 21 31 41 51
 45 TGGCGCGCGG CGGAGCGGAG GGAGATCCGA GCGCGCGCGG CAAGCTGGCT GCGAGCGGCT 60
 GAGCAGCACT CCAAGCTCGC CGGCCTTTGG TCTCCAGGAC TTGTCCAGC AGCCCTCGA 120
 ACTGAGAATT ACACCATCGG ACCCTTGGCT CTGAGGCTT CAGACTTGA CTGTGTACA 180
 CTGCCAGGCT TCCAGGGCTC CAACTTGACG ACCGCTGTT GTGGGACAGT CTCTGTAATC 240
 50 GCGAAAGCAA CCATGGAAGA CCTGGGGGAA AACACCATGG TTTTATCCAC CTTGAGATCT 300
 TTGAACAAT TCATCTCTCA GCGTGTGGAG GGAGGCTCTG GACTGGATAT TTCTACTCG 360
 GCGCCAGGTT CTCTGCAGAT GCAGTACCAG CAGAGCATGC AGCTGGAGGA AAGAGCAGAG 420
 CAGATCGGTT CGAAGTCCCA CCTCATCCAG GTGGAGCGGG AGAAATGCA GATGGAGCTG 480
 AGTCACAAGA GGGCTCGAGT GGAGCTGGAG AGAGCAGCCA GCACCACTGC CAGGAACCTAC 540
 55 GAGCGTGAGG TCGACCGCAA CCAGGAGCTC CTGACCGGCA TCCGGCAGCT TCAGGAGCGG 600
 GAGGCGCGGG CGGAGGAGAA GATGACAGAG CAGCTGGAGC GCAACAGGCA GTGTGACAG 660
 AACTTGGATG CTGCCAGCAA GAGGCTGCGT GAGAAAGAGG ACAGTCTGGC CCAGGCTGGC 720
 GAGACATCA ACCCACTGAA GGGGAGGATC TCGAACTGC AGTGGAGCGT GATGGACCA 780
 GAGATGCGGG TGAAGCGCCT GGAGTGGAG AAGCAGGAGC TGCAGGAGCA GCTGGACCTG 840
 60 CAACACAAA AATGCCAGGA AGCCAATCAG AAAATCCAGG AACTCCAGGC CAGCCAAGAA 900
 GCAAGAGCAG ACCACGAGCA GCAGATTAA GATCTGGAGC AGAAGCTGTC CCTGCAAGAG 960
 CAGGATGCA GATTGTGAA GAACATGAAG TCTGAGCTGG TACGGCTCCC TAGGCTGGAA 1020
 CGGAGCTGTA AGCAGCTGCG GGAGGAGAGC GCGCACCTGC GGGAGATGAG AGAGACCAAC 1080
 GGGCTGCTCC AGGAAGAGCT GGAAGGGCTG CAGAGGAAGC TGGGGGCCCA GGAGAAGATG 1140
 CAGGAGACGC TGGTTGGCTT GGAGCTGGAG AACGAGAGGC TGCTGGCCAA GCTGCAAGGC 1200
 65 TGGGAGAGCT TGGACAGAC CATGGGCTTG AGCATCAGGA CTCCAGAAAG CTTTCCAGA 1260
 TTCGTGGTTG AGCTGCAGCA GAGGAGCTT GCCTTGAAG ACAAGAACAG CGCCGTCAAC 1320
 AGCAGCGCCC GGGGGCTGGA GAAGGCCAGG CAGCAGCTGC AGGAGGAGCT CCGCAGGTC 1380
 AGGGCGCAGC TGTGGAGGA GAGGAAGAAG CGCGAGACCC ACGAGGCGCT GCGCCGAGG 1440
 70 CTCCAGAAAC GGGTCTGCT GCTCACCAG GAGCGGAGC GTATGCGGGC CATCTGGGG 1500
 TCCTAGGACA GCGAGCTGAC CCGGCGGAG TACTCACCCC AGCTGACGCG GCGCATGCGG 1560
 GAGGCTGAGG ATATGGTGCA GAAGGTGCAC AGCCACAGCG CCGAGATGGA GGCTCAGCTG 1620
 TCCGAGGCC TGGAGGAGCT GGGAGGCCAG AAACAAGAG CAGACATGCT GGAGATGGAG 1680
 CTGAAGATGC TGAAGTCTCA GTCCAGCTCT GCCGAACAGA GCTTCTGTG TCCAGGGAG 1740
 75 GAGCGGACA CGCTCAGGTT GAAGTTCGAG GAGCTGGAAG GCGAGCGGAG TCGGCTGGAG 1800
 GAGGAAAAA GGAATGCTGGA GGCACAGCTG GAGCGGCGAG CTCTGACAGG TGACTATGAC 1860
 CAGAGCAGGA CCAAGTGTCT GCACATGAGC CTGAACCCCA CAGTGTGGC CAGGACAGCG 1920
 CTGCGCGAG ACCACAGCCA GCTGCAGGCG GAGTGCAGC GACTGCGCG GCTCTGCGC 1980
 80 GCCATGGAGA GAGGAGGCAC GGTCCAGCG GACTTGTAGG CTGCGCGCG GAGTCTGCCA 2040
 TCGTCAAGG AGGTGCGAGA GCTGAAGAAG CAGGTGGAGA GTGCGGAGCT GAAGAACCA 2100
 CGGCTCAAGG AGGTTTTCCA GACCAAGATC CAGGAGTTCC GCAAGGCGCT CTACACGCTC 2160
 ACCGGCTACC AGATGACAT CACCAAGGAG AACCACTACC GGCTGACCTC GCTGTACGCC 2220
 GAGCACCCAG GCGACTGCTT CATCTTCAAG GCCACAGCC CCGGGGTTT CAAGATGCAG 2280
 CTACTGGAGA CAGAGTTTCT ACACACGCTG TCGAGGTGCA CTTGCGGCGC 2340
 CAGGACAGCA TCCCTGCTT CCTCAGCTCG CTCACCTCG AGCTCTTCA GCGCCAGACC 2400

5 GTGGCGTAGC CTGACGGCTC GGGGGCATAG CCGGAGCCAC TCTGCTTGGC CTGACCTGCA 2460
 GGTCCCCCTGC CCGGCCAGCC ACAGGCTGGG TGCAGTCTCT GCCTCTCCAG CCCACAGGG 2520
 CAGCAGCATG ACTGACAGAC ACCTGCGGAC CTACGTCGGG CTTCCTGCTG GGGCGGCCAG 2580
 CACCTCTTCC ACGTGCAGAC CCGATGCCGC CCGGAGCCTG GTGTGTGGGC GTCGGCCACC 2640
 AGCCTGGGTT CCTCACCTTG TGAATAAAAA TCTTCTCCCC TAG 2683

Seq ID NO: 180 DNA Sequence

Nucleic Acid Accession #: NM_000273.1

Coding sequence: 1..1275

10 1 11 21 31 41 51
 | | | | |
 ATGACCCAGG CAGGCGCGCG GGGTCTTGGC ACACCCGAGC CGGCTCCGCG AACACAGCCC 60
 ATGGCCTCCC CGGCGCTAGG GACCTTCTGC TGGCCACAGC GGGACGACAG CACGACAGTC 120
 GTGCTGAGCT TCCAGCGCGG GGCTTCCAC GCGCTCTGCC TGGGACGCGG CCGGCTCCGC 180
 15 TTGGCGCTGG GCCTTCTGCA GCTGCTGCCG GCGCGCGCGC CCGCGGCGCC CCGGTCCGCC 240
 CGGATGGGCC CGCGGCGCTC GGTCCGCATC CTGCGGCTG CCGCTGCCTG CGACCTTCTC 300
 GGCTGCTCGG GTATGGTGTG CCGGTCCACC GTGTGGTTAG GATTCCCAAA TTTTGTGAC 360
 AGCGTCTCGG ATATGAACCA CAGGAAATTT TGGCTTCTGC CTTCCTGCGT GGGGAGTGGG 420
 ATGTGGATCC AGCTGTGTGA CAGTGCCTGC TTCTGGTGGC TGTTTTGCTA TGCAGTGGAT 480
 20 GCTTATCTGG TGATCCGGAG ATCGGCAGGA CTGAGCAGCA TCCTGCTGTA TCACATCATG 540
 GCGTGGGGCC TGCCACACCT GCTCTGTGTG GAGGAGCCG CCACTGCTTA CTACCTTCC 600
 GTGTCCAGGT GTGAGCGGGG CCTGGACCAC GCCATCCCCC ACTATGTAC CATGTACCTG 660
 CCCCTGCTGC TGGTCTCGT GCGAAGCCCT ATCCTGTCC AAAAGACAGT GACTGCAGTG 720
 GCGCTTTTAC TTAAGGAAG ACAAGGCATT TACAAGGAGA ACGAGAGGAG GATGGGAGCC 780
 25 GTGATCAAGA TCCGATTTTT CAAAATCATG CTGGTTTTAA TTATTTGTG GTTGTGGAAT 840
 ATCATCAATG AAAGCCTTTT ATTCTATCTT GAGATGCAAA CAGATATCAA TGGAGGTCTT 900
 TTGAAACCTG TCAGAACTGC AGCCAAGACC ACATGGTTTA TTATGGGAAT CCTGAATCCA 960
 GCCCAGGAGT TTCTCTGTTC TTGGCCCTTC TACGGCTGGA CAGGATGCAG CCTGGGTTTT 1020
 CAGTCTTCCA GGAAGGAGAT CCAAGTGGAA TCACTGACCA CTCGCGCTGC TGAGGGGGCT 1080
 30 CACCCATCCC CACTGATGCC CCAAGAAAC CCTGCTCCG GGAAGGTGTC TCAAGTGGGT 1140
 GGCAGAGCTT GGCAGAACG CTTGAGCATG CTGTCTGAAG GTTCTGATGC CAGCACAATT 1200
 GAAATTCACA CTGCAAGTGA ATCTGCAAC AAAAAAGAG GTGACCCTGC TCTCCCAACC 1260
 CATGAGAGCC TATGAAGGGG ATGTGCTGGG GGTCCAGACC CCATATTCTC CAGACTCAAC 1320
 35 AATTCTTGT CTTTAGAACT GTTTCTCAC CTTCCTCAAC CTGCACTGCC GAAGTGTAGC 1380
 GGCCTCCAAA CCTGCTCTC ATCCACAGCT AGAGCTTCTT CCGCAAGGGC CTTTAGGATA 1440
 GGAGAAAGGG TCTATGCACA CACGTGTGAG AATGGAAGAG CCCCCTCCAG ACCACTCTAC 1500
 AGCTGCTCTA GCCTTAGTTG CCACTAGGAA GTTTCTGAG GCTGGCTGTA AAGTAAGTGT 1560
 AAGGTCCACA TCCTTGGGGA AGTAGTTAAA TAAAAAGATT ATGACTG 1607

Seq ID NO: 181 DNA Sequence

Nucleic Acid Accession #: NM_139317.1

Coding sequence: 174..1070

45 1 11 21 31 41 51
 | | | | |
 CCCTGGGATA CTCCCCTCCC AGGGTGTCTG GTGGCAGGCC TGTGCCTATC CCTGCTGTCC 60
 CCAGGGTGGG CCGCGGGGGT CAGGAGCTCC AGAAGGCCCA GCTGGGCATA TTCTGAGATT 120
 GGCCATCAGC CCCCATTCTC GCTGCAAAAC TGGTCAGAGC CAGTGTTCCT TCCATGGGAC 180
 CTAAGACAGC TGCCAAGTGC CTGCAACGTC GACCACAGCC GAGCCACTGG GCAGCCGGTG 240
 50 ATGGTCCCAC GCAGGAGCGC TGTGGACCCC GCTCTCTGGG CAGCCCTGTC CTAGGCGCTG 300
 ACACCTGCAG AGCCTGGGAC CACGTGGATG GGCAGATCCT GGGCCAGCTG CCGCCCTGA 360
 CAGAGGAGGA AGAGGAGTTC GCGCCCGGGG CCACCTTGTG CAGGGGGCCT GCCTTCCCGG 420
 GCATGGGCTC TGAGGAGTTG CGTCTGGCCT CCTTCTATGA CTGGCCGCTG ACTGCTGAGG 480
 TGCCACCCGA GCTGCTGGCT GCTGCCGGCT TCTTCCACAC AGGCCATCAG GACAAGGTGA 540
 55 GTGTCTTCTT CTGCTATGGG GGCCTGCAGA GCTGGAAGCG CGGGGACGAC CCCTGGACGG 600
 AGCATGCCAA GTGGTTCCTC AGCTGTCACT TCCTGCTCCG GTCAAAAGGA AGAGACTTTG 660
 TCCACAGTGT SCAGGAGACT CACTCCACGC TGCTGGGCTC CTGGGACCCG TGGGAAGAAC 720
 CGGAAGAGTC AGCCCTGTGT GCCCCTCGG TCCCTGCCTC TGGGTACCTT GAGCTGCCCA 780
 CACCCAGGAG AGAGGTCCAG TCTGAAAGTG CCCAGGAGCC AGGAGGGGTC AGTCCAGCCG 840
 60 AGGCCACAGG GCGGTGGTGG GTTCTTGAGC CCCAGGAGC CAGGAGTGTG GAGGCGCAGC 900
 TGCGCGGCTC GCAGGAGGAG AGGACGTGCA AGGTGTGCCT GGACCGCGCC GTGTCCATCG 960
 TCTTTGTGCC GTGCGGCCAC CTGCTCTGTG CTGAGTGTGC CCCCAGCCTG CAGCTGTGCC 1020
 CCATCTGCAG AGCCCCGCTC CGCAGCCGCG TCGCACCTT CCGTCTCTAG GCCAGGTGCC 1080
 ATGGCCGGCC AGGTGGGCTG CAGAGTGGGC TCCTGCCCCC TCTCTGCTG TTCTGGAAGT 1140
 65 TGTCTTGGGC CTGCTGAGGA TGGCAGAGCT GGTGTCCATC CAGCACTGAC CAGCCCTGAT 1200
 TCCCGGACCA CCGCCAGGGG TGGAGAAGGA GGCCTTGCT TGGCGTGGG GATGGCTTAA 1260
 CTGTACCTGT TTGGATGCTT CTGAATAGAA ATAAAGTGGG TTTTCCCTGG AGGTACCCAG 1320
 CA

Seq ID NO: 182 DNA Sequence

Nucleic Acid Accession #: NM_022161.2

Coding sequence: 174..1016

75 1 11 21 31 41 51
 | | | | |
 CCCTGGGATA CTCCCCTCCC AGGGTGTCTG GTGGCAGGCC TGTGCCTATC CCTGCTGTCC 60
 CCAGGGTGGG CCGCGGGGGT CAGGAGCTCC AGAAGGCCCA GCTGGGCATA TTCTGAGATT 120
 GGCCATCAGC CCCCATTCTC GCTGCAAAAC TGGTCAGAGC CAGTGTTCCT TCCATGGGAC 180
 CTAAGACAGC TGCCAAGTGC CTGCAACGTC GACCACAGCC GAGCCACTGG GCAGCCGGTG 240
 80 ATGGTCCCAC GCAGGAGCGC TGTGGACCCC GCTCTCTGGG CAGCCCTGTC CTAGGCGCTG 300
 ACACCTGCAG AGCCTGGGAC CACGTGGATG GGCAGATCCT GGGCCAGCTG CCGCCCTGA 360
 CAGAGGAGGA AGAGGAGGAG GCGCCCGGGG CCACCTTGTG CAGGGGGCCT GCCTTCCCGG 420
 GCATGGGCTC TGAGGAGTTG CGTCTGGCCT CCTTCTATGA CTGGCCGCTG ACTGCTGAGG 480
 TGCCACCCGA GCTGCTGGCT GCTGCCGGCT TCTTCCACAC AGGCCATCAG GACAAGGTGA 540
 GGTGCTTCTT CTGCTATGGG GGCCTGCAGA GCTGGAAGCG CGGGGACGAC CCCTGGACGG 600
 AGCATGCCAA GTGGTTCCTC AGCTGTCACT TCCTGCTCCG GTCAAAAGGA AGAGACTTTG 660

5 TCCACAGTGT GCAGGAGACT CACTCCCAGC TGCTGGGCTC CTGGGACCCG TGGGAAGAAC 720
 CGGAAGACGC AGCCCCCTGTG GCCCCTCCG TCCCTGCTTC TGGGTACCTT GAGCTGCCCA 780
 CACCCAGGAG AGAGGTCCAG TCTGAAAGTG CCCAGGAGCC AGGAGCCAGG GATGTGGAGG 840
 OGAGCTGGG GCGGCTGCAG GAGGAGAGGA CGTGCAAGGT GTGCCTGGAC CGCGCCGTGT 900
 CCATCGTCTT TGTGCCGTGC GGCCACCTGG TCTGTGCTGA GTGTGCCCCC GGCCTGCGAGC 960
 TGTGCCCAT CTGCAGAGCC CCCGTCGCGA GCCCGCTGCG CACCTTCTCT TCCTAGGCCA 1020
 GGTGCCATGG CCGGCCAGGT GGGCTGCAGA GTGGGCTCCC TGCCCTCTCT TGCCGTCTCT 1080
 GGAAGTGTGT CTGGGCTGCG TGAGGATGGC AGAGCTGGTG TCCATCCAGC ACTGACCCAGC 1140
 10 CCTGATTCCC CGACCAACCG CCAGGGTGGG GAAGGAGGCC CTTGCTTGGC GTGGGGGATG 1200
 GCTTAACTGT ACCTGTTTGG ATGCTTCTGA ATAGAAATAA AGTGGGTTTT CCCTGGAGGT 1260
 ACCCAGCA 1268

Seq ID NO: 183 DNA Sequence

Nucleic Acid Accession #: NM_021020.1

Coding sequence: 112..1902

15 1 11 21 31 41 51
 TGAGGGCTTT GCTATGACCT CAGTCCCCTC ACGGAGCCAC GACTGCCCTT TGCTGCCACA 60
 20 GCTTTTCCAA GACCTTCCCG GCGCCTGCCC CATCTCAGC CCCGAGTCAC CATGGGCAGC 120
 GTGAGTAGCC TCATCTCCCG CCACAGCTTC CACAGCAAGC ACTGCCGGGC TTCCGAGTAC 180
 AAGCTGGCGA AGTCTCTCCA CCTCAAGAAG CTCAACCGGT ATTCGAGCGG GCTGCTGAGG 240
 TTTGGCTTCT CCAGGACTCT GGTTCACGGC AAGTCCAGCT CCAAAATGGG CAAGAGCGAA 300
 GACTTCTTCT ACATCAAGGT CAGCCAGAAA GCCCGGGGCT CCCATCACCC AGATTACACG 360
 25 GCACTGTCCA GCGGGGATTT AGGGGGCCAG GCTGGGGTGG ACTTTGACCC GTCCACACCC 420
 CCCAAGCTCA TGCCCTTCTC CAATCAGCTA GAAATGGGCT CCGAGAAGGG TGCACTGAGG 480
 CCCACAGCCT TCAAGCTCTG GCTGCCACGG TCAGGAGCCA TCCTGCACTC CTCGCCGGAG 540
 AGTGCCAGCC ACCAGCTGCA CCCCGCCCTC CCAGACAAGC CCAAGGAGCA GGAGCTGAAG 600
 CCTGGCTGTG GCTCTGGGGC GCTGTCAAGC TCCGGCCGGA ACTCCATGTC CAGCTGCCCC 660
 30 ACACACAGCA CCAGCAGCAG CTACCAGCTG GACCCGCTGG TCACACCCCTG GGCACCCACA 720
 AGCGCTTTTG AGGCCCTCCG CCACAACATC ACCCAGGGCA TCGTCTCCA GGACAGCAAC 780
 ATGATGAGCG TGAAGGCTCT GTCCCTCTCC GACGGAGGTA GCAAGCTGGG CCATCGAAC 840
 AAGGCAGACA AGGCCCTCTG GTGTGTCCGC TCCCATCTCT CCACGAGCA GTGCAGCATC 900
 CAGGAGCTGG AGCAGAAGCT GTTGAGAGGG GAGGGCGCCC TCCAGAAGCT GCAGCGCAGC 960
 35 TTTGAGGAGA AGGAGCTTGC CTCAGCCTG GCCTACGAGG AGCGGCGCGG GCGCTGCAGG 1020
 GAGGAGCTGG AGGCCCGGGA GCGCAACAAGC TCAAGCAGGC CTCGACAGAG 1080
 AGCCAGCGCG CGCAGCAGGT CCTGCACCTG CAGGTACTGC AGCTTCAGCA GGAGAAGCGG 1140
 CAGCTCCGCG AGGAGCTCGA GAGCCTCATG AAGGAGCAGG ACCTGCTGGA GACCAAGCTC 1200
 AGGTCTTAGC AGAGGGAGAA GACCAGCTTC GCGCCCGCGC TGGAGGAGAC CCACTGGGAG 1260
 40 GTGTGCCAGA AGTCAGGCGA GATCTCCCTC CTGAAGCAGC AGCTGAAGGA GTCCAGACG 1320
 GAGGTGAACG CCAAGGCTAG CGAGATCCTG GGTCTCAAGG CACAGCTGAA GGACACGCGG 1380
 GGCAAGCTGG AGGCCCTGGA GCTGAGGAGC CAGGACCTGG AGGGCGCCCT GCGCACCAAG 1440
 GGCTCGGAGC TGGAGGTCTG TGAGAATGAG CTGCAGCGCA AGAAGAACGA GCGGAGCTG 1500
 CTGCGGAGAG AGGTGAACCT GCTGAGCAG GAGCTGCAGG AGCTGCGGGC CCAGGCCGCC 1560
 45 CTGGCCCGCG ACATGGGGCC GCCCACCTTC CCCGAGGAGC TCCCTGCCCT GCAGCGGGAG 1620
 CTGGAGCGCG TCGGGCCGGA GCTGCGGGAG GAGCGGCAAG GCCATGACCA GATGTCTCTG 1680
 GGCTTCCAGC ATGAGCGGCT CGTGTGGAAG GAGGAGAAGG AGAAGGTGAT TCAGTACCAG 1740
 AACACGCTGC AGCAGAGCTA GTGGCCATG TACCAGCGGA ACCAGCGCCT GGAGAAGGCC 1800
 CTGCAGCAGC TGGCAGCTGG GGACAGCGCC GGGGAGCCCT TGGAGGTGGA CCTGGAAGGG 1860
 50 GCTGACATCC CCTACGAGGA CATCATAGCC ACTGAGATCT GAGGGGCTGC CTGGGAAGGG 1920
 GAGTCTGGGG ACCTGGCACT GGGAGGCAGG GCTCTCCCGT GCATCCCCCC TGCTCAGCAA 1980
 TTCAGACCCC TCTGAGAGAC GCCACTCCCT GGGACACAGA CCCAGGACCC CCGAGGGGAG 2040
 GGCAGGAGCG CCTTCTCTCT CTCTCTGAT GTCCAGTGC TCACCAAGCC TGACGCCAC 2100
 CAGACGTGAG GCCCTGACTC CTCTGGCTTT CCCAGGAGAT GGGTCCAGGG GTCTGTCTGC 2160
 55 TTTGGTTAAG GGCTCCCTAA ACTTTGGCCT TTGTTGGAAG TAGATATCCT CTCGCCCTCC 2220
 TCCAGGGAAG GTGGCCACAG CAAGAACAGC GGCTCCCTTC CGCTTCTCAT CCCAACCTCT 2280
 TTTTCTCTCT GGACACATTG GAATGCCTTG GAAATAGAAA GAAGCCATAT ATGACCAGAA 2340
 GCCTTGGAA CAGCCCATTC AGAACCTGAG CTATTTCTCT CTGGCCGCGA AGGTGTAGGG 2400
 GTGGAATGAG CCGCGGGGAA GCTGGCTTTG AAACCTCAGG GCTGTCCAG CCCCGGCAAG 2460
 60 CCACAGGAAG GAGGGGAGAG ACAGGCGAGC CAGCAGTTGG GAGACCCCTG CACAGCCAGA 2520
 GGAGGGCAGA GGGAGAATCC AAGGGTTGAG AGCCAGTGGC GGGTGTATGGC CAGCCCTGG 2580
 GGCCAGCGCC CTGTTTACTG GTTCTTGCAA ATGGAGAGTG AGCAGCCTCT GGACAGCCAG 2640
 TGACCTTTGA CCTCGGTGAC CACTCTTCTT TAAGCCATAG ACCCTGAGGC CCTGGCTGG 2700
 65 GTGCTGGGAA GGGAGGGTTG AAACCAACCGT GAACAGAGG GTGTGGCTTT CCAGGCACCC 2760
 TCAGGAGAGC TCCCATCTCT TCCAGCTGGG GCCAGAGGCT GGGAGTCCCT ACCTGCTTCA 2820
 CGTTGGCCGG CGGCTACTCT GGAATGTTTT TCCCTCCCA GAATCAAGCT TTTGCTTGAT 2880
 CCAGAAGAGC CCATATCACT AAGATGGCAT ATATGTGATC TGGGCATTTT CCTCTCTCG 2940
 CTACAGCCAG GTTTAGCGGC AAACCTTTCC CCCTTAGCAC CTTGAGGCT GAGTTCTGGG 3000
 70 TTTCTAGAG TCAGGACGGC TCCTCAGAGC GCCAGGAAGC CAGAGCCCCA AGCAGGACGA 3060
 AAAAGAGGCA TACACACAGC AGTGTGAATA GCCTGGCCAC CAGCCATCCT CCTCCACCT 3120
 CAAGACCCCC ATTTGTCCCA GACTAAAGGA TCCAGAGAGC AGCTCCCTTT CTCAGGAGCT 3180
 TGGCAGTGC CCCAGGAGT CCAGGGTTTC TCTGCAGATG TCGGAGCGG GAGGCGGTGG 3240
 TAGAGAGAGA TAAAGGTGG AGTTTCTCTG TTGTTTGGTT CAGGGATTTT ATTTTAAAT 3300
 75 TTATGAGACA GGGTCTTGCT CTGCCCCCA GCGTGGAGTG CAGTGGCATG ATCATAGCTC 3360
 ACTGACGCT CATACTCCTG GGTCAAGCA ATCTCTCTGC CTCAGCCTTC CAATAGCTG 3420
 GGACTACAGG TCGCGGCCAC GGTGCTGGC TAACTTTTCA TTTTTTTGT AGGGACGGGG 3480
 TCTCGTTTTG TTGCAAAAGC TGGTCTCAA CTGTGGCCT CAAGCAATCC ACCTGCCTTG 3540
 80 GCCTCCCAA GTGCTGAGAT TGCAGATGTG AGCCACCGTG CCTGGCCAGA TTTTCTTTT 3600
 ATTCTTCTT CTTTTCTTCT TTGCTTTTCA GAAAGCAAGCC AGACCTAGCA 3660
 GGCTGTTCCT TGTTCTATTT TTGACTGTAG CCACAGCTGC TGTTCTCAGG ACAGCATCCC 3720
 TTCCCATG CTGCGGCTCT CTGCTGCTG AGATGAGGAG GGGAGCGTCT GGGAACTTGC 3780
 GAGTCCAAGG CCACTCCCA TTTCTGCTC GCTCACCGCT GGCCTTAGA GACCCGAGG 3840
 TAGGGGTGGG GAGATGCTTC TCTCTTGCC CCCCGCCCTC ATGGGTCTTA GCCCTTCTCT 3900
 GAGTGGGGG TGAGGCCAGA GTACCTTTT CTGTGGCTG CTCTACCTTC CTGTCCTGA 3960
 GGTAAACCG TGCCCATCTC GCCATCTCA AACGACAGAG GAGCTTTTCT GGAATTTCAA 4020

5
10
15
20
25

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ACCATTGCTC TTAGTCCCAA GCTAGGCTTA AACCTGGAAT CTACAAGCCA AAAGTCCCTC 4080
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Seq ID NO: 184 DNA Sequence
Nucleic Acid Accession #: AF265577
Coding sequence: 1..2193

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Seq ID NO: 185 DNA Sequence
Nucleic Acid Accession #: NM_031945.1
Coding sequence: 65..1132

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CCCATGCTG GGGCTGGCAC TGGGAGGGCT GGTGGTCAG GCAGCGAGCC TGGCTGGCTG 480
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5 AGACAGCCTG GAGCACACCC TGGTGTGGC CATCGCCAC TACCAGGACG ACCCAGACCT 660
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20 Seq ID NO: 186 DNA Sequence
 Nucleic Acid Accession #: AF475085.1
 Coding sequence: 54..1715

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Seq ID NO: 187 DNA Sequence
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 Coding sequence: 194..910

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Seq ID NO: 188 DNA Sequence
Nucleic Acid Accession #: NM_005356.2
Coding sequence: 52..1581

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Seq ID NO: 189 DNA Sequence
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Coding sequence: 1504..2658

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| | TTGATGGCCA | TTGCTTACCT | GGGATCCTCA | TGCCCCCTAC | AACCAACCAG | CTCCCTAGCT | 1560 |
| 5 | CTCTCCCTCT | CCCCCACCCC | CTCAGACTTC | GAGCAGGAGT | CGGGCATTGA | GACAGCCATG | 1620 |
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| | CCAGCCACCA | GCCCCCTGGT | GGTGACAGAA | GTCCCGGAAG | AGCCCAGCCA | GAGAGCCACC | 1800 |
| | ACCGTCTCCA | CTACCATGGC | TACCACTGCT | GCCACAAGCA | CAGGGGACCC | GACTGTGGCC | 1860 |
| 10 | ACAGTGCCTG | CCACAGTGGC | CACCCACCAC | CCCAGCACCC | CTGCAGCACC | CCCTTTTACG | 1920 |
| | GCCACCACTG | CTGTTATAAG | GACCACTGGC | GTACGGAGGC | TTCTGCCTCT | CCCCTGACC | 1980 |
| | ACAGTGGCTA | CGGCACGGGC | CATACCCCC | GAGGCGCCCT | CCCCGCCAC | CACGGCGGCT | 2040 |
| | GTCTTGGACA | CGGAGGCCCC | AACACCCAGG | CTGGTCAGCA | CAGCTACCTC | CCGGCCCAAG | 2100 |
| | GCCCTTCCCA | GGCGGCCAC | CACCCAGGAG | CCTGACATCC | CTGAGAGGAG | CACCTGCCCC | 2160 |
| 15 | CTGGGGACCA | CTGCCCTTGG | ACCCACAGAG | GTGGCTCAGA | CCCCAATCC | AGAGACCTTC | 2220 |
| | CTGACCACAA | TCCGGGATGA | GCCAGAGGTT | CCGGTGAGTG | GGGGGCCAG | TGGAGACTTC | 2280 |
| | GAGCTGGCAG | AAGAAGAGAC | CACACAACCA | GACACAGCCA | ATGAGGTGGT | AGCTGTGGGA | 2340 |
| | GGGGTCCGG | CAAGGCCATC | ATCTCCACCT | GGGACACTGC | CCAAGGGTGC | CCGGCCGGGC | 2400 |
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| 20 | AGTATCTCG | AGCGGAAGGA | GGTGCTCGTA | GCTGTGATTG | TGGGCGGGGT | GGTGGCGGCC | 2520 |
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| | AGCTACACGC | TGGAGGAACC | CAAGCAGGGC | AGCGTCACAT | ACCAGAAGCC | TGACAAGCAG | 2640 |
| | GAGGAGTTCT | ATGCCCTAGT | GAGCCACAGT | GCCTCCCTGC | AGCCTCAACA | CCACCTGCT | 2700 |
| | GTCCAGTCCC | CAGCCTGGCC | CCACCAGCCC | AAGCCTGGGA | CTGGGCTTGG | AACCTGGCCC | 2760 |
| 25 | CAGTCTCTCT | CTGCCCTCTC | TCCCAGGTC | TGCCCAGGCT | GCCAGCCTCA | CACAGATCTT | 2820 |
| | CCCCGAGGAA | GAGGGGCTGC | TGCCATCTGC | CCCAGACTGT | GCCCTTACGA | GCTCATCTCT | 2880 |
| | TGTTCCCTCC | ATCCCTGCCA | CCAGTCTGGG | GCTTCAGGAC | CTCATGTCTG | ATGGATGGGA | 2940 |
| | GGAGAAAGC | TCTGATTGG | CTGGTGGTGG | AAGAAAGGGT | GGGGCTTGAG | ATGAGCCTGA | 3000 |
| | GCCTGACTTT | GGCACCCACA | GTGCTCACTG | AGATCTCCTT | TTTGGGGCAG | AGAGGCACTC | 3060 |
| 30 | AGGCTGGTTT | CCAGGACAAA | CATTTGGTAA | ACACAGCCCT | TGAAATCATC | TAGACACTGC | 3120 |
| | AACTCTTGTC | TGCTATCCCA | GGGCCCTCTC | CTAGCTGGGT | GAGAGGGTGT | CCCTTGTCTC | 3180 |
| | CAGCCTGTTT | TGCTCTGGTC | TCTCTGGGGT | TGTTGAATCT | CTCCTCTTGC | CTGCCAAGTA | 3240 |
| | CACATGTACC | GCAACTTCAT | TTCTTCTGTC | ATCTTCCCCC | AAGAAACAGC | TTCTGAGGG | 3300 |
| | TGCTGGGGCA | GCCACTGGTG | AGGAGGGGCT | GCTCTGATGT | CCCTCCTATG | AGGGGACTCT | 3360 |
| 35 | GCACAGACAC | CATTGGCCAC | ACTATCACCA | TATTTTCACT | CAGTCACACA | CAAGACAAAA | 3420 |
| | GCATGCAATG | ACAAAACCAT | ACGCAATCCT | GACCGCCAG | CCAATCAAGA | CATATCACAG | 3480 |
| | AACACACGGC | TCCTTCCAAG | AATGTTTATC | CTCATGCATC | ACTTACACAC | CCCCAGACAC | 3540 |
| | GTACTGCAAT | GCAAGTCACT | AGTCATGGTC | ACATGACAGT | GACAGTGTGG | CCTCCTCTTA | 3600 |
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| 40 | GGAGGGTGGG | ATCGAGCCAG | AACAATCAGC | CCATATTGGG | TCCCCCTAAG | TGCCCCCGTC | 3720 |
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| 45 | AGAGGGGGAG | GTGTTGGGGC | AGACCCCCAC | TAGCTGGGAG | CCTGGGGGCT | CCTCTAAGGC | 4020 |
| | TGAGGAAGGA | AAATTGGCCC | CAGGTTGTTG | GGGGGCTCTG | GGTCTCCAG | GACGGAAGGC | 4080 |
| | CCAGGGCAGG | GAGGGGGCAT | GTGGTTGGGC | TCCTTTATCT | CCCTGTGTCC | CCTTCTGCT | 4140 |
| | TTGAGCTAGG | GGGCTGACTC | TGCCCTCCAG | GACACAAGTC | TCCAAGTGC | CTGTGAGGGC | 4200 |
| | GGGCCCTCCG | CACCCCTCTG | CCTCTGCCTG | GCAGGCCAAC | CTCAGCCAC | CTGCCCAGAG | 4260 |
| 50 | GCCTCCCTCG | TGGACACCCC | CTCACCTATT | TGGCCAAACA | ATTCTGGCTG | CAGCTTCAGG | 4320 |
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| 55 | CCCTCACC | ACATCCCA | TTCAAGTCAG | GAAGGCAGGT | TTTATTTCAG | GGCCCTTTTC | 4620 |
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| | GAAGAGTGGG | CATGGGGGGC | CCCTGATATC | TGGAGGGGGC | GGGTGGCCCT | CAGTCATCTT | 4860 |
| 60 | TGGAGCAGAA | GGGCTGGGTC | CTGGGGCCAC | AGACCAACAG | GCTCAGCCTC | CCTACCTGTC | 4920 |
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| 65 | GGCTTGGGCT | CCAGGCACCTG | GCTTCTCTTC | TCTGTGCTCT | TAGCATTGGA | GAGAAGAGGC | 5220 |
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| 70 | GCACAGGGAG | TTCCAAATGA | GAGGGAGCTT | CTGTGGCTTG | AGAGCCTCTG | GGGCCCTTGG | 5520 |
| | TGCCAGAGCA | CGAGGCAGGC | CAGGACCTGG | AGAGCCCAAG | CCCTGTCTCC | AGGAGGCCAG | 5580 |
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| | AGCCGCTGCT | GACCCCTCTC | GGTGGGGGCC | CCTGGACACA | GGGAGCAGAC | CCTCTGCCTC | 5760 |
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| 75 | CTGGACTTGC | CTCCCCAGGC | CTCTTGCCTG | TAAATAGAAG | CCCGCAAACT | GTACAGATTT | 5880 |
| | ACAGAGGCAT | CGAGACTGGG | CCCTGGGAGT | TGCCATCTGA | GAGCGATGG | CCCCAGCATC | 5940 |
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Seq ID NO: 190 DNA Sequence
Nucleic Acid Accession #: NM_006917.2
Coding sequence: 189..1580

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Seq ID NO: 191 DNA Sequence
Nucleic Acid Accession #: NM_002185.1
Coding sequence: 23..1402

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Seq ID NO: 192 DNA Sequence
Nucleic Acid Accession #: NM_006272.1
Coding sequence: 73..351

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Seq ID NO: 193 DNA Sequence

Nucleic Acid Accession #: NM_006157.1

Coding sequence: 103..2535

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Seq ID NO: 194 DNA Sequence

Nucleic Acid Accession #: NM_016180.1

Coding sequence: 26..1618

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GGGCATGGAC TGGCCACCC TCACATGCAAT GGTGCAGCTG GCTCAGATCC TGGTCGGAGG 1500
TGGCCTGGGC TTTCTGGTCA ACACAGCCGG GACCGTTGTC GTCTGTGTA TCACAGCGTC 1560
TGCCTGGGCA CTGATAGGCT GTTCTTTGT CGCTCTCTT GTTAGATATG TGGATTAGGT 1620
CAATAAAGAG ACAATGACCC TAAAAAATA 1650

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20
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35
40
45
50
55
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65
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Seq ID NO: 195 DNA Sequence
Nucleic Acid Accession #: NM_012400.2
Coding sequence: 18..455

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1      11      21      31      41      51
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TGATTCGAAT CCAGGGGGGG ATCTGAAAC TGAACAAGAT GGTCAAGCAA GTGACTGGGA 120
AAATGCCCAT CCTCTCTAC TGGCCCTAC GCTGTCACT CGGACTAGGT GGCAGAGGCC 180
AACCCAAAGA TGCCACGGAC TGGTGCTGCC AGACCCATGA CTGCTGTAT GACCACTGA 240
AGACCCAGGG GTGCAGATC TACAAGGACT ATTACAGATA CAACCTTTCC CAGGGGAACA 300
TCCACTGCTC TGACAAGGGA AGCTGGTGTG AGCAGCAGCT GTGTGCTGT GACAAGGAGG 360
TGGCCTTCTG CCTGAAGCGC AACCTGGACA CCTACCAGAA GCGACTGCGT TTCTACTGGC 420
GGCCCCACTG CCGGGGCGAG ACCCTGGGT GCTAGAAGCC CACACCTCT ACCTGTTCC 480
TCAGCATGGA GCTCTGGCAT CCCCACCTCA GTATCTAAC TGAACAGCC TGGCTTTTCA 540
AACACTCCGG GGGAGGAGT TCCCAGCCTC CCCCAGAAC CTCTACCAAT GCCTTCTGAC 600
CTTCTGAAGC TTTCGAATC CTCCAGTTG AGGCAGTAGC TGTGCTCTT GAGGGTGGAT 660
GGGAATCTTG GGAGAAGCCC AAGCAAGGGA GCGCTCAGAG GTGGTGTITG GACCAAAACA 720
TGGGGGTGGG GGAGGGGTCT GCCCTGTGCC CCCACCTGCT GGGCCCTTG TCCTTCTCA 780
CCCCCTCCAA TATAGTCTCG GAGCTACAAC CGCAGCAGCC ACTATAAAG GCAATATTGA 840
TCTTCTGTCT CATGTGGCTC TATCTTTTAA AACCTCAAGG CCTCCACTG TCCTAAGATA 900
AAGCCTCTCA TAGGCACTGG GGACCCTGCA CAGTCTGGCC ATGTGACCCT CTCGCCAGC 960
AAGCTCTGAA GTCCCTCGAG GTGGAGGCCA TGCTGTCTT AAACCTCAGT GCATCCCTGG 1020
TGCCCAAGAG AACACAGAA CCAAGAAGGA GCTCCATAAA TCCTTCTGG GTGAAGCCTA 1080
GACAAAGCCG CCAGGTCTTG TGGCTCCAGG CACCAGAGCC TTGAGTACTT TCTCTGCCT 1140
CCAGGCATTT GCTCAGGGTG AATTACAAGG GGCTACTGAA TGGCTATTAC TTTCATCAG 1200
ACTGATCCCC CCTCTCTCAG GGTCAAAGGG CTACTTCTG GAAGTCTCCC CAGGCTGACT 1260
CCTTCTCCCT GACTGCAAGG GCTCACTCCC TCCTCCAAGC TCCCACAATG CTTCATGGCT 1320
CTGCCGCTTA CTAGCTTGG CTTAGAGTGG CAAATGSAAC TTCTCTGATC TCCCCCACT 1380
AGACTGGAGC CCCCAGGAAG TGGAGACCAT GTCTGTGCCA TCTGTGTTT CCCTGTTTT 1440
CCACATACTA GGTGCTCAAT TCATGCCGTG GAATGGCGTG AGCCCAATAT GGATACACAG 1500
AGGTTGAGCG CATGTGGTGG GTTACCTCAC CCAGATATCA TCCAGGCCCA AGGCCCTCT 1560
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CTGCCCTGGT CTAGTGGGAG CTGCCCTTCC CTTGCCCCAC CTCTCCACCC AAGAGGCCAC 1680
CTGTCACTCA TGGCCAGGAG AGTGACACCA TGGAGGGTAC AATTGGCCAG TCCCCGCTG 1740
CTGTGCAGGA TTGTCTGGGT TGAATGACAC TCTCAAATTG TTCTGGGAT CGGGCTGAGG 1800
CAGGCCTCT CTTGGAACCA CCTCTGTGCT TGGTCTGACC CCTTGGCCTA TCCAGTTTTC 1860
CTGGTCCCT CACAGGTTTC TCCAGAAAGT ACTCCCTCAG TAAAGCATTT GCACAAGAAT 1920
CCTTGTCTCA GGCTCTGCTT CTAAGAAAG AGACTGAAGA GGGACAACCT TTTCCTATGA 1980
GGACTCCCAA CTCGCCATT GTGTGTGGCT AGCTGTTTCC AGCCAGGGG CTGAGGCACC 2040
TGCACTCACC CACTCTGGG GCCTGTGGCA CCATCTGTGC CTGAGCTGAC TGAGCAGTTT 2100
TGAGATGTGG TACTCATGT GAAATGGTGT CATAGGAATG AAGGACTGTG GGCCTGGGT 2160
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TGTGGGGGAA CAGGTGAGG AATCTCCAT ACCTTCTCAA TTTTGTGTG AACCTAAAC 2280
TGCCATATAA AGATAAAGTC TAGGCCAGGC ATGGTGGCTC ATGCTGTAA TCCCAACACT 2340
TAGGTTGGCT GAGGCAGGCA GATCACTGG GGTGAGGAT TCAAGACCA CCTGCCAAC 2400
ATGGCAAAAC CTCGTCTCTA CTAAATAATC AAAAATTAGC CAGGCATCGT GGTGGGTGCC 2460
TGTAATCCCA GCTATTGAG AGGCTGAGGC AGGAGAATCA CTTGACCTG GGAGGCAGAG 2520
GTTTCAAGTA GCCCAGATCG CGACACTGCA CTCACGCTG GGCAACAGAG TGACACTCTG 2580
TCTCAAAAAA TAAAAATAAA TAAAAATAAA TAAAAATAAA TAAAAATAAA 2640
AAAAAATAAA TAAAAATAAA TAAAAATAAA TAAAAATAAA TAAAAATAAA 2700
AAAAAATAAA TAAAAATAAA TAAAAATAAA TAAAAATAAA TAAAAATAAA 2747

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75
80

Seq ID NO: 196 DNA Sequence
Nucleic Acid Accession #: NM_018833.1
Coding sequence: 80..2041

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TCCCGGCGCG GGCTGAGCCA TGCGGCTCCC TGACCTGAGA CCCTGGACCT CCCTGCTGCT 120
GGTGGACGCG GCTTACTGTG GGCTGTCTCA GGGCCCTCTG GGGACTTTGC TTCTCAAGG 180
GCTGCCAGGA CTATGGCTGG AGGGGACCTC GCGCTGGGA GGGCTGTGGG GGTGCTAAA 240
GCTAAGAGGG CTGCTGGGAT TTGTGGGGAC ACTGCTGCTC CCGCTCTGTC TGGCCACCCC 300
CCTGACTGTC TCCCTGAGAG CCCTGGTTCG GGGGGCTCA CGTGTCCCC CAGCCAGAGT 360
CGCTTCAAGC CTTGAGACT GGCTGCTGGT GGGGTACGGG GCTGCGGGCC TCAGCTGGTC 420
ACTGTGGGCT GTTCTGAGCC CTCCTGGAGC CCAGGAGAAG GAGCAGGACC AGGTGAACAA 480
CAAAGTCTTG ATGTGGAGGC TGCTGAAGCT CTCAGGCCG GACCTGCTTC TCCTGTTGCT 540

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| | | | | | | | |
|----|-------------------------------------|-------------|------------|-------------|------------|-------------|------|
| 5 | CGCCTTCTTC | TTCTTGTGCC | TTGCTGTTTT | GGGTGAGACA | TTAATCCCTC | ACTATTCTGG | 600 |
| | TGTTGTCAIT | GACATCTGGG | GAGGTGATT | TGACCCCAT | GCCTTTGCCA | GTGCCATCTT | 660 |
| | CTTCATGTGC | CTCTTCTCCT | TTGGCAGCTC | ACTGTCTGCA | GGCTGCCGAG | GAGGCTGCTT | 720 |
| | CACCTACACC | ATGTCTCGAA | TCAACTTGCG | GATCCGGGAG | CAGCTTTTCT | CCTCCCTGCT | 780 |
| | GGCCACAGAC | CTCGGTTTCT | TCCAGGAGAC | TAAGACAGGG | GAGCTGAAC | CACGGCTGAG | 840 |
| | CTCGGATACC | ACCCTGATGA | GTAACCTGGT | TCCTTTAAAT | GCCAATGTGC | TCTTGCGAAG | 900 |
| | CCTGGTGAAT | GTCGTGGGGC | TGTATGGCTT | CATGCTCAGC | ATATCGCCTC | GACTCACCTC | 960 |
| | CCTTTCTCTG | CTGCACATGC | CCTTCACAAT | AGCAGCGGAG | AAGGTGTACA | ACACCCGCCA | 1020 |
| 10 | TCAGGAAGTG | CTTCGGGAGA | TCCAGGATGC | AGTGGCCAGG | GGCGGGCAGG | TGGTCCGGGA | 1080 |
| | AGCCGTTGGA | GGAGTGCAGA | CCGTTGCGAG | TTTTGGGGCC | GAGGAGCATG | AAGTCTGTGC | 1140 |
| | CTATAAGAG | GGCCTTGAA | AATGTGCGCA | GCTGTATTGG | CGGAGAGACC | TGGAACGGCG | 1200 |
| | CTTGATACCT | CTCATAAGGA | GGGTGCTGCA | CTTGGGTGTG | CAGATGCTGA | TGCTGAGCTG | 1260 |
| | TGGGCTGCG | CAGATGCAGG | ATGGGGAGCT | ACCCAGGGC | AGCCTGCTTT | CCTTTATGAT | 1320 |
| | CTACAGGAG | AGCGTGGGGA | GCTATGTGCA | GACCTGGTA | TACATATATG | GGGATATGCT | 1380 |
| 15 | CAGCAACGTG | GGAGCTGCAG | AGAAAGTTT | CTCCTACATG | GACCGACAGC | CAAACTCTGCC | 1440 |
| | TTCACTCTGC | AGCCTTGCCC | CCACCACTCT | GCAGGGGGTT | GTGAAATTC | AAGACGTCTC | 1500 |
| | CTTCGATAT | CCCAATCGCC | CTGACAGGCC | TGTGCTCAAG | GGGCTGACGT | TTACCTTACG | 1560 |
| | TCTCGTGTG | GTGACGGGCG | TGTTGGGACC | CAATGGGTCT | GGGAAGAGCA | CAGTGGCTGC | 1620 |
| 20 | CCTGTCTGAG | AATCTGTACC | AGCCCAACAG | GGGACAGGTG | CTGCTGGATG | AAAAGCCCAT | 1680 |
| | CTCACAGTAT | GAACACTGCT | ACCTGCACAG | CCAGGTGGTT | TCAGTTGGGC | AGGAGCCTGT | 1740 |
| | GCTGTCTTCC | GGTCTGTGTA | GGAAACAAT | TGCTTATGGG | CTGCAGAGCT | GCGAAGATGA | 1800 |
| | TAAGGTGATG | GGCGCTGCCC | GGGCTGCCCA | CGCAGATGAC | TTATCCAGG | AAATGGAGCA | 1860 |
| | TGGAATATAC | ACAGATGTAG | GGGAGAAGGG | AGCCAGCTG | GCTGCCGGAC | AGAAACAACG | 1920 |
| 25 | TCCTGCCATT | GGCCGGGGCC | TTGTACGAGA | CCGCGGGGTC | CTCATCTCGG | ATGAGGCTAC | 1980 |
| | TAGTGCCCTA | GATGTGCAGT | GGGAGCAGGC | CAAAACCCCT | TGGAAGTTCA | TGATATTTTG | 2040 |
| | AATTTCAATG | GATTTTCTCT | GGGAATAATG | AGTTCAAATG | AACGAATATG | TGGAACAAGG | 2100 |
| | CATCACCAAT | ATTATTTTTT | TCAAGATGAG | GTGATGGACA | AAACCATCAC | AGGGAATTTG | 2160 |
| | AGGCAATATG | TACATGTAAA | ACAATACTTC | GGGTGAGTCC | ACCTATCCCA | AAGTCGTATC | 2220 |
| 30 | AAAGAAAGTG | CTGCAGATTG | GAGCCCAAG | CCTTTGGTTC | CTCAGTTTCC | AAATGGATTG | 2280 |
| | TCTAGTAGTG | GGATCATGAG | TTTGCTTTGG | ACACCCCAAA | TTCTAACTAT | TTCTTTTGT | 2340 |
| | TCTTACATCC | TTTCCCTCTT | CCCCAGCCCC | TTCCCTCAT | GTTACACCTC | TTGCTGGTTT | 2400 |
| | GAGAGCTCAA | TCACCACTGA | AAAGAATTA | AACCAATATT | TTGAGCTGGC | AAAATTTCTA | 2460 |
| | GCCTAGTACA | ATTCTTCTAA | TTAACTGTA | GCTCAAC | | | 2497 |
| 35 | Seq ID NO: 197 DNA Sequence | | | | | | |
| | Nucleic Acid Accession #: NM_002416 | | | | | | |
| | Coding sequence: 40-417 | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| 40 | ATCCAATACA | GGAGTGACTT | GGAACCTCAT | TCTATCACTA | TGAAGAAAAG | TGGTGTCTCT | 60 |
| | TTCTCTTGG | GCATCATCTT | GCTGGTTCTG | ATTGGAGTGC | AAGGAACCCC | AGTAGTGAGA | 120 |
| | AAGGGTGCCT | GTTCCTGCAT | CAGCACCAAC | CAAGGGACTA | TCCACCTACA | ATCCTTGAAA | 180 |
| | GACCTTAAAC | AAATTGCCCC | AAGCCCTTCC | TGGGAGAAAA | TTGAAATCAT | TGCTACACTG | 240 |
| 45 | AAGAATGGAG | TTCAAAACATG | TCTAAACCCA | GATTTCAGCAG | ATGTGAAGGA | ACTGATTAAA | 300 |
| | AAGTGGGAGA | AACAGTCTCAG | CCAAAAGAAA | AAGCAAAAGA | ATGGGAAAAA | ACATCAAAAA | 360 |
| | AAGAAAGTTC | TGAAAGTTGG | AAAATCTCAA | CGTTCTCGTC | AAAAGAAGAC | TACATAAGAG | 420 |
| | ACCACTTCAC | CAATAAGTAT | TCTGTGTTAA | AAATGTTCTA | TTTTAATTAT | ACCGTATCA | 480 |
| | TTCCAAAGGA | GGATGTCATA | TAATACAAAG | GCTTATTAA | TTGACTAGAA | AAITTTAAAC | 540 |
| 50 | ATTACTCTGA | AAATGTAAC | AAAGTTAGAA | AGTTGATTTT | AAGAATCCAA | ACGTTAAGAA | 600 |
| | TTGTTAAAGG | CTATGATTGT | CTTTGTTCTT | CTACCAACCA | CCAGTTGAAT | TTCAATCATG | 660 |
| | TTAAGGCCAT | GATTTTAGCA | ATACCCATGT | CTACACAGAT | GTTCAACCAA | CCACATCCCA | 720 |
| | CTCACAAACG | CTGCCGTGAA | GAGCAGCCCT | AGGCTTCCAC | GTACTGCAGC | CTCCAGAGAG | 780 |
| 55 | TATCTGAGGC | ACATGTCAGC | AAGTCTTAAG | CCTGTTAGCA | TGCTGGTGAG | CCAAGCAGTT | 840 |
| | TGAAATTTAG | CTGGACCTCA | CCAAGCTGCT | GTGGCCATCA | ACCTCTGTAT | TTGAATCAGC | 900 |
| | CTACAGGCC | CACACACAAT | GTGCTGAGCA | GATTCATGCT | GATTGTTATT | GGGTATCACC | 960 |
| | ACTGGAGATC | ACCAGTGTGT | GGCTTTTCAA | GCCTCTCTTC | TGGCTTTGGA | AGCCATGTGA | 1020 |
| | TTCCATCTTG | CCCCTCAGG | CTGACCACTT | TATTTCTTTT | TGTTCCCTTT | TGCTTCATTC | 1080 |
| 60 | AAGTCAGCTC | TTCTCCATCC | TACCACAATG | CAGTGCCTTT | CTTCTCTCCA | GTGCACCTGT | 1140 |
| | CATATGCTCT | GATTATCTG | AGTCAACTCC | TTTCTCATCT | TGTCCTCAAC | ACCCACAGAG | 1200 |
| | AGTGTCTTCT | TCTCCCAATT | CATCCTCACT | CAGTCCAGCT | TAGTTCAAGT | CCTGCCTCTT | 1260 |
| | AAATAAACCT | TTTTGGACAC | ACAAATTATC | TTAAACTCC | TGTTTCACTT | GGTTCAGTAC | 1320 |
| | CACATGGGTG | AACACTCAAT | GGTTAACTAA | TTCTTGGGTG | TTTATCCTAT | CTTCCCAACC | 1380 |
| 65 | AGATTGTGAG | CTCCTTGAGG | GCAAGAGCCA | CAGTATATTT | CCCTGTTTCT | TCCACAGTGC | 1440 |
| | CTAATAATAC | TGTGGAACCT | GGTTTAAATA | ATTTTAAAT | TGATGTTGTT | ATGGGCAGGA | 1500 |
| | TGGCAACCCG | ACCAATTGCT | CAGAGCAGGT | GCTGGCTCTT | TCCTGGCTAC | TCCATGTTGG | 1560 |
| | CTAGCCTCTG | GTAACCTCTT | ACTTATTATC | TTCAAGACAC | TCACTACAGG | GACCCAGGAT | 1620 |
| | GATGCAACAT | CCTTGTCTTT | TTATGACAGG | ATGTTTGCTC | AGCTTCTCCA | ACAATAAGAA | 1680 |
| 70 | GCACGTGGTA | AAACACTTGC | GGATATTCTG | GACTGTTTTT | AAAAAATATA | CAGTTTACCG | 1740 |
| | AAAAATCATAT | AATCTTACAA | TGAAAAGGAC | TTTATAGATC | AGCCAGTGAC | CAACCTTTTC | 1800 |
| | CCAAACATAC | AAAAATTCCT | TTTCCCGAAG | GAAAAGGGCT | TTCTCAATAA | GCCTCAGCTT | 1860 |
| | TCTAAGATCT | AACAAGATAG | CCACCGAGAT | CCTTATCGAA | ACTCATTTTA | GGCAATATG | 1920 |
| | AGTTTTATTG | TCCGTTTACT | TGTTTCAGAG | TTTGTTATTG | GATTATCAAT | TACCACACCA | 1980 |
| 75 | TCTCCCATGA | AGAAAGGGAA | CGGTGAAGTA | CTAAGCGCTA | GAGGAAGCAG | CAAGTCGGT | 2040 |
| | TAGTGGAAAG | ATGATTGGTG | CCCAGTTAGC | CTCTGCAGGA | TGTGGAAACC | TCCTTCCAGG | 2100 |
| | GGAGGTTTCT | TGAATTGTGT | AGGAGAGGTT | GTCTGTGGCC | AGAATTTAAA | CCTATCTCA | 2160 |
| | CTTTCCCAAA | TTGAATCACT | GCTCACACTG | CTGATGATTT | AGAGTGCTGT | CCGGTGAGGA | 2220 |
| 80 | TCCCAACCGA | AGGTCTTATC | TAATCATGAA | ACTCCCTAGT | TCCTTCATGT | AACTTCCCTG | 2280 |
| | AAAAATCTAA | GTGTTTCTATA | AATTTGAGAG | TCTGTGACCC | ACTTACCTGT | CATCTCACAG | 2340 |
| | GTAGACAGTA | TATAACTAAC | AACCAAGAC | TACATATTGT | CACTGACACA | CACGTTATAA | 2400 |
| | TCTATTATCA | TATATATACA | TACATGCATA | CACCTCTCAA | GCAAAATAAT | TTTCACTTCA | 2460 |
| | AAACAGTATT | GACTTGTATA | CCTTGTAAAT | TGAAATATTT | TCTTTGTATA | AATAGATATG | 2520 |
| | TATCAATAAA | TAGACCATTA | ATCAG | | | | |

Seq ID NO: 198 DNA Sequence

Nucleic Acid Accession #: NM_006533.1

Coding sequence: 72..467

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 TCTCCGACC TGGTGTGAGG GGTGGTCTTA TGCCCAAGCT GGCTGACCGG AAGCTGTGTG 180
 CGGACCAGGA GTGCAGCCAC CCTATCTCCA TGGCTGTGGC CCTTCAGGAC TACATGGCCC 240
 10 CCGACTGCCG ATTCTTGACC ATTCACCGG GCCAAGTGGT GTATGTCTTC TCCAAGCTGA 300
 AGGGCCGTCG GCGGCTCTTC TGGGGAGGCA GCGTTCAGGG AGATTACTAT GGAGATCTGG 360
 CTGCTCGCTC GGGCTATTTT CCGAGTAGCA TTGTCCGAGA GGACCAGACC CTGAAACCTG 420
 GCAAAGTCGA TGTGAAGACA GACAAATGGG ATTTCTACTG CAGGTGAGCT CAGCCTACCG 480
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Seq ID NO: 199 Protein sequence

Protein Accession #: NP_002412.1

1 11 21 31 41 51
 20 MHSFPLLLL LFWGVVSHSF PATLETQEQD VDLVQKYLEK YYNLKNDGRQ VEKRRNSGPV 60
 VEKLKQMKEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN 120
 YTPDLPRADV DHAIEKAPQL WSNVTPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180
 LAHAFOQPGP IGGDAHFDEED ERWTNNFREY NLHRAVAHEL GHSGLSLSHST DIGALMYPST 240
 TFSGDVQLAQ DDIDIGIAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMPFKDR 300
 25 FYMRTNPFYP EVELNPFISV WPQLPNGLEA AYEFAADRDEV RFFKGNKYWA VQGNVNLHGY 360
 PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFFVANKYWR DEYKRSMDPG YPKMIAHDFP 420
 GIGHKVDAVF MKDGFYFFH GTRQYKFDPK TKRILTQKA NSWFNCRKN

Seq ID NO: 200 Protein sequence

Protein Accession #: NP_002412.1

1 11 21 31 41 51
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 VEKLKQMKEF FGLKVTGKPD AETLKVMKQP RCGVPDVAQF VLTEGNPRWE QTHLTYRIEN 120
 35 YTPDLPRADV DHAIEKAPQL WSNVTPLTFT KVSEGGADIM ISFVRGDHRD NSPFDGPGGN 180
 LAHAFOQPGP IGGDAHFDEED ERWTNNFREY NLHRAVAHEL GHSGLSLSHST DIGALMYPST 240
 TFSGDVQLAQ DDIDIGIAIY GRSQNPVQPI GPQTPKACDS KLTFDAITTI RGEVMPFKDR 300
 FYMRTNPFYP EVELNPFISV WPQLPNGLEA AYEFAADRDEV RFFKGNKYWA VQGNVNLHGY 360
 PKDIYSSFGF PRTVKHIDAA LSEENTGKTY FFFVANKYWR DEYKRSMDPG YPKMIAHDFP 420
 40 GIGHKVDAVF MKDGFYFFH GTRQYKFDPK TKRILTQKA NSWFNCRKN

Seq ID NO: 201 Protein sequence

Protein Accession #: NP_002413

1 11 21 31 41 51
 45 MKSLPILLLL CVAVCSAYPL DGAARGEDTS MNLVQKYLEN YYDLEKDVQK FVRRKDSGPV 60
 VKKIREMQKF LGLLEVTKGLD SDTLEVMRKP RCGVPDVGHF RTFPGIPKWR KTHLTYRIVN 120
 YTPDLPKADV DSAVEKALKV WEEVTPLTFS RLYEGEADIM ISFAVREHGD FYFPGDGPVN 180
 LAHAAYAPGP INGDHAFDDD EQMTKDTTGT NLFLVAHAHEI GHSGLGLFSA NTEALMYPST 240
 50 HSLTDLTRAV LSLDDINGIQ SLYGPPDPS ETPLVPTPEV PPEPGTPANC DPALSFDASV 300
 TLRGEILIFK DRHFWRKSLR KLEPELHLIS SFWSPSPGV DAAYEVTSKD LVFIFKGNQF 360
 WAIRGNEVRA GYPRGIHTLG FPPTVRKIDA AISDKENKNT YFFVEDKYWR FDEKRNSEMP 420
 GPPKIAEDF PGIDSKIDAV FEFPFFYFF TGSSQLEFDP NAKKVTHTLK SNSWLNC

Seq ID NO: 202 Protein Sequence

Protein Accession #: NP_001845

1 11 21 31 41 51
 55 MEPWSSRWKT KRWLWDFTVT TLALTFLFQA REVRGAAPVD VLKALDFHNS PEGISKTTGF 60
 CTNRKNSKGS DTAYRVSKQA QLSAPTKQLF PGFTFPEDFS ILFTVKPKKG IQSFLLSIYN 120
 60 EHQIQQIGVE VGRSPVFLFE DHTGKPAED YPLFRVTNIA DGKWHRAIS VEKKTVTMIV 180
 DCKKTKTKPL DRSERAIVDT NGITVFGTRI LDEEVFEGDI QOFLITGDPK AAYDYCEHYS 240
 PDCDSSAPKA AQAQEPQIDE YAPEDIIEYD YEYGEAEYKE AESVTGPTV TEETIAQTEA 300
 NIVDDPFQYEN YGTMESYQTE APRHVSQTNE PNPVEEIPTE EYLTGEDYDS QRKNSEDTLY 360
 65 ENKEIDGRDS DLLVDGLGE YDFYKEYE DKPTSPPNEE FGPVPAETD ITETSINGHG 420
 AYGEKGQKGE PAVVEPGLMV EGPPGPAGPA GIMGPPGLQG PTGPPGDPGD RGPGRPGPLP 480
 GADGLPGPPG TMLMLPFYRG GDGSKGPTIS AQEAQAQAIL QQARIALRGP PGPMLTGRP 540
 GPVGGPGSSG AKGESGDPG QGPRGVQCPP GPTGKPGKRG RPDAGGGRGM PGEPAKGRD 600
 GFDGLPLPG DKGHRGERGP QGPPGPPGDD GMRGEDGEIG PRGLPGEAGP RGLLGPRTGP 660
 70 GAPGQPGMAG VDGPPGPKGN MGPQGERGPP QQQGNPGPQG LPGPOGPFGP PGEKGPQKGP 720
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 GEDGPPGFKG DMGLKGRGE VQIGPRGXD GREPKGRAG PTGDPGPGSQ AGEKGLGVP 840
 GLPGYPGRGP PKGSTGPPGF PGANGKGRG GVAGKPGPRG QRGPPTGPRG RGARGPTGKP 900
 GPKGTSGGDD PPGPPGERGP QGPQGPVGF PPKPPGPPG RMGCPGHPGQ RGETGPGKGT 960
 75 GPPGPGVVG POGPTGETGT IGERGYGPP GPPGEQGLPG AAGKEGAKGD PGPOGISGKD 1020
 GPAGLRGFP ERGLPGAQGA PGLKGGEGPQ GPPGVPVSPG ERGSAGTAGP IGLRGRPGPQ 1080
 GPPGPAGEKG APGEKGPQGP AGRDGVQGPV GLPGPAGPAG SPGEDGDKGE IGEPPGKGSK 1140
 GKGEGNPGP PGLGQPVGA PGIAGDGEPP GPRGQQGMFG QKGDGARGF PGPPGPIGLQ 1200
 GLPGPPGEKG ENGDDVGMGP PGPGRGPGPQ GPNAGDGPQG PPGSVGSVGG VGEKGEPEGA 1260
 80 GNPGPGEAGE VGGPPGERGE KGEAGPPGAA GPPGAKGPPG DDGPKGNRGP VGFPGDPGPP 1320
 GELGPAQDQD VGGDKGEDGD PQQPGPPGPS GEAGPPGPPG KRGPAGAAGA EGRQSEKGA 1380
 GEAGAEGPPG KTGVPVGP GPAGKPPGGLR GIPGPVGEQG LPGAAGQDGP PGPMPGPPGL 1440
 GLKGDGSGK EKGHPGLIGL IGPPGEQGEK GDRGLPGTQG SPGAKGDGGI PGAPGLGPP 1500
 GPPGLPGPQG PKGNKSGTGP AQKGDGSLP GPPGPPGPPG EVIQPLPILS SKKTRRHTG 1560
 MQADADDNIL DYSDMGEIIF GSNLSLKQDI EHMKPPMGTP TNPARTCKDL QLSHPDFPDG 1620

EYWDPNQGC SGDSFKVYCN FTSGGETCIY PDKKSEGVRI SSWPKEKPGS WPSEFKRGKL 1680
 LSYLDVEGNS INMVMTFLK LLTASARQNF TYHCHQSAAM YDVSSGSYDK ALRFLGSNDE 1740
 EMSYDNNFFI KTLYDGCTSR KGYEKTVEIE NTPKIDQVPI VDMISDFGD QNQKFGFEVG 1800
 PVCFLG

Seq ID NO: 203 Protein sequence
 Protein Accession #: XP_057014

1 11 21 31 41 51
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 10 MRPGQPAASP QRLRGLLLLL LLQLPAPSSA SEIPKKGKKA QLRQREVVDL YNGMCLQGPA 60
 GVPGRDGGSPG ANGIPGTGPI PGDRDGFKEK GECLRESFEE SWTPNYKQCS WSSLNYGIDL 120
 GKIAECTFTK MRSNSALRVL FSGSLRLKCR NACCQRWYFT FNGAECSGPL PIEAIIYLDQ 180
 GSPFNSTIN IHRTSSVEGL CEGIGAGLVD VAIWVGTCSD YPKGDASTGW NSVSRIIEE 240
 LPK

Seq ID NO: 204 Protein sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
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 20 MPGTLKTRTG APADYRVILK TSQEDELQVP DDISVRVMSS QSVLVSVDLP VLEKQKKVVA 60
 SRQYTVRYRE KGLARWYK QIANRRVLIE NLIPDTVYEF AVRIQGERD GKWSTSVFQR 120
 TPESAPTTAP ENLNWVPNG KPTVVAASWD ALPETEGVKV VCLLDGTGLFS VSSFQPSAKS 180
 FQNTFFHTPR LSNHLEQSPS PILETLLLPW WMVCSLGNAI FSKSGPQTGE AWDLTTPKPSL 240
 25 SLQCCQECST QKDFCLAYL IDIQTKQVMK DPQLEGSVFG PCFLFYFLTF MLDIGGFSFI 300
 MCYEDPVSSL TGNLSKVA SKADVQNTTE DNGKPEKPEP SSPSPRAPAS SQHPSVPASP 360
 QGRNAKDLLL DLKNKILANG GAPRKPQLRA KKAEEELDQS TEITGEEELG SREDSPPSPS 420
 DTQDQKTRLP PPSRHHGSHV APGRTAVRAR MPALPRREGV DKPGFSLATQ PRPGAPPSAS 480
 ASPAHASTQ GTSRHSPLPA SLNDNDLVDS DEDERAVGSL HPGGAFAQPR PALSPSRQSP 540
 30 SSVLRDRSSV HPGAKPASPA RRTPHSGAAE EDSSASAPPS RLSPPHGGSS RLLPTQPHLS 600
 SPLSKGGKDG EDAPATNSNA PSRSTMSSSV SSSLRSRTQV SEGAESDGE SHGDGDRDRE 660
 GRQAETAATQ LRARPASGHF HLLRHKKFAA NGRSPSRFSI GRGPRLPQSS SPQSTVPSRA 720
 HPRVPSHSDS HPKLSSGSHG DEEDEKPLPA TVVNDHVPSS SRQPISRGWE DLRRSPQRGA 780
 SLHRKEPIPE NPKSTGADTH PQGKYSSLAS KAQDVQQSTD ADTEGHSKPA QPGSTDRHAS 840
 35 PARPPAARSQ QHPSVPRMT PGRAPEQQPP PPVATSQHHP GPQSRDAGRS PSQPRLSLTQ 900
 AGRPRPTSQG RSHSSSDPYT ASSRGMLPTA LQNDQEDAQG SYDDSTEVE AQDVRAPAHA 960
 ARAKEAASL PKHQVESPT GAGAGGDHRS QRGHAASPAR PSRPGGPQSR ARVPSRAAPG 1020
 KSEPPSKRPL SSKSQSVSA EDEEEDAGF FKGGKEDLLS SSVPKWPSSS TPRGGKDADG 1080
 SLAKEEREPA IALAPRGGS L APVKRPLPPP PGSSPRASHV PSRPPPSRAA TVSPVAGTHP 1140
 40 WPRYTTRAPP GHFSTTPMLS LRQRMHARF RNPLSRQPAR PSYRQYNGR PNVEGKVLPG 1200
 SNGKPNQORI INGPQGTKWV VDLDRGLVLN AEGRYLQDSH GNPLRIKLG GDRITVDLGG 1260
 TPVVSDELPL LFGQGRHGTG LANAQDKPIL SLGGKPLVLG EVIKKTTTHP TTTMQPTTTT 1320
 TPLPTTTTPR PTTATTMQPT TTTTLPPTTT PRPTTATTRR TTTTRPTTTV RTTTRTTTTT 1380
 TPKPTTPIPT CPPTGLERHD DDGNLIMSSN GIPECYAEED EFGSLETDTA VPTEAYVIY 1440
 45 DEDYEFETSR PPTTTEPSTT ATTPRVIPEE GAISFFPEEE FDLAGRKRKF APYVTYLNKD 1500
 PSAPCSLTD LDFHFDVDSL EIIIPNDLKS DLPPQHAPRN ITVVAVEGCH SFVIVDWDKA 1560
 TPGDLVTGYL VYSASYEDI RNKFSTQASS VTHLPIENLK PNTRYFVKVQ AQNPFGYGI 1620
 SPSVSFVTES DNPLLVVRPP GGELSGSHSL SNMIPATRTA MDGNM

Seq ID NO: 205 Protein Sequence
 Protein Accession #: NP_055059

1 11 21 31 41 51
 | | | | |
 50 MDPPAGAARR LLCFALLLLL LLLPPPLLP PPPPANARLA AAADPPGGPI GHGAERILAV 60
 PVRTAQGRRL VSHVSAATS RAGVRARRAA PVRTSPFPFG NEEEPGSHLF YNVTVFGRL 120
 55 HLRLRNARL VAPGATMEHQ GEKCTTRVEP LLGSLCYLVG VAGLAESSV ALSNCDLAG 180
 LIRMEEEFF IEPLEKGLAA QEAQGRVHV VYRRPPTSP LGGPQALDTG ASLDSLDSLS 240
 RALGVLEHA NSSRRARRH AADDYNIIEV LLGVDDSVVQ FHGKEHVQKY LLTLMNIVNE 300
 IYHDESLGAH INVVLVRIIL LSYGKSMSLI EIGNPSQSLE NVCRWAYLQQ KPDTHGDEYH 360
 60 DHAIFLTRQD FGPSGMQGYA PVTGMCHPVR SCTLNHEDGF SSAPVVAHET GHVLGMEHDG 420
 QGNRCGDEVR LGSIMAPLVQ AAFHRFHWRS CSQQELSRYL HSYDCLDDP FAHDWALPQ 480
 LPGLHYSMNE QCRDFGLGY MMCTAFRTFD PCKQLWCSHP DNPYFCKTKK GPPLDGTMCA 540
 PGKHCFKGNH IWLTPDILKR DGSWGAWSPP GSCSRTCTGT VKFRTRQCDN PHPANGGRTC 600
 SGLAYDFQLC SRQDCPDLSA DFREEQCRQW DLYFEHDAQ HHMLPHEHRD AKERCHLYCE 660
 65 SRETGEVVM KRMVHDGTRC SYKDAFSLCV RGDCKRVGCD GVIGSSKQED KCGVCGGDNS 720
 HCKVVKGTFT RSPKHGYIK MFEIPAGARH LLIQEV DATS HHLAVKNLET GKFI LNEEND 780
 VDASSKTFIA MGVWEYERDE DGRTELQTMG PLHGTITVLV IPVGDTRVSL TYKMIHEDS 840
 LNVDDNNVLE EDSVVYEWAL KKWSPCKSKC GGSQFTKYG CRRRLDHKMV HRGFCAALSK 900
 PKAIRACNP QECSPQVWVT GEWEPCSQTC GRTGMQVRSV RCIQPLHNT TRSVHAKHCN 960
 70 DARPESRRAC SRELCPGRWR AGPWSQCSVT CGNGTQERP PV PCRTADDSFG ICQEERPETA 1020
 RTCLRGPCPR NISDPKSKSY VVQWLSRPDP DSPIRKISSK GHCQGDKSIF CRMEVLSRYC 1080
 SIPGYNKLSK KSCNLYNNLT NVEGRIEPPP GKHNDIDVFM PTLPVPTVAM EVRPSSTPL 1140
 EVPLNASSTN ATEHPETNA VDEPKIHGL EDEVQPPNLI PRRSPYEKT RNQRIQELID 1200
 EMRKKEMLGK F 1211

Seq ID NO: 206 Protein sequence
 Protein Accession #: NP_076927

1 11 21 31 41 51
 | | | | |
 80 MGENDPPAVE APFSPRSLFG LDDLKISPA PDADAVAAQI LSLPLKFFP IIVIGIALI 60
 LALAIGLGIH FDCSGKYRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVQLVF 120
 TAASWKTMCS DDWKGHYANV ACAQLGFPYS VSSDNLRVSS LEGQFREEFV SIDHLLPDDK 180
 VTALHSHVYV REGCASHGV TLQCTACGHR RGYSSRIVGG NMSLLSQMPW QASLQFGYH 240
 LCGGSVITPL WIITAAHCYV DLYLPKSWTI QVGLVSLLDN PAPSHLVEKI VYHSKYKPKR 300
 LGNDIALMKL AGPLTFNEMI QPVCLPNSEE NFPDGKVCWT SGWGATEDGG DASPVLNHAA 360

Seq ID NO: 207 Protein Sequence
Protein Accession #: CAC03433.2

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20      NETLDEDLDFH KLIGQQD
      Seq ID NO: 208 Protein Sequence
      Protein Accession #: NP_114433.1
      1      11      21      31      41      51
      |      |      |      |      |      |
25      MASRSMRLLL LLSLACKATGV LGDIIMRPSC APGWFYHKSN CYGYFRKLRN WSDAELECOS 60
      YGNGAHLASI LSLKEASTIA EYISGYQRSQ PIWIGLHDPQ KRQQNQWMDG APYLTRYSWG 120
      KSMGGNGHKCA ELSNNNFLT WSSNECNKRG HPLCKYRP 158

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Seq ID NO: 209 Protein Sequence
Protein Accession #: XP_051860.2

| | | |
|----|--|---|
| | Seq ID NO: 210 Protein Sequence | |
| | Protein Accession #: NP_036244.1 | |
| 60 | <pre> 1 11 21 31 41 51 MSQVKSSYSY DAPSDFINFS SLDDEGDTQN IDSWEFEKAN LENKLLGKNG TGGFLQGGKTP LRKANLQQA1 VTLPLKPVNDT YYKEAEKENL VEQSIPSNAC SSLEVEAAIS RKTPAQFQRR SLRSLAQDQD EQKEKHVHKM KAKRCAATVI IDEILPSKMM KVSNNKKKPE EEGSAHQDTA EKNASSPEKA KGHRTYPCMP PAQKQFLKST EQELEKSMK MQQEVVEMRK HPEFKKLAL AGIGQPVVKS VSQVTKSVDF HFRTDLERIK HPEQLEKSMK VNFTSELRIKH PSSPARVTKG CTIVKPFNLS QGKKRTFDET VSTYVPLAQQ VEDFHKRTPN RYHLRSKKND INLLPSKSSV TKICRDPTPT VLQTKHRRAR TQCSSTABLE ADELEKLLQY KFKARELDPR ILEGGPILPK KPPVKPQEPF IGFDLEIEKR IQERESKKTL IDEHFEFHSR PCPTKILEDV VGVPEKKVLP ITVPKSPAPA LKNRIRMPKT EDEEEDPVP IKAQPVPHYG VPFKQPIPEA RTVEICPFSS DSRDKERQLQ KEKKIKELQK GEVPKFKALP LHPFDTINLP EKKVKNVTQI EFCFLETDRR GALKAAQTKW QLEELRQOQ EAACFKARP N TVISQEPFVP KKEKKSVAEG LSGSLVQEPF QLATEKRAKE RQELEKRMKE VEAAKQAQLE EARLQEEBQK KEELARLRLE LVHKANPRLT YOGLEIKSSD QPLTVPVSPK FSTRFHC </pre> | <pre> 60 120 180 240 300 360 420 480 540 600 660 720 747 </pre> |

Seq ID NO: 211 Protein Sequence
Protein Accession #: NP_065169.1

| | | | | | | | | | | | |
|-----|----------------------------------|-------------|-------------|------------|------------|------------|--|--|--|-----|--|
| 75 | Seq ID NO: 211 Protein Sequence | | | | | | | | | | |
| | Protein Accession #: NP_065169.1 | | | | | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | | | | | |
| 80. | MSRRKQAKPQ | HINSEEDQGE | QQPQQQTPEF | ADAAPAAPAA | GELGAPVNH | GNDEVADE | | | | 60 | |
| | ATVKRLRREE | THVCKCAAE | FFSISEFLH | KKNCTKNPPV | LIMNDSEGPV | PSEDFSGAVL | | | | 120 | |
| | SHQPTSPGSK | DCHRENGGSS | EDMKCKDAE | SVVYLKTETA | LPPTPDISY | LAKGKVANTN | | | | 180 | |
| | VTLQALRGRL | VAVNQRSADA | LPAPVPVGANS | IPVWLEQLIC | LQQQQQLQIQ | LTEQIRIQVN | | | | 240 | |
| | WMASHALHSS | GAGADTLTKLT | GSHMSQQVSA | AVALLSQKAG | SGQLSLDALK | QAKLPHANTP | | | | 300 | |
| | SATSSSPGL | APFTLKPDTG | PLVPNVMSVA | PSALLPQAPG | SVLFQSPFST | VALDTSKKKG | | | | 360 | |

5 GKPPNISAVD VKPKDEAALY KHKCKYCSKV FGTDSLSLQIH LRSHTGERPF VCSVCGHRT 420
TKGNLKVHFM RHPQVKANPQ LFAEFQDKVA AGNGIPYALS VPDPIDEPSL SLDSPVLVT 480
TSVGLPQNLK SGTNPDKLDTG GSLPGDLQPG PSPSEGGPT LPGAQPNYNS PRAGGFGGSG 540
TPEPGSETLK LQQLVENIDK ATTDNNECLI CHRVLSCQSS LKMHYRTHTG ERPFQCKICG 600
15 RAFSTKGNLK THLGVHRTNT SIKTQHSCEPI CQKKFTNAV M LQQHIRMGMG QQIPNTPLPE 660
NPCDPTGSEP MTVGENGSTG AICHDDVIES IDVEEVSSQE APSSSSKVPT PLPSIHSASP 720
TLGFAMMASL DAPGKVGAP FNLQRQGSRE NGSVESDGLT NDSSSLMGDQ EYQSRSPDIL 780
ETTSFQALSP ANSQAESIKS KSPDAGSKAE SSENSRTEME GRSSLPTSTFI RAPPTTVKVE 840
10 VPGETFVGPST LSPGMTPLLA AOPRRQAKQH GCTRCGNFIS SASALQIHER THTGEKPFVC 900
NIGGRAFTTK GNLKVHYMTH GANNNSARRG RKLAIENTMA LLGTGDKRVS EIFPKEILAP 960
SVNVDPVVMN QYTSMLNGGL AVKTNESIVI QSGGVPTLPV SLGATSVVMN ATVSKMDGSG 1020
SGISADVEKP SATDGVPKHQ FPHFLEENKI AVS 1053

15 Seq ID NO: 212 Protein Sequence
Protein Accession #: NP_005092
1 11 21 31 41 51
| | | | |
MGWDLTVKML AGNEFQVSL SSMVSVELKA QITQKIGVHA PQQLAVHPS GVALQDRVPL 60
ASQGLGPGST VLLVVDKDE PLSILVRNNK GRSTYEVRL TQTVHLKQK VSGLEGVQDD 120
20 LFWLTPECKP LEDQLPLGEY GLKPLSTVFM NLRLRGGTE PGRS 165

Seq ID NO: 213 Protein sequence
Protein Accession #: Eos sequence
1 11 21 31 41 51
| | | | |
25 MIILYLFLL LWEDTQGWGF KDGIFHNSIW LERAAGVYHR EARSQKYKLT YAEAKAVCEF 60
EGGHLATYKQ LEAARKIGFH VCAAGWMAKG RVGYPIVKPG PNCXPGKTGI IDYGIRLNRS 120
ERWDAYCYNP HAKECGGVFT DPKRIFKSPG FPNEYEDNQI CYWHIRLKYG QRIHLSFLDF 180
30 DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPPDDIIS TGNVMTLKL SDAVSTAGGF 240
QIKYVAMPDV SKSSQGNKTS TTSTGNKNFL AGRFSL

Seq ID NO: 214 Protein sequence
Protein Accession #: NP_009046.1
1 11 21 31 41 51
| | | | |
35 MIILYLFLL LWEDTQGWGF KDGIFHNSIW LERAAGVYHR EARSQKYKLT YAEAKAVCEF 60
EGGHLATYKQ LEAARKIGFH VCAAGWMAKG RVGYPIVKPG PNCXPGKTGI IDYGIRLNRS 120
ERWDAYCYNP HAKECGGVFT DPKRIFKSPG FPNEYEDNQI CYWHIRLKYG QRIHLSFLDF 180
40 DLEDDPGCLA DYVEIYDSYD DVHGFVGRYC GDELPPDDIIS TGNVMTLKL SDAVSTAGGF 240
QIKYVAMPDV SKSSQGNKTS TTSTGNKNFL AGRFSL

Seq ID NO: 215 Protein Sequence
Protein Accession #: NP_006389.1
1 11 21 31 41 51
| | | | |
45 MAPNASCLCV HVRSEWDLN TFDANPYDSV KKIKEHVRSK TKVPVQDQVL LLGSKILKPR 60
RSLSSYGIQK EKTIIHLTKV VKPSDEELPL FLVESGDEAK RHLLQVRRSS SVAQVKAMIE 120
TKTGIIPETQ IVTCNGKRL DGMAMADYGI RKGNNLLFLAS YCIGG 165

50 Seq ID NO: 216 Protein Sequence
Protein Accession #: NP_002349.1
1 11 21 31 41 51
| | | | |
55 MALQLSREQG ITLRGSAEIV AEFFSFGINS ILYQRGIYPS ETFTRVQKYG LTLVTTDL 60
LILYLANVVE QLKDWLYKCS VQKLVVVISN IESGEVLERN QFDIECDKTA KDSAPREKS 120
QKAIQDEIRS VIRQITATVT FLPLLEVSCS FDLIYTDKD LVVPEKWEES GPQFITNSEE 180
VRLRSFTTTI HKVNSMVAYK IPVND 205

60 Seq ID NO: 217 Protein sequence
Protein Accession #: NP_001889.1
1 11 21 31 41 51
| | | | |
65 MAQYLSTLLL LLATLAVALA WSPKEEDRII PGGIYNADLN DEWVQALHF AISEYNKATK 60
DDYYRRPLRV LRARQQTGG VNYFFDVEVG RTICTKSQPN LDTCAFHEQP ELQKQQLCSF 120
EIEYEVWENR RSLVKSRCQE S

70 Seq ID NO: 218 Protein sequence
Protein Accession #: NP_009162.1
1 11 21 31 41 51
| | | | |
MDKLKCPSPF KCREKEKVA SSENHVGGEN DENQDRGNWS KKS DYLLSMI GYAVGLGNVW 60
RFPYLYSNG GGAFLIPYAI MLALACLPLF FLECSLQQA SLGPVSVWRI LPLFQGVGIT 120
MVLISIFVTI YYNVIAIYSL YYMFASFQSE LPWKNCSWS DKNCRSPIV THCNVSTVVK 180
75 GIQEIIMNK SWDINNFTC INGSEIYQPG QLPSEYWNK VALQRSSGMN ETGVIVHYLA 240
LCLLLAWLIV GAALFKGKIS SGKVYFTAL FPVYVLLILL VRGATLEGAS KGISYYIGA 300
SNFTKLKAE VWKDAATQIF YLSVAHGGL VALSSYNKFK NNCPSDAIVV CLTNCLTSVF 360
AGFAIFSILG HMAHISGKEV SQVVKSGFDL AFIAYPEALA QLPGGPFWSI LFFFMLLTLG 420
LDSQFASIEI ITTTIQDLFP KVMKKMRVPI TLGCCLVLF LGLVCVTQAG IYVWHLIDHF 480
80 CAGWGLIAA ILELVGIMI YGGRNFIEDT EMMIGAKRWI FMLWWRACWF VITPILLIAI 540
FIWSLVQFHR PNYGAIPYD WGVALGWCHI VFCIIWIPIM AIIKIIQAKG NIFQRLISCC 600
RPASNWGPYL BQHRGERYKD MVDPKKADH EIPTVSGSRK PE

Seq ID NO: 219 Protein sequence
Protein Accession #: NP_006389.1

| | | | | | | | |
|-----------------------------------|-------------|-------------|------------|------------|------------|------------|------|
| 5 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | MAPNASCLCV | HVRSEEDWLM | TFDANPYDSV | KKIKEHVRSK | TKVPVQDQVL | LLGSKILKPR | 60 |
| | RSLSSYGIDK | EKTIHLTLKV | VKPSDEELPL | FLVESGDEAK | RHLLQVRRSS | SVAQVKAMIE | 120 |
| | TKTGIIPEQT | IVTCNGKRLE | DGKMMADYGI | RKGNLLFLAS | YCIGG | | |
| Seq ID NO: 220 Protein sequence | | | | | | | |
| Protein Accession #: XP_094741.1 | | | | | | | |
| 10 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | MKANYSAEER | FLLLGPSDWP | SLQPVLFALV | LLCYLLTLTG | NSALVLLAVR | DPRLHTPMYY | 60 |
| | FLCHLALVDA | GFTTSVVPPL | LANLRGPALW | LPRSHCTAQL | CASLAIGSAE | CVLLAVMALD | 120 |
| | RAAAVCRPLR | YAGLVSPRLC | RTLASASWLS | GLTNSVAQTA | LLAERPLCAP | RLLDHFCICL | 180 |
| 15 | PALLKLACGG | DGDTTENQMF | AARVVILLPL | FAVILASYGA | VARAVCCMRP | SGRRRAVGT | 240 |
| | CGSHLTAVCL | FYGSATYTYL | QPAQRYNQAR | GKPVSLFTTV | VTPALNPLIY | TLRNQKVKGK | 300 |
| | ARRLRLSLGR | GQAGQ | | | | | |
| Seq ID NO: 221 Protein Sequence | | | | | | | |
| Protein Accession #: NP_061155.1 | | | | | | | |
| 20 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | MDPFTEKLE | RTRARRENLO | RMAERPTAA | PRSMTHAKRA | RQPLSEASNQ | QPLSGGEEKS | 60 |
| | CTKPSPSKKR | CSDNTEVEVS | NLENKQPVES | TSAKSCSPSP | VSPQVQPOAA | DTISDSVAVP | 120 |
| 25 | ASLLGMRRLG | NSRLKATAAS | SVKTRMQKLA | EQRRRWNDND | MTDDIPESSL | FSPMPSEEKA | 180 |
| | ASPPKPLLNS | ASATPVGRRG | RLANLAATIC | SWEDDVNHSP | AKQNSVQEQP | GTACLKSFSS | 240 |
| | ASGASARINS | SSVKQEAATFC | SQRDGDASLN | KALSSSADDA | SLVNASISSS | VKATSPVKST | 300 |
| 30 | TSITDAKSC | QNPPELLPKT | PISPLKTGVS | KPIVKSTLSQ | TVPSKGELSR | EICLQSQSKD | 360 |
| | KSTTPGGTGI | KPFLERFGER | CQHSKESPA | RSTPHRTPII | TPNTKAIQER | LFKQDTSSST | 420 |
| | THLAQQLKQE | RQKELACLGR | RFDKGNWSA | EKGNSKSKQ | LETQETHCQ | STPLKKHQGV | 480 |
| 35 | SKTQSLPVT | KVTENQIPAK | NSSTEPKGF | ECMTKSSPL | KITLFLEEDK | SLKVTSDPKV | 540 |
| | EQKIEVIREI | EMSVDDDDIN | SSKVINDLFS | DVLEEGELDM | EKSQEQMDQA | LAESSEEQED | 600 |
| | ALNISSMSLL | APLAQTVGVV | SPESLVSTPR | LELKDTSRSD | ESPPGKGFQR | TRVPRAESGD | 660 |
| 40 | SLGSEDRDLL | YSIDAYRSQR | FKETERPSIK | QVIVRKEDVT | SKLDEKNAF | PCQVNIKQKM | 720 |
| | QELANNEINMO | QTVIYQASQA | LNCCVDEEHG | KGSLEEAEAE | RLLLIATGKR | TLIDELNKL | 780 |
| | KNEGPRKRNK | ASPOSEFMPS | KGSVTLSEIR | LPLKADFVCS | TVQKPDAAHY | YYLIILKAGA | 840 |
| 45 | ENMVATPLAS | TSNSLNGDAL | TFTTFTLQD | VSNDFEINIE | VYSLVQKKDP | SGLDKKKTS | 900 |
| | KSKAITPKRL | LTSITTKSNI | HSSVMASPGG | LSAVRTSNFA | LVGSYTLSSS | SVGNTKFXLD | 960 |
| | KVPFLSSLEG | HIYLKIKCOV | NSSVEERGFL | TIFEDVSGFG | AWHRRWCVL | GNCISYNTYP | 1020 |
| 50 | DDEKRNKPIG | RINLANCTSR | QIEPANREFC | ARRNTFELIT | VRPQREDDRE | TLVSQCRDYL | 1080 |
| | CVTKNWLSAD | TKEERDLWMO | KLNQVLVDIR | LWQPDACYKP | IGKP | | 1124 |
| Seq ID NO: 222 Protein Sequence | | | | | | | |
| Protein Accession #: Q9H8V3 | | | | | | | |
| 45 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | MAENSVLTST | TGRTSLADSS | IFDSKVTEIS | KENLLIGSTS | YVEEEMPQIE | TRVILVQEAG | 60 |
| | KQEELTKALK | DIKGVGVKME | SVEEFGELDS | PEFENVFVVT | DFQDSVFNDL | YKADCRVIGP | 120 |
| 50 | PVVLNCSQKG | EPLPFSCRPL | YCTSMNLVL | CFTGFRKKEE | LVLRLTLVHH | MGGVIRKDFN | 180 |
| | SKVTHLVANC | TQGEKFRVAV | SLGTPIMKPE | WIYKAWERRN | EQDFYAAVDD | FRNEFKVPFP | 240 |
| | QDCIFSLFGF | SDEEKTNME | MTEMQGGKYL | PLGDERCTHL | VVEENIVKDL | PFEPSSKLYV | 300 |
| 55 | VKQEWFWGSI | QMDARAGETM | LYEKANTPE | LKKSVMLSL | NTFNSNRKRR | RLKETLAQLS | 360 |
| | RDTDVSPPPP | RKRPASAEHSL | SIGSLDLISN | TPSEINSYGD | TPKSTCKSSK | SSTPVPSKQS | 420 |
| | ARWQVAKELY | QTESNYVNIL | ATIIQLFQVP | LEEEGQGRGP | ILAPEEIKTI | FGSIDPIDFV | 480 |
| 60 | HTKIKDDLED | LIVNWDESKS | IGDIFLKYSK | DLVKTYPPFV | NFFEMSKETI | IKCEKQKPRF | 540 |
| | HAFLKINQAK | PEGCRQSIVE | LLIRPVQRLP | SVALLLNDLK | KHTADENPDK | STLEKAIGSL | 600 |
| | KEVMTHINED | KRKTEAQKI | FDVVYEVDGC | PANLLSSHRS | LVORVETISL | GEHPCDRGEQ | 660 |
| 65 | VTLFLFNCLC | BIARKRHKVI | GTFRSPHGQT | RPPASLKHHI | LMPLSQIKKV | LDIRETEDCH | 720 |
| | NAPALLVRPP | TEQANVLLSF | QMTSDELPKE | NWLKMLCRHV | ANTICKADAE | NLIYTADPES | 780 |
| | FEVNTKDMDS | TLRSASRAIK | KTSKKVTRAF | SFSKTPKRAL | RRALMTSHGS | VEGRSPSSND | 840 |
| | KHVMRLSST | SSLAGIPSPS | LVSLPSFFER | RSHTLSRSTT | HLI | | 883 |
| Seq ID NO: 223 Protein Sequence | | | | | | | |
| Protein Accession #: NP_002488.1 | | | | | | | |
| 65 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | MPSRAEDYEV | LYTIGTGSYG | RCQKIRKSD | GKILVWKELD | YGSMTAEAKQ | MLVSEVNLLR | 60 |
| | ELKHPNIVRY | YDRIIDRTNT | TLIYVMEYCE | GGDLASVITK | GTKERQYLDE | EFVLRVMTQL | 120 |
| 70 | TLALKKECHRR | SDGQHTVLHR | DLKPANVFLD | GKQNVKLQDF | GLARILNHDT | SFAKTAVGTP | 180 |
| | YMSPEQMNR | MSYNEKSDIW | SLGCLLYELC | ALMPPTAFS | QKELAGKIRE | GKFRPIPYRY | 240 |
| | SDELNEIITR | MLNLKDYHRP | SVEEILENPL | IADLVADEQR | RNLERRGRQL | GEPEKSQDSS | 300 |
| 75 | PVLSLKLKE | IQLOQERERL | KAREERLEQK | EQELCVRERL | AEDKLARAEN | LLKNYSLLKE | 360 |
| | RKFLSLASNP | ELLNLPSVSI | KKKVHFSGES | KENIMRSNS | ESQLTSKSKC | KDLKKRLHAA | 420 |
| | QLRAQALSDI | EKNYQLKSRQ | ILGMR | | | | 445 |
| Seq ID NO: 224 Protein Sequence | | | | | | | |
| Protein Accession #: Eos sequence | | | | | | | |
| 80 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | DISYENENYN | SSWIPGSHIV | SPSLLNLNN | GQLLPLOLQG | PLNSWIPFSS | GILQOQQQAQ | 60 |
| | IPGLSQFSL | ALDQFAGLLP | NQIPLTGEAS | FAQGAQAGQV | DPLQLQTPPQ | TQPGSHVMP | 120 |
| 85 | YVFSFKMPQE | QQQMFQYYPV | YMLVPWEQPP | QTVPRSPQQT | RQQQYEEQIP | FYAQPGYIPQ | 180 |
| | LAEPALSGGG | QQALFDPQLG | TAPEIAVMST | GEEIPYLQKE | AINFRHDSAG | VFMPSTSPKP | 240 |
| | STTNVFTSAV | DQTIITPELPE | EKDKTDSIRE | P | | | 271 |

Seq ID NO: 225 Protein Sequence
Protein Accession #: eos sequence

5 1 11 21 31 41 51
| | | | |
RGEKHSRMV QIFLFRSRK IYHTMKIII LLGFLGATLS APLIPQRLMS ASNSNELLN 60
LNNGQLLPQ LQGPLNSWIP PFSGLQQQQ QAQIPGLSQF SLSALDQFAG LLPNQIPLTG 120
EASFAQQA QGVDPQLQT PPQTQPGPSH VMPYVFSFKM PQEQGQMFQY YPVYMLPWE 180
10 PQQTVPRSP QTRTQQQYEE QIPFYAQFGY IPQLAEPAS GQQQLAFDP QLGTAPETIAV 240
MSTGEEIPYL QKEAIFNRHD SAGVFMPSST PKPSTTNVFT SAVDQITITPE LPEEKDKTDS 300
LREP 304

Seq ID NO: 226 Protein Sequence
Protein Accession #: NP_003970.1

15 1 11 21 31 41 51
| | | | |
MATTVPDGR NGLSKYYRL CDKAEAWGIV LETVATAGVV TSVAFMLTL ILVCKVQDSN 60
RRKMLTQPL FLGLVGLIFG LTFAPILGLD GSTGPTRFLL FGILFISICFS CLLAHAVSLT 120
KLVRGRKPLS LLVILGLAVG FSLVQDVIAI EYIVLTNRT NVNVFSELSA PRNRNDFVLL 180
20 LTYVLFMLAL TFLMSSFTFC GSFTGWRHG AHYILTMLS IAIWVANITL LMLPDFDRRW 240
DDTILSSALA ANGWVFLLAY VSPFVLLTK QRNPMQYVPE DAFCKPQLVK KSYGVENRAY 300
SQEETQCFE ETGDTLYAPY STHFQLQNQP PQKEFSIPRA HAWPSYKDY EVKKEGS 357

Seq ID NO: 227 Protein Sequence
Protein Accession #: NP_116575.1

25 1 11 21 31 41 51
| | | | |
MPKIVLNGVT VDFPFQPYKC QQEYMTKVLE CLQQKVNGL ESPTGTGKTL CLLCTTLAWR 60
EHLRDGISAR KIAERAQGL FPDRLSSWG NAAAAAGDPI ACYTDIPKII YASRTHSOLT 120
30 QVINELRNTS YRPKVCVLGS RQQLCIHPEV KQESNHLQI HLCRKKVASR SCHFYNNVEE 180
KSLEQELASP ILDIEDLVKS GSKHRVCPYY LSRNLKQAD IIFMPYNYLL DAKSRRAHNI 240
DLKGTVVIFD EAHNVKMCCE ESASFOLDTPH DLASGLDVID QVLEEQTAA QQGEHPPEFS 300
ADSPSPGLNM ELEDIAKLKM ILLRLEGAID AVELPGDDSG VTKPGSYIFE LFAEAQITFQ 360
35 TKGCILSLD QIIQHLGRA GVFTNTAGLQ KLADIIQIVF SVDPSGSPG SPAGLGALQS 420
YKVHIHPDAG HRTTAQRSDA WSTTAARKRG KVLSYNCFSP GHSMHLEVRQ GVRSLILTS 480
TLAPVSSPAL EMQIPFPVCL ENPHIIDKHQ IWGVVPRGP DGAQLSSAFD RRFSEELSS 540
LGKALGNIR VVPYGLLIFF PSYPVMEKSL EFWARDLAR KMEALKPLFV EPRSKGSFSE 600
TISAYARVA APGSTGATFL AVCRGKASEG LDFSOTNCRG VIIVTGLPYPP RMDPRVVLKM 660
40 QFLDEMKGQ GAGGQFLSGQ EYRQASRA VNQAIGRVIR HRQDYGAVFL CDHRFAFADA 720
RAQLPSWVRP HVRVYDNFGH VIRDAQFFR VAERTMPAPA PRATAPSVRG EDAVSEAKSP 780
GPFFSTRKAK SLDLHVP SLK QRSAGSPAAG DPESLCEVEY EQEPVPARQR PRGLLALEH 840
SEQRAGSPGE EAHNSCSTLS LLSEKPAEE PRGGRKKIRL VSHPEEPVAG AQTDRAKLFM 900
VAVKQELSQA NFATFTQALQ DYKGSDDFAA LAACLGPLFA EDPKKNLLQ GFYQFVRPHH 960
45 KQQFEVCIC LTGRGCGYRP EHSIPRRQRA QVLDPTGRT APDPKLTVST AAAQQLDPOE 1020
HLNQGRPHLS PRPPPTGDPG SQPQWGSVP RAGKQGHAV SAYLADARRA LGSAGCSQLL 1080
AALTAYKQDD DLQKVLAVLA ALTTAKPEDF PLLHRFSMFV RPHHKQRFQ TCTDLTGRPY 1140
PGMEPPGPQE ERLAVPPVLT HRAPOGPSPR SEKTGKTQSK ISSFLRQSPA GTVGAGGEDA 1200
GPSQSSGPPH GPAASEWGL HGRDIAGQQA TCAPGGPLSA GCVCQCGGAE DVVPFQCPAC 1260
50 DPQRQCAWQ RHLQASRMCP ACHTASRKQS VMQVFWPEPH KDHEGAGGAR PVAAPVGUGA 1320
ACPAAGAGCT RSGRNLHPL AGRDRGAAG VCFVPPRHLC AAAPVPRQPH DVMPVSTAPL 1380
HAVLELPGAL PLLQPLRGA 1400

Seq ID NO: 228 Protein Sequence
Protein Accession #: NP_057518.1

55 1 11 21 31 41 51
| | | | |
MPKIVLNGVT VDFPFQPYKC QQEYMTKVLE CLQQKVNGL ESPTGTGKTL CLLCTTLAWR 60
EHLRDGISAR KIAERAQGL FPDRLSSWG NAAAAAGDPI ACYTDIPKII YASRTHSOLT 120
60 QVINELRNTS YRPKVCVLGS RQQLCIHPEV KQESNHLQI HLCRKKVASR SCHFYNNVEE 180
KSLEQELASP ILDIEDLVKS GSKHRVCPYY LSRNLKQAD IIFMPYNYLL DAKSRRAHNI 240
DLKGTVVIFD EAHNVKMCCE ESASFOLDTPH DLASGLDVID QVLEEQTAA QQGEHPPEFS 300
ADSPSPGLNM ELEDIAKLKM ILLRLEGAID AVELPGDDSG VTKPGSYIFE LFAEAQITFQ 360
35 TKGCILSLD QIIQHLGRA GVFTNTAGLQ KLADIIQIVF SVDPSGSPG SPAGLGALQS 420
YKVHIHPDAG HRTTAQRSDA WSTTAARKRG KVLSYNCFSP GHSMHLEVRQ GVRSLILTS 480
TLAPVSSPAL EMQIPFPVCL ENPHIIDKHQ IWGVVPRGP DGAQLSSAFD RRFSEELSS 540
LGKALGNIR VVPYGLLIFF PSYPVMEKSL EFWARDLAR KMEALKPLFV EPRSKGSFSE 600
TISAYARVA APGSTGATFL AVCRGKASEG LDFSOTNCRG VIIVTGLPYPP RMDPRVVLKM 660
40 QFLDEMKGQ GAGGQFLSGQ EYRQASRA VNQAIGRVIR HRQDYGAVFL CDHRFAFADA 720
RAQLPSWVRP HVRVYDNFGH VIRDAQFFR VAERTMPAPA PRATAPSVRG EDAVSEAKSP 780
GPFFSTRKAK SLDLHVP SLK QRSAGSPAAG DPESLCEVEY EQEPVPARQR PRGLLALEH 840
SEQRAGSPGE EAHNSCSTLS LLSEKPAEE PRGGRKKIRL VSHPEEPVAG AQTDRAKLFM 900
VAVKQELSQA NFATFTQALQ DYKGSDDFAA LAACLGPLFA EDPKKNLLQ GFYQFVRPHH 960
45 KQQFEVCIC LTGRGCGYRP EHSIPRRQRA QVLDPTGRT APDPKLTVST AAAQQLDPOE 1020
HLNQGRPHLS PRPPPTGDPG SQPQWGSVP RAGKQGHAV SAYLADARRA LGSAGCSQLL 1080
AALTAYKQDD DLQKVLAVLA ALTTAKPEDF PLLHRFSMFV RPHHKQRFQ TCTDLTGRPY 1140
PGMEPPGPQE ERLAVPPVLT HRAPOGPSPR SEKTGKTQSK ISSFLRQSPA GTVGAGGEDA 1200
75 GPSQSSGPPH GPAASEWGL 1219

Seq ID NO: 229 Protein Sequence
Protein Accession #: NP_056462.1

80 1 11 21 31 41 51
| | | | |
MPAPAPRATA PSVRGEDAVS EAKSPGPFFS TRKAKSLDLH VPSLKQRSSG SPAAGDPSS 60
LCVEYEQEPV PARQPRGLL AALEHSEORA GSPGEEQAHS CSTLSLLSEK RPAEEPRGGR 120

5 KKIRLVSHPE EPVAGATQDR AKLFMVAVKQ ELSQANFATF TQALQDYKGS DDFAALAACL 180
 GPLFAEDPKK HNLQGFYQF VRPHKQKFE EVCIQLTGRG GGYRPEHSIP RRQRAQPVLD 240
 PTGRTAPDFK LTVSTAAQ LDPQEHNLQG RPHLSRPPPP TGDGPGSQPW GSGVPRAGKQ 300
 QHAVASAYLA DARRALGSAG CSQLLAALTA YKQDDLDKV LAVLAALTTA KPEDFPLLHR 360
 FSMFVRPHHK QRSQTCTDL TGRPYPGMEP PGQOEERLAV PPVLTHRAPO PGPSRSEKTK 420
 KTQSKISSLF RQRPAITVGA GGEDAGPSQS SGPPHGPAAS EWGEPHGRDI AGQATGAPC 480
 GPLSAGCVQ CCGAEDVVPF QCPACDFQRC QACWQRHLQA SRMCPACHTA SRKQSVMQVF 540
 WPEPQ 545

10 Seq ID NO: 230 Protein Sequence
 Protein Accession #: NP_003814.1

1 11 21 31 41 51
 | | | | |
 15 MRALEGPGLS LLCLVLALPA LLPVPAVRGV AETPTYPRWD AETGERLVCA QCPPGTFVQR 60
 PCRRDSPPTC GPCPPRHYTQ FWNLYERCRY CNVLCGEREE EARACHATHN RACRCRTGFF 120
 AHAGFCLEHA SCPPGAGVIA PGTPSQNTQC QCPPGTFPSA SSSSSEQCQP HRNCTALGLA 180
 LNVPGSSSDH TLCTSTCTGFP LSTRVPGAEE CERAVIDFVA PQDISIKRLQ RLLQALEAPE 240
 GWGPTPRAGR AALQKLKRRR LTELGAQDG ALLVRLQLAL RVARMPGLER SVRERFLPVH 300

20 Seq ID NO: 231 Protein Sequence
 Protein Accession #: NP_116563.1

1 11 21 31 41 51
 | | | | |
 25 MRALEGPGLS LLCLVLALPA LLPVPAVRGV AETPTYPRWD AETGERLVCA QCPPGTFVQR 60
 PCRRDSPPTC GPCPPRHYTQ FWNLYERCRY CNVLCGEREE EARACHATHN RACRCRTGFF 120
 AHAGFCLEHA SCPPGAGVIA PGTPSQNTQC QCPPGTFPSA SSSSSEQCQP HRNCTALGLA 180
 LNVPGSSSDH TLCTSTCTGFP LSTRVPGAEE CERAVIDFVA PQDISIKRLQ RLLQALEAPE 240
 GWGPTPRAGR AALQKLKRRR LTELGAQDG ALLVRLQLAL RVARMPGLER SVRERFLPVH 300

30 Seq ID NO: 232 Protein Sequence
 Protein Accession #: NP_000584.2

1 11 21 31 41 51
 | | | | |
 35 MAELLASAGS ACSWDFPRAP PSFPPPAASR GGLGGTRSFH PHRGAESPRP GRDRDGVVRP 60
 MASSRCAPAP GCRCLPGASL AMLGTIVLLL ADWVLLRTAL PRIFSLVET ALPLLVRVAV 120
 GLSRWAVLWL GAGCVLRATV GSKSENAGAQ GWLAALKPLA AALGLALPGL ALFRELISWG 180
 APGSADSTRL LHMGSHTAF VVSYAAALPA AALWHKLGSL WVPGGQGGSG NPVRRLLGCL 240
 GSETRRLSLF LVLVLSLGL EMAIPFTTGR LTDWILQDGS ADTFTNRLTL MSILTIASAV 300
 LEFVGDIYN NTMGHVHSHL QGEVFGAVLR QETEFQOQNG TGNIMSRVTE DTSTLSDLSL 360
 40 ENLSLFLWYL VRGLCLLIGM LMGSVSLTMV TLITLPLLEL LPKKVKGWYQ LLEVQVRESL 420
 AKSSQVAIEA LSAMPTVRSF ANEEGEAQKF REKIQEIKTL NQKEAVAYAV NSWTTISISM 480
 LLKVGLIYIG GQLVTSAGVS SGNLVTFLVY QMQFTQAVEV LLSIYPRVQK AVGSSEKIFE 540
 YLDRTPRCPP SGLLTPLHLE GLVQFQDVSE AYPNRPDVLV LQGLTFTLRP GEVTALVGNP 600
 GSGKSTVAAL LQNLVQFTGG QLLDGKPLP QYEHRYLHRQ VAAVGQEPQV FGRLSQENIA 660
 45 YGLTQKPTME EITAAAVKSG AHSFISGLPQ GYDTEVDEAG SOLSGGQRA VALARALIRK 720
 PCVLILDDAT SALDANSQIQ VEQLLYESPE RYSRSVLLIT QHLSLVEQAD HILFLEGGAI 780
 REGGTHQQLM EKGCTWAMV QAPADAPE 808

50 Seq ID NO: 233 Protein Sequence
 Protein Accession #: NP_002414.1

1 11 21 31 41 51
 | | | | |
 55 MRLTVLCAVC LLPGSLALPL PQEAGGMSSEL QWEQAQDYLK RFYLYDSETK NANSLEAKLK 60
 EMQKFGFLPI TGMNLSRVIE IMQKPRCGVP DVAEYSLFPN SPKWTSKVVT YRIVSYTRDL 120
 PHITVDRLVS KALNMWKEI PLHFRKVWVG TADIMIGFAR GAHGDSYFPD GPGNTLAHAF 180
 APGTGLGDA HFDEDERWTD GSSLGINFLY AATHELGHSL GMHGSSDPNA VMYPTYGND 240
 PQNFKLSQDD IKGIQKLYGK RNSRKK 267

60 Seq ID NO: 234 Protein Sequence
 Protein Accession #: NP_061144

1 11 21 31 41 51
 | | | | |
 65 MPPIEVCKIK FAEEDAKPKE KEAGDEQSLG GAVAPGAAPR DLATFASTST LHGLGRACGP 60
 GPHGLRRTLW ALALLTSLAA FLYQAAGLAR GYLTRPHLVA MDPAPAPVA GFPAVTLQNI 120
 NFRHSAISLD ADIFHLANLT GLPPKDRDGH RAAGLRYPEP DMVDILNRTG HQLADMLKSC 180
 NFSGHHCAS NFSVYTRYG KCYTFNADPR SSLPSRAGGH GSGLEIMLDI QQEYLPINR 240
 ETNETSFEG IRVQHSQEE PPYIHQLGFG VSPGFQTFVS CQEQLRTYLP QPWGNCRAES 300
 ELREPELQGY SAYSVSACRL RCEKEAVLQR CHCRMVHMPG NETICPPNIY IECADHTLDS 360
 LGGPGEPCFP CFTPCNLTRY GKEISMVRIP NRGSAARYLAR KYNRNETYIR ENFLVDVFF 420
 70 EALTSEAMEQ RAAYGLSALL GDLGGQMGFL IGASILTLE ILDYIYEVSW DRLKRVWRRP 480
 KTPLRTSTGG ISTLGLQELK EQSPCPSLGR AEGGGVSSLL PNHHHPHGPP GGLFEDFAC 539

75 Seq ID NO: 235 Protein Sequence
 Protein Accession #: BAC03567

1 11 21 31 41 51
 | | | | |
 80 MEVSSPSPAQ RLRRKKRPMV QGPAGCQVFQ PSPSGGTAGD PGGLSDPFYP PRSGSLALGD 60
 PSSDPACSQS GPMEAEEDSL PEQPEDSAQL QQEKPSLYIG VRGTVVRSMQ EVLWTRLREL 120
 PDPVLSEEVV EGIAAGIEAA LWDLTQGTNG RYKTKYRSL FNLDRPNLD LFLKVHVGDD 180
 TPYDLVRMSS MQLAPQELAR WRDQEEKRGL NIIEQQQKEP CRLPASKMTH KGEVEIQRDM 240
 DQTLTLEDLV GPQMFMDSCP QALPIASEDT TGQHDHFFLD PNCHICKDWE PSNELLGSFE 300
 AAKSCGDNIF QKALSQTPMP APEMPKTREL SPTEPQDRVP PSGLHVPAAP TKALPLCPW 360
 EGVLDMSFIK RFRARAQLVS GHSCRLVQAL PTVIRSAGCI PSNIVMDLLA SICPAKADV 420
 CVVRLCPHGA RDTQNCRLLY SYLNDQRHG LASVEHMGWV LLPLPAFQPL PTRLRPLGGP 480

| | | | | | | | | |
|----|--|----------------------------------|-------------|-------------|-------------|-------------|-------------|-----|
| | | GLEVTHSSLL | LAULLPKKEGL | PDTAGSSPWL | GKVQKMVSFN | SKVEKRYYP | DDRRPNVPLK | 540 |
| | | GTPPPGGAWQ | QSQGRGSIAP | RGISAWQRP | RGRGRWLWPEP | ENWQHPRGQ | WPPEPGLRQS | 600 |
| | | QHPYSPVAPG | HGFGRGQHFH | RDSCPHQALL | RHLESATMS | HQLQALLCPQ | TKSSIPRPLQ | 660 |
| | | RLSSALAAPE | PPGPARDSSL | GPTDEAGSEC | FFPRKA | | | 696 |
| 5 | | Seq ID NO: 236 Protein Sequence | | | | | | |
| | | Protein Accession #: NP_005282 | | | | | | |
| | | 1 | 11 | 21 | 31 | 41 | 51 | |
| 10 | | MSKRSWWAGS | RKPPREMLKL | SGSDSSQSMN | GLEVAPPGLI | TNFSLATAEQ | CGQETPLENM | 60 |
| | | LFASFYLLDF | ILALVGNLTA | LWLFIRDHKS | GTPANVFLMH | LAVADLSCVL | VLPTRLVYHF | 120 |
| | | SGNHWPFGEI | ACRLTGFLPY | LNMYASIFYL | TCISADRFLA | IVHPVKSLLK | RRPLYAHLAC | 180 |
| | | AFLLVVVAVA | MAPLLVSPQT | VQTNHTVVCL | QLYREKASHH | ALVSLAVAPT | FPFITVTVCY | 240 |
| 15 | | LLIIRSLROG | LRVEKRLKTK | AVRMIAIVLA | IFLVCFVPYH | VNRSVYVLHY | RSHGASCATQ | 300 |
| | | RILALANRIT | SCLTSLNGAL | DPIMYFFVAE | KFRHALCNLL | CGKRLKGPPP | SFEGKTNES | 360 |
| | | LSAKSEL | | | | | | 367 |
| | | Seq ID NO: 237 Protein Sequence | | | | | | |
| | | Protein Accession #: NP_061113 | | | | | | |
| | | 1 | 11 | 21 | 31 | 41 | 51 | |
| 20 | | MRKTRLWGLL | WMLFVSELRA | ATKLTEEKYE | LKEGQTLQVK | CDYLEKFA | SQKAWQIIRD | 60 |
| | | GEMPKTLACT | ERPSKNSHPV | QVGRILEEDY | HDHGLLRVRM | VNLQVEDSGL | YQCVIYQPPK | 120 |
| 25 | | EPHMLFDIIR | LVTYKGFSTQ | PGSNENSTON | VYKIPPTTK | ALCELYTSPR | TVTQAPPKST | 180 |
| | | ADVSTPDSEI | NLTNVTDIIR | VPVFNIVILL | AGGFLSKSLV | FSVLFAVTLR | SFVP | 234 |
| | | Seq ID NO: 238 Protein Sequence | | | | | | |
| | | Protein Accession #: NP_003458 | | | | | | |
| | | 1 | 11 | 21 | 31 | 41 | 51 | |
| 30 | | MEGISIYTSD | NYTEEMSGSD | YDSMKKEPCFR | EENANFNKIF | LPTIYSIIFL | TGIVGNGLVI | 60 |
| | | LVMGYQKKLR | SMTDKYRLHL | SVADLLFVIT | LPFWAVDAVA | NWYFGNPLCK | AVHVIYTVNL | 120 |
| | | YSSVLILAFI | SLDRYLAIHV | ATNSQRPRKL | LAEKVVYVGV | WIPALLLTIP | DFIFANVSEA | 180 |
| 35 | | DDRYICDRFY | PNDLWVVVFQ | FQHMVGLIL | PGIVILSCYC | IIISKLSHSK | GHQKRKALKT | 240 |
| | | TVILILAFFA | CWLPYYIGIS | IDSFILLEII | KQGCDEFNTV | HKWISITEAL | APFFHCCLNPI | 300 |
| | | LYAFILGAFK | TSQAHALTSV | SRGSSSLKILS | KGKRGGHSSV | STESSESSFH | SS | 352 |
| | | Seq ID NO: 239 Protein Sequence | | | | | | |
| | | Protein Accession #: NP_036338.1 | | | | | | |
| | | 1 | 11 | 21 | 31 | 41 | 51 | |
| 40 | | MHPQVILSL | ILHLADSVAG | SVKVGGEAGP | SVTLPCHYSG | AVTSMCWNRG | SCSLFTQONG | 60 |
| | | IWNTNGTHVT | YRKDTRYKLL | GDLSRRDVS | TIENTAVSDS | GVYCCRVEHR | GWFNDMKITV | 120 |
| | | SLBIVPPKFI | TPTIVTIVPT | VTTVRTSTIV | PTTTTVPIT | VPTIMSIPIT | TIVPTMTVS | 180 |
| 45 | | TTISVPTTIS | IPITTSVPVT | TTVSTFVPPM | PLPRQNHPEV | ATSPSSSQPA | ETHPTTLQGA | 240 |
| | | IRREPTSSPL | YSYTTDGNIT | VTSSDGLWN | NNQTQLFLEH | SLLTANTTKG | IYAGVCISVL | 300 |
| | | VLLALGLVII | AKKYFFKKEV | QQLSVSFSSL | QIKALQNAVE | KEVQAEDNIY | IENSLYATD | 359 |
| | | Seq ID NO: 240 Protein Sequence | | | | | | |
| | | Protein Accession #: NP_004923.1 | | | | | | |
| | | 1 | 11 | 21 | 31 | 41 | 51 | |
| 50 | | MRTYRYFLLL | FWVGQPYPTL | STPLSKRTSG | FPAKKRALEL | SGNSKNELNR | SKRSWMWNOF | 60 |
| | | FLLEEYTGSD | YQYVGKLHSD | QDRGDGSLKY | ILSGDGAGDL | FIINENTGDI | QATKRLDREE | 120 |
| 55 | | KPVYILRAQA | INRRTGRPVE | PESEFIKIH | DINDNEPIFT | KEYVTATVPE | MSDVGTFFVQ | 180 |
| | | VTATADDDPT | YGNSAKVVS | ILQGQPYFSV | ESETGIIKTA | LLNMDRENRE | QYQVVIQAKD | 240 |
| | | MGGQMGGLSG | TTTVNITLTD | VNDNPPRFPO | STYQFKTPES | SPPGTPIGRI | KASDADVGEN | 300 |
| | | AETEYSITDG | EGLDMFDVIT | DQETQEGIIT | VKKLLDFEKK | KVYTLKVEAS | NPYVEPRFLY | 360 |
| 60 | | LGPFFKDSATV | RIVVEDVDEP | PVFSKLAYIL | QIREDAQINT | TIGSVTAQDP | DAARNPVKYS | 420 |
| | | VDRHTDMORI | FNIDSGNGSI | FTSKLLDRET | LLWHNITVIA | TEINNPKQSS | RVPLYIKVLD | 480 |
| | | VNDNAPEFAE | FYETFVCEKA | KADQLIQLTH | AVDKDDPYSG | HQFSFSLAPE | AASGNSFTIQ | 540 |
| | | DNKDNTAGIL | TRKNGYNRHE | MSTYLLPVVI | SDNDYPVQSS | TGTVTIVRCA | CDHHGNMQSC | 600 |
| | | HAEALHTPTG | LSTGALVAIL | LCIVILLVTV | VLFAALRRQR | KKEPLIISKE | DIRDNIVSYN | 660 |
| 65 | | DEGGGEDTQ | AFDIGTLRNP | EAIEDNKLRR | DIVPEALFLP | RRTPTARDNT | DVRDFINQRL | 720 |
| | | KENDTDPTAP | PYDSLATYAY | EGTGSVADSL | SSLESVTDA | DQDYDYLSDW | GPRFKKLADM | 780 |
| | | YGGVDSDDKS | | | | | | 790 |
| | | Seq ID NO: 241 Protein Sequence | | | | | | |
| | | Protein Accession #: BAB14227.1 | | | | | | |
| | | 1 | 11 | 21 | 31 | 41 | 51 | |
| 70 | | MRLTRRLVL | PVFGVLWITV | LLFFWVTKRK | LEVPTGPEVO | TPKVMSLFFK | VAGMSPHAPQ | 60 |
| | | VPVSPTPPYQ | RGLHPTGGHL | AVCHFPCLLQ | EAQPHLQTV | FLQVRCTLLV | YCTDLPTPTSI | 120 |
| | | IITFHNEARS | TLLRTIRSVL | NRTPTHLIRE | IILVDDFSND | PDDCKQLIKL | PKVKCLRNNE | 180 |
| 75 | | RQGLVRSRIR | GADIAQGTTL | TFLDSHCEVN | RDWLQPLLHR | VKEDYTRVVC | PVIDIINLDT | 240 |
| | | FTYIESASEL | RGGFDWSLHF | QWEQLSPEQK | ARRLDPTPEI | RTPIIAGGLF | VIDKAWFDYL | 300 |
| | | GKYDMDMDIW | GGENFEISFR | VWMCSSLEI | VPCSRVGHVF | RKXHPYVFPD | GNANTYIKNT | 360 |
| | | KRTAEVWMD | YKQYAAARP | FALERPPGNV | ESRLDLRKNL | RCQSFKWYLE | NIYPELSIPK | 420 |
| | | ESSIQKGNIR | QRQKLESQR | QNNQETPNLK | LSPCAKVKEG | DAKSQVWAPT | YTQILQEEL | 480 |
| 80 | | CLSVITLFP | APVVLVLCNK | GDDRQQWTKT | GSHIEHIA | LCLDITDMFGD | GTENGKEIVV | 540 |
| | | NPCSSLSMQ | HWMVSS | | | | | 557 |
| | | Seq ID NO: 242 Protein Sequence | | | | | | |
| | | Protein Accession #: AAH10659 | | | | | | |

| | | | | | | | |
|----|----------------------------------|-------------|------------|------------|-------------|-------------|-----|
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| | MRLRLRLVL | PVFGVLWITV | LLFFWVTKRK | LEVPTGPEVQ | TPKPSDADWD | DLWDQFDERR | 60 |
| 5 | YLNKKKRVG | DDPYKLYAFN | QRESERISSN | RAIPDTRHLR | CTLVYCTDL | PPTSIIITFH | 120 |
| | NEARSTLLRT | IRSVLNRTP | HLIREIILVD | DFSNDPDDCK | QLIKLPKVKC | LRNNRQGLV | 180 |
| | RSRIRGADIA | QGTTLTFLDS | RCEVNRDLQ | PLLRVVKEDY | TRVVCVIDI | INLDTFTYIE | 240 |
| | SASELRGGFD | WSLHFQWEQL | SPDQKARRLD | PTEPIRTPII | AGGLEFVIDKA | WFDYLGKYDM | 300 |
| | DMDIINGGFN | EISFRVVMCG | GSLEIVPCSR | VGHVFRKQHP | YVFPDGNANT | YIKNTKRTAE | 360 |
| 10 | VWMDYKQYY | YAARPFALER | PFGNVESRLD | LRKNLRCSQF | KWYLENIYPE | LSIPKESSIQ | 420 |
| | KGNIRQKQC | LESQRQNNQE | TPNLKLSPCA | KVKGEDAKSQ | VWAFYTYQOI | LQEECLQSVI | 480 |
| | TLFPAGPVVL | LSQKNGDDRQ | QWTKTGSHE | HIASHLCLDT | DMFGDGTENG | KEIVVNPCE | 540 |
| | SLMSQHWDMV | SS | | | | | 552 |
| | Seq ID NO: 243 Protein Sequence | | | | | | |
| 15 | Protein Accession #: AAH10659.1 | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| | MRLRLRLVL | PVFGVLWITV | LLFFWVTKRK | LEVPTGPEVQ | TPKPSDADWD | DLWDQFDERR | 60 |
| 20 | YLNKKKRVG | DDPYKLYAFN | QRESERISSN | RAIPDTRHLR | VLRNTPHTLI | REIILVDDFS | 120 |
| | NDPDDCKQLI | KLPKVKCLRN | NERQGLVRSR | IRGADIAQGT | TLTFLDSHCE | VNRDLWQLPL | 180 |
| | HRVKEDYTRV | VCPVIDIINL | DTFTYIESAS | ELRGGFDWSL | HFQWEQLSPE | QKARRLDOTE | 240 |
| | PIRTPIIAGG | LFVIDKAWFD | YLGKYDMDMD | IWGGENFEIS | FRVVMCGGSL | EIVPCSRVGH | 300 |
| | VFRKHPPYVF | PDGNANTYIK | NTKRTAEVWM | DEYKRYYYAA | RPFALERPFQ | NVESRLDLRK | 360 |
| | NLRQCSFKWY | LENIYPELSI | PKESSIQKGN | IRQRQKCLCS | QRQNNQETPN | LKLSPCAQVK | 420 |
| 25 | GEDAKSQVWA | FTYTYQQLQE | ELCLSVITLF | PGAPVVLVLC | KNGDDRQQWT | KTGSHIEHIA | 480 |
| | SHLCLDTDMF | GDGTENGKEI | VVNPCESSLM | SQHWDMVSS | | | 519 |
| | Seq ID NO: 244 Protein Sequence | | | | | | |
| 30 | Protein Accession #: NP_078848.1 | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| | MNGKVMSPGP | FGALTSAPRAH | SDFLDHCEV | NRDLWQLPLH | RVKEDYTRVV | CPVIDIINLD | 60 |
| | TFTYIESASE | LRGGFDWSLH | FQWEQLSPEQ | KARRLDPTPE | IRTPIIAGGL | FVIDKAWFDY | 120 |
| 35 | LGKYDMDMDI | WGGENFEISF | RVMCMGGSLE | IVPCSRVGHV | FRKKHPYVFP | DGNANTYIKN | 180 |
| | TKRTAEVWMD | EYKQYVYAA | PFALERPFQ | VESRLDLRKN | LRCQSFKNYL | ENIYPELSIP | 240 |
| | KESSIQKGN | RQRQKCLCS | RQNNQETPNL | KLSPCAKVK | EDAKSQVWAF | TYTYQQLQEE | 300 |
| | LCLSVITLFP | GAPVVLVLC | NGDDRQQWTK | TGSHIEHIA | HLCLDTDMFG | DGTENGKEIV | 360 |
| | VNPCESSLMS | QHWDMVSS | | | | | 378 |
| 40 | Seq ID NO: 245 Protein Sequence | | | | | | |
| | Protein Accession #: NP_001209.1 | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| | MRRSLHAAA | VLLLVILKEQ | PSSPAPVNGS | KWTYFGPDGE | NSWSKKYPSC | GGLLQSPIDL | 60 |
| 45 | HSDILQVDAS | LTPLEFGQYN | LSANKQFLLT | NNGHSVKLNL | PSDMHIQGLQ | SRYSATQLHL | 120 |
| | HWGNPNDPHG | SEHTVSGQHF | AAELHIVHYN | SDLYPDASTA | SNKSEGLAVL | AVLIEMGSFN | 180 |
| | PSYDKIFSHL | QHVYKQGEA | FVPGFNIEEL | LPERTAAYYR | YRGSLLTPPC | NPTVLWTVFR | 240 |
| | NPVQISQEQ | LALLETALYCT | HMDDPSPREM | INNFRQVQKF | DERLVYTSFS | QVQVCTAAGL | 300 |
| 50 | SLGIILSLAL | AGILGICIVV | VVSINLFRRK | SIKKGDNKGV | IYKPKATMET | EAAH | 354 |
| | Seq ID NO: 246 Protein Sequence | | | | | | |
| | Protein Accession #: BC000278 | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| 55 | MRRSLHAAA | VLLLVILKEQ | PSSPAPVNGS | KWTYFGPDGE | NSWSKKYPSC | GGLLQSPIDL | 60 |
| | HSDILQVDAS | LTPLEFGQYN | LSANKQFLLT | NNGHSVKLNL | PSDMHIQGLQ | SRYSATQLHL | 120 |
| | HWGNPNDPHG | SEHTVSGQHF | AAELHIVHYN | SDLYPDASTA | SNKSEGLAVL | AVLIEMGSFN | 180 |
| | PSYDKIFSHL | QHVYKQGEA | FVPGFNIEEL | LPERTAAYYR | YRGSLLTPPC | NPTVLWTVFR | 240 |
| | NPVQISQEQ | LALLETALYCT | HMDDPSPREM | INNFRQVQKF | DERLVYTSFS | QGIILSLALA | 300 |
| 60 | GILGICIVVV | VSIWLFRKRS | IKKGDNGKVI | YKPKATMETE | AHA | | 343 |
| | Seq ID NO: 247 Protein Sequence | | | | | | |
| | Protein Accession #: NP_006623.1 | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| 65 | MQVDETLPFR | KGPSLCSARY | GIALVLHFCN | FTTIAQNVIM | NITMVAMVNS | TSPQSQNLDS | 60 |
| | SEVLVPVDSFG | GLSKAPKSLP | AKSSILGGQF | AIWEKWPPO | ERSRLCSIAL | SGMLLGCFPTA | 120 |
| | ILIGGFISET | LGWPFVYFIF | GGVGCVCCLL | WFVVIYDDPF | SYPWISTSEK | EYIISLKKQ | 180 |
| | VGSSKQPLPI | KAMLRSLPIW | SICLGCFSHQ | WLVTMVVYI | PTYISSVYHV | NIRDNGLLSA | 240 |
| 70 | LPFIVAMVIG | MVGGYLDLFL | LTKKFRITV | RKIATILGSL | PSSALIVSLP | YLNCGYITAT | 300 |
| | ALLTLSCGLS | TLCQSGIYIN | VLDIAPRYSS | FLMGASRGFS | SIAPVIVPTV | SGFLLSQDPE | 360 |
| | FGWRNVFFLL | FAVNLGLLLF | YLIFGEADVQ | EWAKERKLTR | L | | 401 |
| 75 | Seq ID NO: 248 Protein Sequence | | | | | | |
| | Protein Accession #: NP_003049.1 | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| | MPTTVDDVLE | HGGEFHFQK | QMFLLALLS | ATFAPYVGI | VFLGFTPDHR | CRSPGVAELS | 60 |
| | LRCGWSPAEE | LNVTVPQGP | AGEASPRQCR | RYEVDWQST | FDCVDPLASL | DTNRSRLPLG | 120 |
| 80 | PCRDGWVYET | PGSSIVTEFN | LVCANSWMLD | LFQSSVNVGF | FIGSMSIGYI | ADRFGRKLCL | 180 |
| | LTTVLINAAA | GVLMAISPTY | TWMLIFRLIQ | GLVSKAGWLI | GYILITEFVG | RRYRTTVGIF | 240 |
| | YQVATYGLL | VLAVAYALP | HWRWLQFTVA | LPNFFFLYY | WCIPESPRWL | ISQNKNAEAM | 300 |
| | RIIKHIAKKN | GKSLPASLQR | LRLEEETGKK | LNPSFLDLVR | TPQIRKHTMI | LMYNWFTSSV | 360 |
| | LYQGLIMHMG | LACDNIYLD | FYSALVEFPA | AFMIILTIDR | IGRRYPWAAS | NMVAGAACLA | 420 |

SVFIPGDLQW LKIIISCLGR MGITMAYEIV CLVNAELYPT FIRNLGVHIC SSMCDIGGII 480
 TPFLVYRLTN IWLEPLMVF GVLGLVAGGL VLLLPETGK ALPETIEEAE NMQRPRKNKE 540
 KMIYLVQQL DIPLN 555

5

Seq ID NO: 249 Protein Sequence
 Protein Accession #: Eos sequence

1 11 21 31 41 51
 | | | | |
 MQPAIQWVFG EDLPLSPRSP LTPRHGPGLA NVCQYDEWIA VRHEATLLPM QEDLSIWLSG 60
 LLGIKVKAEK LLEELDNGVL LCQLIDVLQN MVKTCNEES GNPPMRKVPC KKDAASGSFF 120
 ARDNTANFLH WCRDYGVDET YLFESEGLVL HKDPRQVYLC LLEIGRIVSR YGVEPPVLVK 180
 LEKEIELEET LNTSGPEDS ISIPKSCCRH EELHEAVKHI AEDPPCSCSH RFSIEYLSG 240
 RYRLGDKILF IRMLHGKHMV VRVGGGWDTL QGFLLYDPC RILQFATLEQ KILAFQKGV 300
 NESVPDSPAR TPQPPENPL SAVNMFQKQN SKPSVPVSIP KSKEQGRPP GALVPASSLK 360
 GGNLGSMSVR SKLPNSPAAS SHPKLKSSKG ITKKPQAPSN NASSSLASLN PVGKNTSSPA 420
 LPRTPACISE SPRKCISSPN TPKAKVIPAQ NSADLPSTL LPNKCSGKTQ PKYLKHNHIS 480
 SRDNAVSHLA AHSNSSSKCP KLPKANIPVR PKPSFQSSAK MTKTSSKTIA TGLGTQSQPS 540
 DGAPQAKPVP AQKLKSAALN NQPVSVSVS PVKATQKSKD KNIVSATKKQ PQNKSAFQKT 600
 GPSSLKSPGR TPLSVSLPQ SSTKTQTAPK SAQTVAKSQH STKGPPRSRG TPASIRKPPS 660
 SVKADSSGDK KPTAKKEDD DHYFVMTGSK KPRK 694

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Seq ID NO: 250 Protein Sequence
 Protein Accession #: NP_001035.1

1 11 21 31 41 51
 | | | | |
 MSKSKCSVGL MSSVAPAKE PNAVGPKEVE LILVKEQNGV QLTSSLTNP RQSPVEAQR 60
 ETWKKIDFL LSVIGFAVDL ANVWRFPYLC YKNGGGAFLV PYLLPMVIAG MPLFYMLAL 120
 GQFNREGAAG VWKICPILKG VGPTVILISL YVGFFYNVII AWALHYLFSS FTTELPMIHC 180
 NNSWNPNCS DAHPGDSGSD SSGLNDTFGT TPAAEYFERG VILHLQSHGI DDLGPPRWQL 240
 TACLVLVIVL LYFSLWKGVK TSGKVVWITA TMPYVLTAL LLRGVTLPGA IDGIRAYLSV 300
 DFYRLCEASV WIDATAQVCF SLGVGFGVLI AFSSYNKFTN NCYRDAIVTT SINSLTSFSS 360
 GFVVSFLGY MAQKHSVPIG DVAKDGPGLI FIIYPEAIAT LPLSSAWAVV FFIMLLTLGI 420
 DSAMGMESV ITGLIDEFQL LHRHRELFTL FIVLATFLLS LFCVTNGGIY VFTLLDHFAA 480
 GTSILFGLVI EAIGVAVFYG VGQFSDDIQ MTGQRPSLYW RLCWKLVSPC FLLFVVVVSI 540
 VTFRPPHYGA YIFPDWANAL GWVIATSSMA MPPIYAAYKF CSLPGSFREK LAYAIAPKED 600
 RELVDRGEVR QFTLRHKLK 620

40

45

Seq ID NO: 251 Protein Sequence
 Protein Accession #: NP_071356.1

1 11 21 31 41 51
 | | | | |
 MPLGHIMRLD LEKIALEYIV PCLHEVGFCY LDNFLGEVVG DCVLERVKQL HCTGALRDQ 60
 LAGPRAGVSK RHLRGDQITW IGGNEEGCEA ISFLLSLIDR LVLYCGSRLG KYVVKERSKA 120
 MVACYPGNT GYVRHVDNPN GDGRICITCI YLNKNWDAKL HGGILRIFFE GKSFIADVEP 180
 IFDRLLFFWS DRRNPHVQF SYATRYAMTV WYFDAEERA AKKKFRNLTR KTESALTED 239

50

55

Seq ID NO: 252 Protein Sequence
 Protein Accession #: NP_647475.1

1 11 21 31 41 51
 | | | | |
 MSGAPTAGAA LMLCAATAVL LSAQGGPVQS KSPRFASWDE MVLVLAHLQ LGQGLREHAE 60
 RTRSQLSALE RRLSACGSAC QGTEGSTDL PAPSERSVDPE VLHSLQTLK AQNSRIQQLF 120
 HKVAQQQRHL EKQHLRIQHL QSQFGLLDHK HLDHEVAKPA RKRRLPEMAQ PVDPAHNVSR 180
 LHLRLPRDQCE LFQVGERQSG LFEIQPGQSP PFLVNCIMTS DGGWTVIQRH HDGSVDFNRP 240
 WEAYKAGFGD PHGEFWLGLK KVSITGDRN SRLAVQLRDW DGNAAELLQFS VHLGGEDTAY 300
 SLQLTAPVAG QLGAATVPVS GLSVPFSTWD QDHDLRRDKN CAKSLSGGWV FGTCSHSNLN 360
 GQYFRSIPQ RQKLKKGIFW KTRWGRYYP LQATTMLIQPM AEAAS 406

60

65

70

Seq ID NO: 253 Protein Sequence
 Protein Accession #: NP_001207.1

1 11 21 31 41 51
 | | | | |
 MAPLCPSWL PLLIPAPAG LTVQLLSLL LIMPVHPQRL PRMQEDSPIG GGSSGEDDPL 60
 GEEDLPSEED SPREEDPGE EDLPGEEDLP GEEDLPEVKP KSEEBGSLKL EDLPTVEAPG 120
 DPQEPQNAH RDKEGDDQSH WRYGGDPWP RVSPACAGRF QSPVDIRPQL AAFCPALRPL 180
 ELLGFLPPL PELRLRNNGH SVQLTLPPGL EMALGPGREY RALQLHLHWG AAGRPGSEHT 240
 VEGHRPFAEI HVVHLSTAFV RVDEALGRPG GLAVLAAFL EGPENSAYE QLSRLLEEIA 300
 EEGSETQVPG LDISALLPSD FSRYFYEGS LTPPCAQGV IWTVPNTVM LSAQLHTLS 360
 DTLWPGDSR LQLNFRATQ LNRVIEASF PAGVDSSPA AEPVQLNSCL AAGDILALVF 420
 GLLFAVTSVA FLVQMRQHR RGTGKGVSYR PAEVAETGA 459

75

80

Seq ID NO: 254 Protein Sequence
 Protein Accession #: NP_003030.1

1 11 21 31 41 51
 | | | | |
 MEQDQDSMKE GRLLTLVLALA TLIAAFGSSF QYGVNVAAVN SPALLMQQFY NETYYGRTGE 60
 FMEDFPLTL WSVTVSMFPF GGFIGSLLVG PLVNFGRKG ALLFNIFSI VPAILMGCSR 120
 VATSFELIII SLLVIGICAG VSSNVVPMYL GELAPKNLRG ALGVVPQLFI TVGILVAQIF 180
 GLRNLNAV DWPILLGLTG VPAALQLLLL PFPESPRLY LIQKDEAAA KKALQTLRGW 240
 DSVREVAEI RQDEAEKAA GFISVLKLF MRSLRWOLLS IIVLMGGQQL SGVNAIYYA 300
 DQIYLSAGVP EEHVQYVTAG TGAVNVMTF CAVFVVELL RRLLLLLGFS ICLIAACVLT 360
 AALALQDTS WMPYISIVCV ISYVIGHALG PSPIPALLIT EIFLQSSRPS AFMVGGSVHW 420
 LSNFTVGLIF PFIQELGPHY SFIVFAVICL LTTIYIFLIV PETKARTIE INQIFTMKNK 480
 VSEVYPEKEE LKELPPVTSE Q 501

| | |
|-----------------------------------|--|
| Seq ID NO: 255 Protein Sequence | |
| Protein Accession #: NP_001243.1 | |
| 5 | 1 11 21 31 41 51 |
| | MPEEGSGCSV RRRPYGCVLR AALVPLVAGL VICLVVCIQR FAQAQQQLPL ESLGWDVAEL 60 |
| | QLNHTGPOOD PRLYWQGGPA LGRSFLHGPE LDKGQLRIHR DGIYMHIOV TLAICSSSTA 120 |
| | SRHHPTLAV GICSPASRSI SLLRLSFHQG CTIASQRLTP LARGDTLCTN LTGTLLPSRN 180 |
| 10 | TDETFFGVQW VRP 193 |
| Seq ID NO: 256 Protein Sequence | |
| Protein Accession #: NP_060562.2 | |
| 15 | 1 11 21 31 41 51 |
| | MLFTSFVEQK KKAGVFEQIT KTHGTIIGIT SGIVLVLLII SILVQVKQPR KKMACKTAP 60 |
| | NKTGFQEVFD PPHYELFSLR DKEISADLAD LSEELDNYQR MRRSSTASRC IHDHHCQSQA 120 |
| | SSVKQSRITNL SSMELPLRND FAQPQPMKTF NSTFKKSSYT FKQGHCEPQK ALEDRVMEEI 180 |
| | PCEIYVRGRE DSAQASISID F 201 |
| Seq ID NO: 257 Protein Sequence | |
| Protein Accession #: Eos sequence | |
| 20 | 1 11 21 31 41 51 |
| | IIAATINNAS MTSPIDNAGL AADDFKMNAS LQTQISTDAE AVSSAKSEIM ELKQVLQSLQ 60 |
| 25 | HELQSVLMAQ SSPBGTADT EAGYVAQLSE IKMYISILEE QICQIRGETE YQNTQYALQ 120 |
| | DIKTRLEVEI ETYHRLGGE GGSEAREAES KG 152 |
| Seq ID NO: 258 Protein Sequence | |
| Protein Accession #: NP_003256.1 | |
| 30 | 1 11 21 31 41 51 |
| | MRQTLPCIYF WQGLLPFGML CASSTTKCTV SHEVADCSHL KLTQVPDDL P T NITVLNLTH 60 |
| | NQLRRLPAAN PTRYSQLTSL DVGFTNTISKL EPELCQKLPK LKVLNLQHNE LSQLSDKTFA 120 |
| 35 | FCNTLTELHL MSNSIQIKIN NPFVKQKNLI TLDLSHNGLS STKLGTVQVL ENLQELLN 180 |
| | NKIQALKSEE LDIFANSSLK KLELSSNQIK EFSPGCFHAI GRLFLGLFNN VQLGPSLTEK 240 |
| | LCELEANTSI RNLSLSNSQL STTSNTTFLG LKWTNLTMLO LSYNNLNVVG NDSFAWLPOL 300 |
| | EYFLEYNNI QHLFSHSLHG LFNVRVNLK RSFTKQSISL ASLPKIDDFS FQWLKCLEHL 360 |
| | NMEDNDIPGI KSNMFTGLIN LKYLSSLSNSF TSLRLTLNET FVSLAHSPFH ILNLTKNKIS 420 |
| 40 | KIESDAFSWL GHLEVLDLGL NEIGQELTQ EMRGLENIFE IYLSYNKYQL LTRNSFALVP 480 |
| | SLQRLMLRRV ALKNVDSSPS PFQPLRNLT LLDLNNNIAN INDDMLEGLE KLEILDLOHN 540 |
| | NLARLWKHAN PGPIYFLKG LSHLHILNLE SNGFDEIPVE VFKDLFLKID IDLGLNNLNT 600 |
| | LPASVFNQV SLKSLNLQKN LITSVEKKVF GPAFRNLTEL DMRFNPFDCI CESIAWFWNW 660 |
| | INETHNPIE LSSHLYCNTP PHYHGFVRL FDTSSCKDSA PFELFFMINT SILLIFIFIV 720 |
| | LLIHFEGRWI SFYWNVSVHR VLGFKEIDRQ TEQFEYAAYI IHAYKDKDWV WEHFSMEKE 780 |
| 45 | DQSLKFCLEE RDEAGVFEL EAVNSIKRS RKIIFVITHH LKDPPLCKRF KVHHAVQQA 840 |
| | EQNLDSIILV FLEEIPDYKL NHALCLRRGM FKSHCILNWP VQKERIGAFR HKLQVALGSK 900 |
| | NSVH 904 |
| Seq ID NO: 259 Protein Sequence | |
| Protein Accession #: NP_000570.1 | |
| 50 | 1 11 21 31 41 51 |
| | MDYQVSSPIY DINYYTSEPC QKINVKQIAA RLLPPLYSLV FIFGFVGNML VILILINCKR 60 |
| | LKSMTDIYLL NLAISDLFFL LTVPFWAHYA AAQWDFGNTM COLLTLGYFI GFFSGIFFII 120 |
| 55 | LLTIDRYLAV VHAFVALKAR TVTFGVVTSV ITWVAVFAS LPGIIFTRSQ KEGLHYTCSS 180 |
| | HFPYSQYQFW KMFQTLKIVI LGLVPLLVLM VICYSGLIKT LLRCRNEKCR HRAVRLIFTI 240 |
| | MIVYFLFWAP YNIVYLLNTF QEPFLNACS SSNRDQAMQ VTETLGMTHC CINPIIYAFV 300 |
| | GEKFRNYLLV FQKHIAKRF CKCCSIFQOE APERASSVYT RSTGEQEISV GL 352 |
| Seq ID NO: 260 Protein Sequence | |
| Protein Accession #: Eos sequence | |
| 60 | 1 11 21 31 41 51 |
| | PQPPPGPGI PGAKGELGLP GAPGIDGEGK PKGQKGDPEE PGPAKLKGEA GEMGLSGLPG 60 |
| 65 | ADGLKGEKGE SASDSLQESL AQLIVERGPP GPPGPPGPMG LQGIQGPGLG DGAKEGKAS 120 |
| | GERGPSGLPG PVGPPGLIGL PGTKGEKGRP GEPGLDGFPF PRGEKGRDSE RGEKGERGVP 180 |
| | GRKGVKGQKG EPGPPGLDQP CPVGPDGLPV PGCWHK 216 |
| Seq ID NO: 261 Protein Sequence | |
| Protein Accession #: NP_004852.1 | |
| 70 | 1 11 21 31 41 51 |
| | MLPPQKKPWE SMAKGLVLGA LFTSFLLLVY SYAVPPLHAG LASTTPEAAA SCSPPALEPE 60 |
| | AVIRANGSAG EQPRRNIVF LKTHKTASST LLNILFRFGQ KHLKFAFPN GRNDFDYPTF 120 |
| 75 | FARSLVQDYR PGACFNIIICN HMRPHYDEVR GLVPTNAIFI TVLRDPAFLF ESSPHYFGPV 180 |
| | VPLTWKLSAG DKLETFIQDP DRYYPDPNGFN AHYLRNLFF DLGYDNLDP SSPQVQEHIL 240 |
| | EVERRPHLV LQEYFDESIV LKDLCCWEL EDVLYFKLNA RRDSPVRLS GELYGRATAW 300 |
| | NMLDSHLYRH FNASFWRKVE AFRGRMARE VAALRHANER MRTICIDGGH AVDAAAIQDE 360 |
| 80 | AMQPHQLGT KSLIGYLNKK SIGQRHAQLC RMRLTPEIQY LMDLGANLWV TKLWKFIRDF 420 |
| | LRW 423 |
| Seq ID NO: 262 Protein Sequence | |
| Protein Accession #: NP_061130.1 | |
| | 1 11 21 31 41 51 |

| | | | | | | | |
|----|-------------|------------|------------|-------------|------------|------------|-----|
| | MASVLSRRIG | KRSLLGARVL | GPSASEGPSA | APPSEPLLEG | AAPQPFITSD | DTPCQEQPKE | 60 |
| | VLKAPSTSGI | QQVAFQPGQK | VYVWYGGQEC | TGLVEQHSWM | EGQVTWVLE | QKLQVCCRVE | 120 |
| | EVWLAEELQGP | CQAPPLEPG | AQALAYRFVS | RNIDVPKRKS | DAVEMDEMMA | AMVLTSLSCS | 180 |
| 5 | PVVQSPPGTE | ANFSASRAAC | DPWKESGDIS | DSGSSSTTSGH | WSGSSGVSTP | SPPHQASPK | 240 |
| | YLGDAGFSQ | TDHGFETDPD | PFLDEPAPR | KRKNVSKVMY | KCLWPNCGKV | LRSIVGIKRH | 300 |
| | VKALHLGDTV | DSQDFKREED | FYYTEVQLKE | ESAAAAA | AGTPVPGTPT | SEPAPTPSMT | 360 |
| | GLPLSALPPP | LHKAQSSGPE | HPGPSSSLPS | GALSKSAPGS | FWHIQADHAY | QALPSFIQPV | 420 |
| | SPHIYTSVSW | AAAPSAACSL | SPVRSRSLSP | SEPQQAPAPM | KSHLIVTSP | RAQSGARKAR | 480 |
| 10 | GEAKCKRKVY | GIEHRDQWCT | ACRWKKACQR | FLD | | | 513 |

Seq ID NO: 263 Protein Sequence
Protein Accession #: AB058765.2

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|----|------------|-------------|------------|-------------|-------------|-------------|------|
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| 15 | MRENYETLVS | VGTAELLPLS | AFLSPSEPGR | AVGGGSHADE | GQEPAGCGDP | QGGQPRHSLH | 60 |
| | LTALVLQVKE | IPEFLFGEVK | GAMDSPESES | RGASLDGERA | SPEAAAAAREP | CPLRGLLSCL | 120 |
| | PDGPTSQPHL | ATTPTSSCS | SGPTGDGVQ | SPLPIKTADK | PWPTRKEGPG | ALGGEPSPT | 180 |
| | HSPSRKRSR | QGERGTSEAG | ISPGNSPLQG | LINCLKEILV | PGRHPETSP | SFLPPLPSLG | 240 |
| 20 | TSRLTRADLG | PGSPPMVAVKT | EAVSGDCPLQ | GLLHCLKELP | EAQDRHPSPS | GVGNRRILQEN | 300 |
| | PGAWKRGSG | PGYLLTPPPH | PDLGAGGLLS | VKMENSWQVS | PPGPASCQPG | RQPLSPSATG | 360 |
| | DTRGVQPSW | GPEAQASAS | SSPLEALEAC | LKGIPFNGSS | PSQLPPTSCS | QNPQPGDSRS | 420 |
| | QKPELQPHRS | HSEAEATREP | LPLGLQSCVR | DGSPSRPLAPR | GTPTSFSSSS | STDWDLDFGS | 480 |
| | PVGNQGGHQP | KGSPPGSSPL | QGLENCLEKI | PVPVLRPAWP | CSSAADRCPR | RAEPRNWTAD | 540 |
| 25 | KEGLRAEACE | SARLGGQGRGE | APTRSLHLVS | PQVFTSSCPV | ACHQRGFKDP | GATRPGVWRW | 600 |
| | LPEGSAFKPS | PLHCLSEALR | GILPVRPLRP | ACVGGPSPSP | SPGSSSSFSG | SEGEDPRPEP | 660 |
| | ELWKPLPQER | DRLPSCKPPV | PLSPCPGGTP | AGSSGGSPGE | DPRTTEPRYC | SGLGAGTAQD | 720 |
| | PCVVSQLEKR | PRVSEASRGL | ELGHGRPRVA | AKTHERLLPQ | GPPELPSESP | PPELPPPEAA | 780 |
| | PPVLPASSLQ | PPCHCGKPLQ | QELHSLGAAL | AEKLDRLATA | LAGLAQEVAT | MRTQVNRRLR | 840 |
| 30 | RPQGGPGMPE | ASMMWTLPRG | PRWAHGPGHR | HLPYWRQKGP | TRPKPKILRG | QGESCRAQDL | 900 |
| | QGLSRGTARR | ARLPPDPAPP | AEPPLGHCSS | SQQLLSSTPS | CHAAFPAPHL | LAHTGGHQSP | 960 |
| | LPLVPAALP | LQASPPAAS | ADADVPTSGV | APDGIPIPERK | EPSSLLGGVQ | RALQEELWGG | 1020 |
| | EHRDPRWGAH | | | | | | 1030 |

Seq ID NO: 264 Protein Sequence
Protein Accession #: AL831935.1

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|----|------------|------------|------------|------------|------------|------------|-----|
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| 40 | PAGCGDPOGG | QPRHSLHLTA | LVQLVKEIPE | FLFGEVKGAM | DSPESERGA | SLDGERASPE | 60 |
| | AAAREPCPLR | GLLSCLPDGP | TSQPHLATTP | TDSSCSSGPT | GDGVQGSPLP | IKTADKPWPT | 120 |
| | RKEGPGALGG | EPSPTTSPS | RRKSHRQGER | GTSEAGISPG | NSPLQGLINC | LKEILVPGPR | 180 |
| | HPETSPPSLR | PLPSLGTSLR | TRADLPGSP | PWAVKTEAVS | GDCPLQGLLH | CLKELPEAQD | 240 |
| | RHPSPSGVGN | RRLQENPGAM | KRGSGGPGYL | LTPPPHDLG | AGLLSVKME | NSWVQSPPGP | 300 |
| | ASQPGGRQPL | SPSATGDTRG | VQPSWGPPEA | QAASASSSPL | EALACLKGI | PPNGSSPSQL | 360 |
| 45 | PPTSCSQNPQ | PGDSRSQKPE | LQPHRSHEE | ATREPVLPLG | LQSCVRDGP | RPLAPRGTFP | 420 |
| | SFSSSSSTDW | DLDFGSPVGN | QGHHPGKGP | PGSSPLQGLE | NCLKEIPVPV | LRFAPWCSSA | 480 |
| | ADRGPRRAEP | RNWTADKEGS | APKPSPLHCL | ESALRGILPV | RPLRFACVGG | PSPSPSGSS | 540 |
| | SSFGSGEGED | PRPEFDLWKP | LQERDRLPS | CKPPVPLSPC | PGGTPAGSSG | GSPGEDPRRT | 600 |
| 50 | EPRYCSGLGA | GEFGVS | | | | | 616 |

Seq ID NO: 265 Protein Sequence
Protein Accession #: AAH29071.1

| | | | | | | | |
|----|------------|------------|------------|------------|------------|------------|-----|
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| 55 | RTRGRTRGRL | RSGVMMPLAE | AGALAQGGGP | SATEWACILR | RKTPRHKQPT | LLMVRASRRS | 60 |
| | GKTSAILKAG | RQSVSGRKNS | TSKDLVTLGA | SSLREERGHP | LHPRHRKAVH | LRTRGRTRGW | 120 |
| | VQTLARMSRP | TRGVPERAAA | AAAAAAGGDA | GHAPFPFPPA | ADGARAPRSP | QVTPRGLRL | 180 |
| | RLPRRESLLR | GLCRPLRPLL | GFRESDSAKP | ASLRLQLHTP | SARRNYRIAG | ARLMRSNYPP | 240 |
| 60 | PLSSAALRGA | GPTRRN | | | | | 256 |

Seq ID NO: 266 Protein Sequence
Protein Accession #: NP_002095.1

| | | | | | | | |
|----|------------|------------|-------------|------------|------------|------------|-----|
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| 65 | MTKFSSFSLF | FLIVGAYMTH | VCFNMEIIG | KEVSPHSRPF | MASIQYGGHH | VCGGVLDIDQ | 60 |
| | WVLTAAHCQY | RFTKQSQPTV | VLGAHSLSKN | EASKQTLKIK | KFIPFSRVTS | DQSNIDIMLV | 120 |
| | KLQTAALKNK | HVKMLHIRSK | TSLSRGTKCK | VTGWGATDPD | SLRPSDTLRE | VTVTVLSRKL | 180 |
| | CNSQSYNGD | PFITKDMVCA | GDAKGQKQDSC | KDGSGLPLIC | KGVFHAIVSG | GHECGVATKP | 240 |
| 70 | GIYTLTKKY | QTWKSNLVP | PHTN | | | | 264 |

Seq ID NO: 257 Protein Sequence
Protein Accession #: NP_443179.1

| | | | | | | | |
|----|------------|-------------|------------|------------|------------|------------|-----|
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| 75 | MQVNTLFETS | QVPDWSDPQP | VQVQETVRET | ISCSQMPAFS | EPAGEESPFT | GTTTISFSNL | 60 |
| | GGVHKENASL | AQHSEVKPCT | CGPQEEKQD | RDGNIPDNFR | EDLKYEQSIS | EANDETMSPG | 120 |
| | VFSRHLPKDA | RADFPREPVA | SVASPEPTDT | ALTLENVCDE | PRDREAVCAM | ECFEASDQGT | 180 |
| | CFDTIDSLVG | TPVDNYSPPQ | ICSDVTELA | GQNKVSDLCS | SNDKTLEVFF | QTQVSETSVS | 240 |
| | TKSSKDGNS | VMSPLFITST | TLNISHTASE | GATGENLAKV | EKSTYPLAST | VHAGQEQPSP | 300 |
| 80 | SNSGGLDETQ | LSSSENNPLV | QFKEGGDKSP | SPSAADTTAT | PASYSISVSF | PWEKPTTLTA | 360 |
| | NNECFQATRE | TVTITATEVHP | AKYLAVSIP | DKHAGGTEER | FPRASHEKVS | QFSPQVOVDH | 420 |
| | ILSGATIKST | KELLCRAPSV | PGVPHHLVQL | PEGEGFCNS | PLQVDNLSGD | KSQTVDRADF | 480 |
| | RSYEENFQER | GSETKQGVQ | QSLSQGSL | APDFQQLSPT | TSAAQEERNL | VPTAPSPASS | 540 |
| | REGAGQRSGW | GTRVSVVAET | AGEEDSQALS | NVPSLSLILL | EESKEYRPGN | WEAGNKLKII | 600 |

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TLEASASEIWF PPRQLTNSSE KASDGGLIIP DKVWAVPDSL KADAVVPELA PSEIAALAHS 660
 PEDAESALAD SRESHKGEET TISVHWRLS SRGFSQPRLL ESSVDPVDEK ELSVTDLSLA 720
 ASETGGKENV NNVSQDQEEK QLMMDHTAFF KFLTCPKIL ESSVDPIDEI SVIEYTRAGK 780
 PEPSETTPQG AREGGQSNHG NMGHEAEIQS AILQVPCLOQ TILSENRISS SQEGSMKQEA 840
 EQIQPEEAKT AIWQVLQPSG GGERIPSGCS IGQIQESSDG SLGEAEQSKK DKAELISPTS 900
 PLSSCLPMT HSSLDGVDTHN STGQIHDVPE NDIVEPRKRQ YVFPVSQKRG TIENERGKPL 960
 PSSPOLTRFP CTSSPEGNVT DFLSHKMEK PKIEVLQIGE TKPPSSSSSS AKTLAFISGE 1020
 RELEKAPKLL QDPCQKGTG CAKSRERER SLEARAGKSP GTLTAVTGSE EVKRKPEAPG 1080
 SGHLAEGVKK KILSRVAALR LKLEKENIR KNSAFLKKMP KLETSLSHTE EKQDPKKPSC 1140
 KREGRAVLL KKIQAEMFFE HSGNVKLSQO FAEIHEDSTI CWTKDSKSLA QVQASAGDNS 1200
 TVSFAIVQAS PKDQGLYYCC IKNSYGVKTA EFNLTAEVLK QLSRQDTKG CEEIEFSQLI 1260
 FKEDFLHDSY FGRLRGQIA TEELHFGEGV HRKAFRSTVM HGLMPVFKPG HACVLKVHNA 1320
 IAYGTRNDE LIQRNYKLAA QECYVQNTAR YYAKIYAAEA QPLEGFGVEP EIIPFIPIHR 1380
 PENNIPIYATV EEELIGEFVK YSIRDGKEIN FLRRESEAGQ KCCTFQHWVY QKTSGLLVLT 1440
 DMQGVGMKLT DVGIATLAKG YKGFKGNCMS TFIDQFKALH QCNKYCKMLG LKSLQNNNQK 1500
 QKQPSIGSKS VQNSMTVKK AGPETPGEKK T 1531

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25

Seq ID NO: 268 Protein Sequence
 Protein Accession #: NP_602293.1
 1 11 21 31 41 51
 | | | | |
 MGKQNSKLRP EVLQDLRENT EFTDHELQEW YKGLKDCPT GHITVDEFKK IYANFFPYGD 60
 ASKFAEHVFR TFDITNGDGTI DFREFIIALS VTSRGKLEQK LKWAFSMYDL DGNGYISRS 120
 MLEIVQAIYK MVSSVMKME DESTPEKRTD KIFRQMDTNN DGKLSLEEFI RGAKSDPSIV 180
 RLLQCDPSSA SQF 193

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35

Seq ID NO: 269 Protein Sequence
 Protein Accession #: NP_002140.2
 1 11 21 31 41 51
 | | | | |
 MGKQNSKLRP EVLQDLRENT EFTDHELQEW YKGLKDCPT GHITVDEFKK IYANFFPYGD 60
 ASKFAEHVFR TFDITNGDGTI DFREFIIALS VTSRGKLEQK LKWAFSMYDL DGNGYISRS 120
 MLEIVQAIYK MVSSVMKME DESTPEKRTD KIFRQMDTNN DGKLSLEEFI RGAKSDPSIV 180
 RLLQCDPSSA SQF 193

40
45

Seq ID NO: 270 Protein Sequence
 Protein Accession #: NP_003937.1
 1 11 21 31 41 51
 | | | | |
 MGNAQERPE TIDRERKRLV ETLQADSGLL LDALLARGVL TGPEYEALDA LPDAERRVRR 60
 LLLLVQKGG AACQELLRCA QRTAGAPDPA WDQHVGPY RDRSYDPPCP GHWTPEAPGS 120
 GTTCPLPRA SDPDEAGGPE GSEAVQSGTP EEPEPELEAE ASKEAPEPE PEPEPEPEAE 180
 AEPEPELEPE PDPEPEPDFE ERDESEDS 208

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55

Seq ID NO: 271 Protein Sequence
 Protein Accession #: NP_004198.1
 1 11 21 31 41 51
 | | | | |
 MGAUVDEGP TGVKAPDGGH GMAVLFGCFV ITGFSYAFPK AVSVFFKELI QEFGIGYSDT 60
 AWISSILLAM LYGTGPLCSV CVNRFGCRPV MLVGGFLFASL GMVAASFCSR IIQVYLTGV 120
 ITGLGLALNF QPSLIMLNRY FSKRRPMANG LAAAGSPVFL CALSPLGQLL QDRYGNRGGF 180
 LILGGLLLNC CVCAALMRPL VVTAQPGSGP PRPSRRLLDL SVFRDRGFVL YAVAASVMVL 240
 GLFVPPVFVV SYAKDLGVDP TKAALLTIL GFIDIFARPA AGFVAGLGKV RPYSVYLFSP 300
 SMFFNGLADL AGSTAGDYG LVVFCIFFGI SYGMVGALQF EVLMAIVGTH KFSSAIGLVL 360
 LMEAVAVLVC PPSGGKLLDA THVYMYVFIL AGAEVLTSSL ILLGNFFCI RKKPKPEQPE 420
 VAAEEEEKLH KPPADSGVDL REVEHFLKAE PEKNGEVVHT PETSV 465

60
65
70

Seq ID NO: 272 Protein Sequence
 Protein Accession #: NP_060705.1
 1 11 21 31 41 51
 | | | | |
 MAALTTLFKY IDENQDRYIK KLAKWVAIQS VSAWPEKRGE IRRMMEVAAA DVKQLGGSVE 60
 LVDIGKQKLP DGSEIPLPPI LLGRGLSDPQ KKTVCIIYHL DVQPAALDGD WDSEPTLVE 120
 RDGKLYGRGS TDDKGPVAGV INALEAYQKT GQEIIPNVRF CLEGMEESGS EGLDELIFAR 180
 KDTFFKDVYD VCISDNYWLG KKKPCITYGL RGICYFFIEV ECSNKDLHSG VYGGSVHEAM 240
 TDLILLMGS LVDKRGNIILP GINEAVAAVT EEEHKLYDDI DFDIEEFAKD VQAQILLHSH 300
 KQDILMHRWR YPSLSLHGIE GAFSGSGAKT VIPRKVVGKF SIRLVPMNTP EVVGEQVTSY 360
 LTKKFAELRS PNEFKVYMGH GSKPWVSDFS HPHYLGRRA MKTVFVGEVD LTREGGSIPV 420
 TLTFQATGK NVMLLPVGSA DDGAHSQNEK LNRNYNIEGT KMLAAYLYEV SQLKD 475

75
80

Seq ID NO: 273 Protein Sequence
 Protein Accession #: AF258592.1
 1 11 21 31 41 51
 | | | | |
 MAALTTLFKY IDENQDRYIK KLAKWVAIQS VSAWPEKRGE IRRMMEVAAA DVKQLGGSVE 60
 LVDIGKQKLP PNVNRFCLGE MEESGSEGLD ELIFARKDTF FKDVYVCIS DNYWLGKKP 120
 CITYGLRGIC YFFIEVCSN KDLHSGVYGG SVHEAMTDLI LLMGSLVDKR GNILIPGINE 180
 AVAAVTEEEH KLYDDIDFDI EEFKDVGAQ ILLHSHKKDI LMRWRYPSP SLHGIEGAFS 240
 GSGAKTVIPR KVVGKFSIRL VPMNTEPVVG EQVTSYLTKK FAELRSPNEF KVMYMGHGK 300
 WVSDFSHPHY LAGRRAMKT VGVPEDLTRE GGSIPVTLTF QEATGKQVML LPVGSADDGA 360
 HSQNEKLNRY NYIEGTMLA AYLYEVSQK D 391

Seq ID NO: 274 Protein Sequence
 Protein Accession #: NP_060871.1

1 11 21 31 41 51
 5 MGGNHSHKPP VFDENEENF DHFQILRAIG KGSFGKVCIV QKRDTKKMYA MKYMNKQKCI 60
 ERDEVNMFVR ELQIMOGLEH PFLVNLWYSF QDEEDMFHV DILLGGDLRY HLQONVHFT 120
 GTVKLYICEL ALALEYLQRY HIIHRDIKPD NILLDEHGHV HITDFNIATV VKGAERASSM 180
 AGTKPYMAPE VFQVYMDRGP GYSYPVDMWS LGITAYELLR GWRPYEIHVS TPIDEILNMF 240
 KVERVHYSST WCKGMVALLR KLLTKDPESR VSSLHDIQSV PYLADMNWDA VFKKALMPGF 300
 VPKNGRLNCD PTFEELEML ESKPLHKKKK RLAQNRSRDG TKDSCPLNGH LQHCLLETVRE 360
 10 EFIIFNREKL RRQGGGSQL LDTDSRGGGQ AQSKLQDGCN NLLTHTCTR GCSS 414

Seq ID NO: 275 Protein Sequence

Protein Accession #: NP_004198.1

1 11 21 31 41 51
 15 MGGAVVDEGP TGKAPDGGW GWAFLPGCFV ITGFSYAFPK AVSVFFKELI QEFIGYSDT 60
 AWISSILLAM LYGTGPLCSV CVNRFGRCPV MLVGGLFASL GMVAASFCSR IIQVYLTGV 120
 ITGLGLALNF QPSLIMLNRY FSKRRPMANG LAAAGSPVFL CALSPGLQLL QDRYGRWGGF 180
 LIIGGLLLNC CVCAALMRPL VVTAQPGSGP PRPSRRLDL SVFRDRGFVL YAAVASVMVL 240
 20 GLFVPPVFV SYAKDLGVPD TKAAPLLTIL GFIDIFARPA AGFVAGLGKV RPYSVYLFSP 300
 SMFFNLGLAD AGSTAGDYG LVVFCIFPGI SYGMVAGLQF EVLMAIVGTH KFSSAIGLVL 360
 LMEAVAVLWG PPSGGKLLDA THVYMYVIL AGAEVLTSSL ILLGNFFCI RKKPKPEQPE 420
 VAAAEKELH KPPADSGVDL REVEHFLKAE PEKNGEVVHT PETSV 465

Seq ID NO: 276 Protein Sequence

Protein Accession #: NP_006589.1

1 11 21 31 41 51
 25 MPTNFTVVPV EAHADGGDE TAERTEAPGT PEGPEPERPS PGDGNPRENS PFLNNVEEQ 60
 ESFFEGKQMA LFEEMDSNP MVSSLLNKL NYTNLSQGV EHEEDEESRR REAKAPRMGT 120
 30 FIGVYLPCLQ NILGVILFLR LTVIVGVAGV LESFLIVAMC CTCTMLTAIS MSAIATNGVV 180
 PAGGSYIMIS RSLGPEFGGA VGLCFYLTG FAGAMYILGT IEIFLTYISP GAAIFQAEAA 240
 GGEEAAMLNH MRVYGTCTLV LMAVVFVGV KYVNKLALVF LACVLSILA IYAGVKSFA 300
 DPDPDIPVCLL GNRTLRRSRF DACVKAYGIH NNSATSALWG LFCNGSQSPA ACDEYFIQNN 360
 35 VTEIQIGPA ASGVFLENLW STYAHAGAPV EKKGVSPSPV AEEASRSTLP YVLTIDIAAF 420
 TLLVGIYFPS VTGIMAGSNR SGDLKDAQKS IPTGTILAIV TTSFIYLSCL VLFACIEGV 480
 VLRDKFGEAL QGNLVIGMLA WPSPWVIVG SFFSTCGAGL QTLTGAPRL QAIARDGIVP 540
 FLQVFGHGA NEPTWALLL TVLICETGIL TASLDSVAPI LSMFFLMCYL FVNLACAVQT 600
 LLRTPNWRRP FKFYHTLFS LGMSLCLALM FICSMYALS AMLIAGCIYK YIEYRGAEKE 660
 40 WGDGIRGLSL NAARYALLRV EHGPPHTKNW RPOVLVMLNL DAEQAVKHPR LLSFTSQLKA 720
 GKGLTIVGSV LEGTYLDKHM EAQRAENIR SLMSTKTKG FCQLVVSSSL RDGMSHLIQS 780
 AGLGKFLHNT VLMAPWASWK QEDNPFWSKN FVDTVRDTTA AHQALLVARN VDSFPQNER 840
 FGGLGHIDVW IVHDGMLML LPFLLRQHKV WRKCRMRIFT VAQVDDNSIQ MKKDLQMFY 900
 HLRISAEV EVMEVNDISA PTYERTLME QRSQMLKQMQ LSKNEQEEA QLIHDRNTAS 960
 45 HTAAARTQA PPTPDVKQMT WTREKLIAEK YSRDTSLSG FKDLFSMKPD QSNVRRMHTA 1020
 VKLNGVVLNK SDAQVLVLLN MPGPPKNRQG DENYMEFLEV LTEGLNRVLL VRGGGREVIT 1080
 IYS 1083

Seq ID NO: 277 Protein Sequence

Protein Accession #: NP_004576.1

1 11 21 31 41 51
 50 MASPHQEPKP GDLEIFRLG YEHWALYIGD GYVIHLAPPS EYPGAGSSSV FSVLSNSAEV 60
 KRGRLEDVVG GCCYRVNNSL DHEYQPRPVE VIISAKEMV QQKMKYSIVS RNCEHFVAQL 120
 55 RYKSRCKQV EKAKEVGVA TALGILVVAG CSFAIRRYQK KATA 164

Seq ID NO: 278 Protein Sequence

Protein Accession #: NP_004687.1

1 11 21 31 41 51
 60 MLKREGKVQP YTKTLDGGWG WMIVIHFFLV NVFVNGMTKT FAIFVVFQSE EFGTSEQIG 60
 WIGSIMSSLR FCAGPLVAII CDILGEKTS ILGAFVVTGG YLISSWATS I PFLCVTMGLL 120
 PGLGSFLYQ VAAVVTYKYP KKRLALSTAI ARSGMGLTFL LAPFTKFLID LYDWTGALIL 180
 FGAIALNLVP SSMLLRPIHI KSENNSGIKD KGSSLSAHGP EAHATETHCH ETEESTIKDS 240
 65 TTQKAGLPSK NLTVSQNSE EYNGPNRNR LLLKSDEESD KVISWCKQL FDISLFRNPF 300
 FYIFTWSFLL SQLAYFIPTF HLVARAKTLG IDIMDASYLV SVAGILETVS QIISGWVADQ 360
 NMKKYHYHK SYLILCGITN LLAPLATTFP LLMTYTICFA IFAGGYLALI LPVLVDLCRN 420
 STVNRFLGLA SFFAGMAVLS GPPIAGMLYD YQTNGNSFY FSGICYLLSS VSFFVPLAE 480
 RWKNSLT 487

Seq ID NO: 279 Protein Sequence

Protein Accession #: NP_000349.1

1 11 21 31 41 51
 70 MALFVRLAL ALALALGPA TLAGPAKSPY QLVQLHSRLR GRQHGPNVCA VQKVIGTNRK 60
 YFTNCKWYQ RKICGKSTVI SYECCPGYEK VPGEKGCPAA LPLSNLYETL GUVGTTTQL 120
 75 YTDREKLRP ENEGPGSFTI FAPSNEAWAS LPAEVLDSL SNVNIELNA LRYHVMGRRV 180
 LTDELKHGNT LTSYQNSNI QIHYPNGIV TVNCARLLKA DHHATNGVH LIDKIVSTIT 240
 NNIQIIIEIE LTFETLRAAV AASGLNTMLE GNGQYTLAP TNEAFKIPS ETLNRILGDP 300
 80 EALRDLNHL ILKSAMCAEA IVAGLSVETL EGTTLVGCSS GDMLTINGKA IISNKDILAT 360
 NGVIHYDEL LIPDSAKTLF ELAAESDVST AIDLFRQAGL GNHLSGSESL TLLAPLNSVF 420
 KDGTTPPIDAH TRNLRLNHI KDQLASKYLY HGQTLETGG KKLRFVYVRN SLICIENSCIA 480
 AHDKRGRYGT LPTMDRVLT PMGTVMVLK GDNRFSLVA AIQSAGLTET LNRGVYTVF 540
 APTNEAPRAL PPRERSRLLG DAKELANILK YHIGDEILVS GGIGALVRLK SLQGDKLEVS 600
 LKQNVVSVNK EPVAEPDIMA TNGVVHVITN VLQPPANRPQ ERGDELADSA LEIFKQASAF 660

SRASQSVRL APVYQKLLER MKH

683

Seq ID NO: 280 Protein Sequence

Protein Accession #: NP_663623

5
1 11 21 31 41 51
MEGSGGGAGE RAPLLGARRA AAAAAAGAP AGRRACGAV LLETLLERAA FYGITSNLVL 60
FLNGAPFCWE GAQASEALLL FMGLTYLGSP FCGWLADARL GRARAILLSL ALYLLQMLAF 120
10 PLLAAPATRA ALCGSARLLN CTAPGPDAAA RCCSPATFAG LVLVGLGVAT VKANITPFGA 180
DQVKDRGPEA TRRFNWFYV SINLGAILSL GGIAYIQQNV SFVTGYAIPT VCVGLAFVVF 240
LGGQSVFITK PPDGSAFTDM FKILTYSCCS QKRSGERQSN GEGIGVFQOS SKQSLFDSCK 300
MSHGGPFTTE KVEDVKALVK IVPVFLALIP YNTVYFQMT TYVLQSLHLR IPEISNITTT 360
PHTLPAWLT MFDVALLILL IPLKDKLVDP ILRRHGLLPS SLKRIAVGMF FVMCSAFAAG 420
15 ILESKRLNLV KEKTINQITG NVVYHAADLS LNWQVPQYLL IGISEIFASI AGLEFAYSAA 480
PKSMQSAIMG LFFFFSGVGS FVGSGLLALV SIKAIQWMSS HTDFGNINGC YLNTYFFLLA 540
AIQGATLLLF LIISVKYDHH RDHQSRANG VPTSRRR 577

Seq ID NO: 281 Protein Sequence

Protein Accession #: NP_001241.1

20
1 11 21 31 41 51
MYRLPLQCVL WGCILLTAVHP EPPTACREKQ YLINSQCCSL CQPGQKLVSD CTEFTETECL 60
PGGESEFLDT WNRETHCHQH KYCDPNLGLR VQQKGTSETD TICTCEGWH CTSEACESCV 120
LHRSCSPGFG VKQIATGVSD TICEPCPVGP FSNVSSAFEK CHPTWSCETK DLVQQAGTN 180
25 KTDVVCQPQD RLRLVVIPI IFGILFAILL VLVFIKKVAK KPTNKAPHFK QEPQEIFFPD 240
DLPGSNTAAP VQETLHGQCP VTQEDGKESR ISVQERQ 277

Seq ID NO: 282 Protein Sequence

Protein Accession #: NP_003833.3

30
1 11 21 31 41 51
MEQRQGNAPA ASGARKRHGP GPREARGARP GLRVPKTLVL VVAAVLLLVV AESALITQOD 60
LAPQQRAPQ QKRSSPSEGL CPPGHHSIED GRDCISCKYG QDYSTHWNLD LFCLRCTRCD 120
35 SGEVELSPT TTRNTVCQCE EGTFREEDSP EMCRCRTGC PRGMVKVGDG TPWSDIECVH 180
KESGTHSGE APAAEETVTS SPGTSPASPCS LSGIIGVTV AAVVLIVAVF VCKSLWKKV 240
LPYLKIGCSG GGGDPERVDR SSQRPGAEDN VLNEIVSILQ PTQVPEQEME VQEPAEPTGV 300
NMLSPGESEH LLEPAEAERS QRRRLVPAN EGDPTETLRQ CFDDFADLVF FDSWEPLMRK 360
LGLMDNEIKV AKAEAGHRD TLYTMLIKWV NKTGRDASVH TLLDALETGL ERLAKQKIED 420
40 HLLSSGKPMY LEGNADAMS 440

Seq ID NO: 283 Protein Sequence

Protein Accession #: NP_671716.1

45
1 11 21 31 41 51
MEQRQGNAPA ASGARKRHGP GPREARGARP GLRVPKTLVL VVAAVLLLVV AESALITQOD 60
LAPQQRAPQ QKRSSPSEGL CPPGHHSIED GRDCISCKYG QDYSTHWNLD LFCLRCTRCD 120
SGEVELSPT TTRNTVCQCE EGTFREEDSP EMCRCRTGC PRGMVKVGDG TPWSDIECVH 180
KESGTHSGE VAAVVLIVAV FVCKSLWKKV VLPYLKIGCS GGGDPERVDR RSSQRPGAED 240
50 NVLNEIVSIL QPTQVPEQEM EVQEPAEPTG VNMLSPGESE HLLPEAEAR SQRRLVPA 300
NEGDPETELR QCDDFADLV PFDSWEPLMR KLGLMDNEIK VAKAEAGHR DTLTYTMLIKW 360
VNKTGRDASV HTLLDALETG GERLAKQKIE DHLLSSGKFM YLEGNADAMS S 411

Seq ID NO: 284 Protein Sequence

Protein Accession #: NP_002002.2

55
1 11 21 31 41 51
MRLLALLGV LLSVPGPPVL SLEASEEVEL EPCLAPSLEQ QEQLTVALG QPVRLCCGRA 60
ERGGHMYKEG SRLAPAGRVR GWRGRLEIAS FLPEDAGRYL CLARGSMIVL QNLTITGDS 120
60 LTSSNDDDDP KSHRDLNHRH SYPQAPYWT HPQRMKKLH AVPAGNTVKF RCPAAGNPTP 180
TIRWLKDGQA FHGENRIGGI RLRLHQSILV MESVVPDRG TYTCLVENAV GSIRYNYLLD 240
VLERSPHRPI LQAGLPANTT AVVGSDEVEL CKVYSDAQPH IQWLKHIVIN GSSFGADGFP 300
YVQVLKTADI NSSEVEVLYL RNVSADAGE YTCLAGNSIG LSYSQSAWLTV LPEEDPTWTA 360
AAPEARYTDI ILYASGSLAL AVLLLAGLY RGQALHGRHP RPPATVQKLS RFLARQFSL 420
65 ESGSSGKSSS SLVRGVRLSS SGPALLAGLV SLDPLDPLW EFPRDRLVLG KPLGEGCFGQ 480
VVRAEAFGMD PARPDQASTV AVKMLKONAS DKDLADLVSE MEVMKLIGRH KNIINLLGVC 540
TQEGPLYVIV ECAAKGNLRE FLRARRPPGP DLSPDGPRSS EGPLSFFVLV SCAYQVARGH 600
QYLESRKCIH RDLAARNVLV TEDNVMKIAD FGLARGVHHI DYYKTSNGR LPVKWMAPEA 660
LFDREVYTHS DVMSFGILLW EIFTGGSPY PGIPVEELFS LLREGHRMDR PPHCPPELYG 720
70 LMRECVHAAP SQRPTEFKQLV EALDKVLLAV SEEYLDLRLT FGPYSPSGGD ASSTCSSSDS 780
VFSHDPLPLG SSSFPFGSGV QT 802

Seq ID NO: 285 Protein Sequence

Protein Accession #: NP_075252.1

75
1 11 21 31 41 51
MRLLALLGV LLSVPGPPVL SLEASEEVEL EPCLAPSLEQ QEQLTVALG QPVRLCCGRA 60
ERGGHMYKEG SRLAPAGRVR GWRGRLEIAS FLPEDAGRYL CLARGSMIVL QNLTITGDS 120
LTSSNDDDDP KSHRDLNHRH SYPQAPYWT HPQRMKKLH AVPAGNTVKF RCPAAGNPTP 180
TIRWLKDGQA FHGENRIGGI RLRLHQSILV MESVVPDRG TYTCLVENAV GSIRYNYLLD 240
80 VLERSPHRPI LQAGLPANTT AVVGSDEVEL CKVYSDAQPH IQWLKHIVIN GSSFGADGFP 300
YVQVLKTADI NSSEVEVLYL RNVSADAGE YTCLAGNSIG LSYSQSAWLTV LPGTGRIPHL 360
TCDLTPAGR TKSPTLQFSL ESGSSGKSSS SLVRGVRLSS SGPALLAGLV SLDPLDPLW 420
EFPRDRLVLG KPLGEGCFGQ VVRAEAFGMD PARPDQASTV AVKMLKONAS DKDLADLVSE 480
MEVMKLIGRH KNIINLLGVC TQEGPLYVIV ECAAKGNLRE FLRARRPPGP DLSPDGPRSS 540

5
EGPLSFPVLV SCAYQVARGM QYLESRKCIH RDLAARNVLV TEDNMVKIAD FGLARGVHHI 600
DYYKTSNGR LPVKMAPEA LFDRVYTHQS DVWSFGILLW EIFTLGGSFY PGIPVEELFS 660
LLRBGHRMDR PPHCPPELYG LMRECWAAP SQRPTEKQLV EALDKVLLAV SEEYLDLRLT 720
FGPYSPSGGD ASSTCSSSDS VFSHDLPLG SSSFPFGSGV QT 762

Seq ID NO: 286 Protein Sequence
Protein Accession #: NP_002836.2

10
1 11 21 31 41 51
MRGLGTCLAT LAGLLLTAAE ETFSGGCLFD EPYSTCGYSQ SEGDDFNWEQ VNTLTKPTSD 60
PWMPSSGLML VNASGRPEGQ RAHLLLPQLK ENDTHCIDFH YFVSSKSNP PGLLNYYVKV 120
NNGPLGNPIW NISGDPTRTW NRAELAISTF WPNFYQVIFE VITSGHQYL AIDEVKVLGH 180
PCTRTPHFLR IQNVEVNAQO FATPQCSAIG RTVAGDRLWL QGIDVRDAPL KEIKVTSSRR 240
FIASFNVNT TKRDAGKYRC MIRTEGGVGI SNYAEVLVKE PPVPIAPPQL ASVGATYLMW 300
15 QLNANSINGD GPVAREVEY CTASGSWNRD QPVDSTSYKI GHLDPDTEYE ISVLLTRPCE 360
GGTGSPPGAL RTRTKCADPM RGRPKLEVVE VKSRQITIRW EPFGYNVTRC HSYNLTVHYC 420
YQVGGQEQVR EEVSNDTENS HPQHTITNLS PYTNVSVKLI LMNPEGRKES QELIVQTDDE 480
LPGAVPTESI QGSTFEKIF LQWREPTQTY GVITLYEITY KAVSSFDPEI DLSNQSGRVS 540
KLGNETHFLF FGLYPGTYS FTIRASTAGK FGPPATNQPT TKISAPMMPA YELETPLNQ 600
20 DNTVTMLKP AHSRGAPEVS YQIVVEERP RRTKKTTEIL KCYPVPIHFQ NASLLNSQY 660
FAAEFPADSL QAAQPTTIGD NKTNGYWNW PLLPYKSYRI YFQAASRANG ETKIDCVQVA 720
TKGAATPKPV PPEKQTDHT VKIAGVIAGI LLEVIIIFLG VLVMMKKRLA KKRKETSST 780
RQEMTMVMS MOKSYAEQGT NCDEAFSPMD THNLNGRSVS SPSSPTMTKN TLSTSVFNSY 840
YDETHMAS DTSSLVQSHY YKREPADVP YQTGQLHPAI RVADLLQHIT QMKCAEGYGF 900
25 KEEYESPFEG QSAPEDSAKK DENRMKNRYG NIIAYDHSRV RLQTIEGDTN SDYINGNYID 960
GYHRPNHYIA TQGPQETIY DFWRMVWHEN TASIIMVTNL VEVGRVKCK YWPDDEIYK 1020
DIKVTIETE LLAEVIRTF AVEKRGVHEI REIRQFHTG WPDHGVPYHA TGLLGFVRQV 1080
KSKSPPSAGP LVVHCSAGAG RTGCFIVIDI MLDMAEREGV VDIYNCVREL RSRRVNMVQT 1140
EEQYVFIHDA ILEACLCGDT SVPASQVRLS YYDMNKLDQ TNSSQIKEEF RTLMNMTPTL 1200
30 RVEDCSIAL PRNHEKNRCM DILPPDRCLP FLITIDGESS NYINAALMDS YKQPSAFIVT 1260
QHPLPNTVKD FWRVLVDYHC TSVVMLNDVD PAQLCPQYWP ENGVRHGP I QVEFVSADLE 1320
EDIISRFRI YNAARPDQY RMVQFQFLG WPMYRDTVS KRSFLKLIQ VDKWQEEYNG 1380
GEGPTVVHCL NGGGRSGTFC AISIVCEMLR HQTVDVFAH VKTLRNNKPN MVDLLDQYKF 1440
35 CYEVALEYLN SG 1452

Seq ID NO: 287 Protein Sequence
Protein Accession #: NP_057635.1

40
1 11 21 31 41 51
MGFLQLLVVA VLASEHRVAG AAEVFGNSSE GLIEFSVGKF RYFELNRPFP EEAILHDISS 60
NVTFLFIQIH SQYQNTTVSF SPITLLSNSSE TGTASGLVFI LRPEQSTCTW YLGTSGIQPV 120
QNMAILLSYS ERDPVPGGCG LEFDLDIDPN IYLEYNFFET TIKFAPANLG YARGVDPPPC 180
DAGTDQDSRW RLQYDVYQYF LPENDLTEAM LLKHLQRMVS VPQVKASALK VVTLTANDKT 240
45 SVSFSLSLPQ GVYINVIWMD PFLNTSAAYI PAHTYACSPF AGEGSCASLG RVSSKVFFTL 300
FALLGFFICF FGRHFWKTEL FFIIGFIIMGF FFYILITRLT PIKYDVNLIL TAVTGSVGGM 360
FLVAVMWRFG ILSICMLCVG LVLGFLISSV TFFTPLGNLK IFHDDGVFWV TFSCIAILIP 420
VVFMGCLRIL NILTCGVIGS YSVVLAIDSY WSTSLSYITL NVLKRALNKD FHRAFTNVPF 480
50 QTNDFIILAV WGLAVVSGIT LQIRRRERGR FFFPHYKLV KQERERRVTN ILDPSPYHIP 540
LRERLYGRIT QIKGLFQEQ PAGERTPLLL 570

Seq ID NO: 288 Protein Sequence
Protein Accession #: NP_003811.1

55
1 11 21 31 41 51
MEPPGDWGP FWRSTPRTDV LRLVLYLTFL GAPCYAPALP SCKEDEYPVG SECCPKCSPG 60
YRVKEACGEL TGTVCEPCPP GTYIAHLNGL SKCLQCMCD PAMGLRASRN CSRTENAVCG 120
CSPGHFCIVQ DGDHCAACRA YATSSPGQVR QKGTESQDT LCQNCPPGTF SPNGTLEECQ 180
60 HQTKCSWLVT KAGAGTSSSH WWWFLSGSL VIVIVCSTVG LIIICVRRKP RGDVVVKIVS 240
VQRKRQAEQ EATVIEALQA PPDVTTVAE ETIPSFTGRS PNH 283

Seq ID NO: 289 Protein Sequence
Protein Accession #: NP_000943.1

65
1 11 21 31 41 51
MEPHDSSHMD SEFRYTLFPI VYSIIFVLGV IANGYVLWVF ARLYPCKKFN EIKIFMVNLT 60
MADMLFLITL PLWIVYYQNO GNWILPKFLC NVAGCLFFIN TYCSVAFGLV ITYNRFOAVT 120
RPIKTAQANT RKRGISLSLV IWVAIVGAAS YFLILDSTNT VPDSAGSGNV TRCFEHYEKG 180
70 SVPLIIHIF IVFSFFLVFL ILLFCNLVII RTLLMQPVQO QRNAEVKRRR LWMVCTVLAV 240
FIICFVPHHV VQLPWTLAEL GFQDSKFHQA INDAHQVTLCLLSTNCVLDV VIYCFLTKKF 300
RKHLTEKFYS MRSSRKCSRA TDTVTEVVV PFNQIPGNSL KN 342

Seq ID NO: 290 Protein Sequence
Protein Accession #: NP_003262.1

75
1 11 21 31 41 51
GCLGAIKENK CLLLTFFLLL LLVFLLEATI AILFFAYTDK IDRYAQDLK KGLHLYGTQG 60
NVGLTNAWSI IQTDFRCGV SNYTDWEVY NATRVDPSCC LEFSQGLH APGTWKKAPC 120
YETVKVHLQE NLAVGIFGL CTALVQILGL TFAMTMYCQV VKADTYCA 168

80
Seq ID NO: 291 Protein Sequence
Protein Accession #: NP_005620.1

1 11 21 31 41 51
MAKKSANGI YSVSGDEKKG PLIAPGPDGA PAKGDGPVGL GTPGRLAVP PRETWTRQMD 60

| | | | | | | | |
|----|----------------------------------|-------------|------------|-------------|------------|-------------|------|
| | FIMSCVGFV | GLGNVVRFPY | LCYKNGGGVF | LIPYVLIALV | GGIPIFFLEI | SLGQFMKAGS | 120 |
| | INWVNICPLF | KGLGYASPMV | VFYCNYYIM | VLWGFYYLV | KSFTTTLPPA | TCGHTWNTPD | 180 |
| | CVEIFRHEDC | ANASLANLTC | DQLADRRSPV | IEFWENKVL | LSGGLEVPGA | LWVEVTLCLL | 240 |
| 5 | ACWLVVYFCV | WKGVKSTGKI | VYFTATFPYV | VLVLLVRGV | LLPGALDGI | YYLKPDMWSL | 300 |
| | GSPOVWIDAG | TQIFFSYAIG | LGALTALGYS | NRFNNCYKD | AIILALINS | TSFFAGFVVF | 360 |
| | SILGFMAAEQ | GVHISKVAES | GPGLAFIAYP | RAVTLMPVAP | LWAALFFFM | LLGLDSQFV | 420 |
| | GVEGFTITGL | DLPLASYFR | FQREISVALC | CALCFVIDLS | MVTDGGMYVF | QLEFYYSASG | 480 |
| | TLLWQAFWE | CVVAVVYGA | DRFMDDIACM | IGYRPPCPMK | WCWSFPTPLV | CHGIFIFNVV | 540 |
| 10 | YYEPLVYNN | TVYPWVGEAM | GWAFALSSML | CVPLHLGLCL | LRAKGTMAER | WQHLTQPIWG | 600 |
| | LHHLEYTRAQD | ADVRGLTTLT | PVSESSKVVV | VESVM | | | 635 |
| | Seq ID NO: 292 Protein Sequence | | | | | | |
| | Protein Accession #: NP_037464.1 | | | | | | |
| 15 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| | MKHVLNLYLL | GVVLTLLSIF | VRVMESLEGL | LESPPSGTSM | TTRSQLANTE | PTKGLPDHPS | 60 |
| | RSM | | | | | | 63 |
| | Seq ID NO: 293 Protein Sequence | | | | | | |
| | Protein Accession #: NP_064527.1 | | | | | | |
| 20 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| | MAGASLGARF | YRQIKRHPGI | IPMIGLICLG | MGSAAALYLLR | LALRSPDVCW | DRKNNPEPMN | 60 |
| | RLSPNDQYKF | LAVSTDYKKL | KKDRPDF | | | | 87 |
| 25 | Seq ID NO: 294 Protein Sequence | | | | | | |
| | Protein Accession #: NP_002195.1 | | | | | | |
| 30 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| | MGPGPSRAPR | APRLMLCALA | LMVAAGGCVV | SAFNLDTRFL | VVKEAGNPGS | LFGYSVALHR | 60 |
| | QTERQQRILL | LAPAGRELAV | PDGYNTRTGA | VYLCPLTAHK | DDCERNITV | KNDPGHHIE | 120 |
| | DMWLGTVVAS | QGPAGRVLC | AHRYTQVLWS | GSEDQRRMVG | KCYVRGNLE | LDSSDDWQTY | 180 |
| | HNEMCNSNTD | YLETGMCQGL | TSGGFTQNTV | YFGAPGAYNW | KGNSYMIQK | EWDLSEYSYK | 240 |
| | DPEDQGNLYI | GYTMQVGSFI | LHPKNITIVT | GAPRRHRMGA | VFLLSQEAGG | DLRRRQVLEG | 300 |
| 35 | SQVGAYFGSA | IADLADLNDG | WQDLLVGAPY | YFERKEEVGG | AIYVFMNQAG | TSFPAHPSLL | 360 |
| | LHGPGSGAFG | LSVASIGDIN | QDGFQDIAGV | APFEGLGKVV | IYHSSSKGLL | RQPOQVIHGE | 420 |
| | KLGLPGLATF | GYSLSGQMDV | DENFYDILLV | GSLSHDIVLL | RARPVINIVH | KTLPVPRPAVL | 480 |
| | DPALCTATSC | VQVELCFAYN | QSAGNPYR | NITLAYTLEA | DRDRPPRLR | FAGESAVFH | 540 |
| 40 | GFFSMPEMRC | QKLELLMDN | LRDKLRPIII | SMNYSPLRM | PDRPRLGLRS | LDAYPIINQA | 600 |
| | QALENHTEVQ | FQKECGPDNK | CESNLQMRRA | FVSEQQQKLS | RLQYSRDVRK | LLLSINVTNT | 660 |
| | RTSERSGEDA | HEALLTLVVP | PALLSSVRP | PGACQANETI | FCELGNPFKR | NORMELLIAF | 720 |
| | EVIGVTLHTR | DLQVQLQST | SSHQDNLWPM | ILTLVDYTL | QTSLSMVNHR | LQSFPGGTVM | 780 |
| | GESGMKTVED | VGSPLKYEFQ | VGPMGEGLVG | LGLTLVLGLEW | PYEVSNGKWL | LYPTEITVHG | 840 |
| | NGSWPCRPFG | DLINPLNLTL | SDPGDRPSSP | QRRRRQLDPG | GGQGPPTVTL | AAAKKAKSET | 900 |
| 45 | VLTCAATGRAH | CVWLECPIDP | APVVTNVTVK | ARVMNSTFIE | DYRDFDRVRV | NGWATLFLRT | 960 |
| | SIPTINMENK | TTWFSVDIDS | ELVEELPAEI | ELWLVLVAVG | AGLLLLGLII | LLWKCCKFFK | 1020 |
| | RARTRALYEA | KRQKAEMKSG | PSETERLTD | Y | | | 1051 |
| | Seq ID NO: 295 Protein Sequence | | | | | | |
| | Protein Accession #: NP_005492.1 | | | | | | |
| 50 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| | MGPGPSRAPR | APRLMLCALA | LMVAAGGCVV | SAFNLDTRFL | VVKEAGNPGS | LFGYSVALHR | 60 |
| | QTERQQRILL | LAPAGRELAV | PDGYNTRTGA | VYLCPLTAHK | DDCERNITV | KNDPGHHIE | 120 |
| 55 | DMWLGTVVAS | QGPAGRVLC | AHRYTQVLWS | GSEDQRRMVG | KCYVRGNLE | LDSSDDWQTY | 180 |
| | HNEMCNSNTD | YLETGMCQGL | TSGGFTQNTV | YFGAPGAYNW | KGNSYMIQK | EWDLSEYSYK | 240 |
| | DPEDQGNLYI | GYTMQVGSFI | LHPKNITIVT | GAPRRHRMGA | VFLLSQEAGG | DLRRRQVLEG | 300 |
| | SQVGAYFGSA | IADLADLNDG | WQDLLVGAPY | YFERKEEVGG | AIYVFMNQAG | TSFPAHPSLL | 360 |
| | LHGPGSGAFG | LSVASIGDIN | QDGFQDIAGV | APFEGLGKVV | IYHSSSKGLL | RQPOQVIHGE | 420 |
| 60 | KLGLPGLATF | GYSLSGQMDV | DENFYDILLV | GSLSHDIVLL | RARPVINIVH | KTLPVPRPAVL | 480 |
| | DPALCTATSC | VQVELCFAYN | QSAGNPYR | NITLAYTLEA | DRDRPPRLR | FAGESAVFH | 540 |
| | GFFSMPEMRC | QKLELLMDN | LRDKLRPIII | SMNYSPLRM | PDRPRLGLRS | LDAYPIINQA | 600 |
| | QALENHTEVQ | FQKECGPDNK | CESNLQMRRA | FVSEQQQKLS | RLQYSRDVRK | LLLSINVTNT | 660 |
| | RTSERSGEDA | HEALLTLVVP | PALLSSVRP | PGACQANETI | FCELGNPFKR | NORMELLIAF | 720 |
| 65 | EVIGVTLHTR | DLQVQLQST | SSHQDNLWPM | ILTLVDYTL | QTSLSMVNHR | LQSFPGGTVM | 780 |
| | GESGMKTVED | VGSPLKYEFQ | VGPMGEGLVG | LGLTLVLGLEW | PYEVSNGKWL | LYPTEITVHG | 840 |
| | NGSWPCRPFG | DLINPLNLTL | SDPGDRPSSP | QRRRRQLDPG | GGQGPPTVTL | AAAKKAKSET | 900 |
| | VLTCAATGRAH | CVWLECPIDP | APVVTNVTVK | ARVMNSTFIE | DYRDFDRVRV | NGWATLFLRT | 960 |
| | SIPTINMENK | TTWFSVDIDS | ELVEELPAEI | ELWLVLVAVG | AGLLLLGLII | LLWKCCKFFK | 1020 |
| 70 | RTTRYQIMPK | YHVRIRIEEE | RYPPPGSTLP | TKKHVWTSWQ | TRDQYY | | 1066 |
| | Seq ID NO: 296 Protein Sequence | | | | | | |
| | Protein Accession #: NP_003777 | | | | | | |
| 75 | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| | MDALCGSGEL | GSKFWSNLS | VHTENPDLP | CFQNSLLAWV | PCIYLWVALP | CYLLYLRRHC | 60 |
| | RGYIILSHLS | KLKMLVGLVLL | WCVSWADLFY | SFHGLVHGRA | PAPVFFVTPL | VGVMTLLAT | 120 |
| | LLIQYERLQG | VQSSGVLIIF | WFLCVVCAIV | PFRSKILLAK | ABGEISDPFR | FTTFYIHFAL | 180 |
| | VLSALILACF | REKPPFFSAK | NVDPNYPET | SAGFLSRLFF | WMFTQMAIYG | YRHPLEKDL | 240 |
| 80 | WSLKEEDRSQ | MVQQQLLEAW | RKQEKQTARH | KASAAPGKNA | SGDEVLLGA | RPRPKPSFL | 300 |
| | KALLATFGSS | FLISACFKLI | QDLSFINPQ | LLSILIRFIS | NPMAPSWMGF | LVAGLMFLCS | 360 |
| | MMQSLTLQHY | YHYIFVTGVI | FRTGIMGVII | RKALVITNSV | KRASTVGEIV | NLMSVDAQRF | 420 |
| | MDLAPFLNLL | WSAPLQIILA | IYFLWQNLGP | SVLAGVAFMV | LLIPLNGAVA | VKMRAFQVKQ | 480 |
| | MKLKDSRIKL | MSEILNGIKV | LKLYAMEPSF | LKQVEGIRQG | ELQLLRTAAY | LHTTTTFTWM | 540 |

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10
15

CSPFLVTLIT LWVYVYVDPN NVLDAEKAFV SVSLFNILRL PLNMLPQLIS NLQASVSLK 600
 RIQQFLSQEE LDPQSVVERKT ISPGYAITIH SGTFTWAQDL PPTLHSLDIQ VPKGALVAVV 660
 GPVGGGKSSL VSALIGEMEK LEGKVHMKGS VAYVPOQAWI QNCTLQENVL FGKALNPKRY 720
 QQTLEACALL ADLEMLPGGD QTEIGKEGIN LSGGQORQVS LARAVYSDAD IFLLDDPLSA 780
 VDHSVAKHIF DHVIGPEGVL AGKTRVLVTH GISFLPQTDI IIVLADGQVS EMGPYPALLQ 840
 RNGSFANFLC NYAPDEDQGH LEDSWTALEG AEDKEALLIE DTLSNHTDIT DNDPVTYVVQ 900
 KQFMRQLSAL SSDGEGQGRP VPRRHLPSE KVQVTEAKAD GALTQEEKAA IGTVELSVFW 960
 DYAKAVGLCT TLAICLLYVG QSAAAGANV WLSAWTNDAM ADSRQNTSL RLGVYAALGI 1020
 LQGLVLMAL MAMAAGGIIQA ARVLHQALLH NKIRSPQSFF DTPPSGRILN CFSKDIYVVD 1080
 EVLAPVILML LNSPFNAIST LVVIMASTPL FTVVILPLAV LYTIVQRFYA ATSRQLKRL 1140
 SVSRSPYISH FSETVTGASV IRAYNRSRDF EIIISDTKVA NQRSCYPYII SNRWLSIGVE 1200
 FVGNVVLFA ALFAVIGRSS LNPGLVGLSV SYSLOVTFAL NWMIRMSDL ESNIVAVERV 1260
 KEYSKTETEA PWVVEGSRPP EGWPPRGEVE FRNYSVRYRP GLDLVLRLDS LHVHGGEKVG 1320
 IVGRTGAGKS SMTLCFLFRIL EAAKGEIRID GLNVADIGLH DLRSQTLIIP QDPILFSGTL 1380
 RMNLDPPGSE SEEDINWALE LSHLHTFVSS QPAGLDQFCS EGGENLSVQG RQLVCLARAL 1440
 LRKSRILVLD EATAIDLET DNLIQATIRT QFDTCTVLT I AHRNLTIMDY TRVLVLDKGV 1500
 VAEFDSANL IAARGIFYGM ARDAGLA 1527

20

Seq ID NO: 297 Protein Sequence
 Protein Accession #: NP_002692.1

1 11 21 31 41 51
 | | | | |
 MHFYRLFLGA TRRFLNPEWK GEIDNWCYV LTSLLPFKIQ SQDIKALQKE LEQFAKLLKQ 60
 KRITLGYTQA DVGLTLGLVLF GKVSQTITC RFEALQLSFK NMCKLRPLLQ KWVEEADNNE 120
 NLQEICKAET LVQARKRKRT SIENRVGRNL ENLFLQCPKP TLQOISHIAQ QLGLEKDVVR 180
 VWFCNRRQKG KRSSSDYAQR EDFEAGSPF SGGPVSFPLA PGPHFGAPGY GSPHFTALYS 240
 SVFPFEGEAF PPVSVTTLGS PLHSN 265

30

Seq ID NO: 298 Protein Sequence
 Protein Accession #: NP_005449.1

1 11 21 31 41 51
 | | | | |
 MASPRRSQGP GRPPPPPPPP ARLLLLLLLP LLLPLAPGAW GWARGAPRPP PSSPPLSIMG 60
 LMPLTKEVAK GSGRGVLPA VELAIEQIRN ESLLRPYFLD LRLYDTECDN AKGLKAFYDA 120
 IKYGNHLMV FGVCVPSVTS IIAESLQGMN LVQLSFAATT PVLADKKKYP YFFRTVPSDN 180
 AVNPAILKLL KHQWKVRGT LTQDVQRFSE VRNDLTGVLY GEDIEISDTE SFSNDPCTSV 240
 KKLKQNDVRI ILQGFQDNMA AKVFCCAYEE NMYGSKYQHI IPGWYEPSWV EQVHTEANSS 300
 RCLRNLLAA MEGYIGVDPE PLSSKQIKTI SGKTPQYER EYNNKRSVGQ PSKFHGYAYD 360
 GIWVIAKTLQ RAMETHLASS RHQRIQDFNY TDHTLGRILN NAMNETNFFG VTGQVVRFRG 420
 ERMGTIKFTQ FQDSREVKVG EYNAVADTLE IINDTIRPOG SEPPKDKTII LEQLRKISLP 480
 LYSILSALTI LGMIMASAFI FFINKNRQK LIKMSPPYMN NLIIILGMLN YASIFLFLGLD 540
 GSFVSEKTFE TLCTVRTWIL TVGYTTAFGA MFAKTWRVHA IFKNVKKKKK IKDKQLLVI 600
 VGGMLLIDLC ILICQWAVDP LRRTEKYSM EPDPAGRDIS IRPLLEHCEN THMTIWLGI 660
 YAYKGLMLLF GCFLAWETRN VSIPALNDSK YIGMSVYVNG IMCIIGAASV FLTRDQPNVQ 720
 FCIVALVLIIF CSTITLCLVF VPKLITLRTN PDAATQNRRE QFTQNKQKED SKTSTSVTSV 780
 NQASTSRLEG LQSENHRLRM KITELDKLE EVTMLQLOTP EKTYYIKQNH YQELNDILNL 840
 GNFTSTDDG KAILKMHLDQ NPQLQWNTTE PSRTCKOPIE DINSEPIQR RLSLQLPILH 900
 HAYLPSIGGV DASCVCSPVS PTASPRHRHV PPSFRVMVSG L 941

50

Seq ID NO: 299 Protein Sequence
 Protein Accession #: NP_055632

1 11 21 31 41 51
 | | | | |
 MEAARALRL LVVCGCLALP PLAEPVCPER CDCQHPQHLL CTNRGLRVVP KTSSLPSPHD 60
 VLTYSLQGNF ITNITAFDFH RLQQLRRLDL QYNQIRSLHP KTFEKLRLLE ELYLGNLLQ 120
 ALAPGTAPL RKIRILYANG NEISRLSRGS FEGLESVLKL RLDGNALGAL PDAVFAPLGN 180
 LLYLHLESNR IRFLGKNAPA QLGKLRFLNL SANELQPSLR HAATFAPLRS LSSLILSANS 240
 LQHLGPRIF HLPRLGLLSL RGNQLTHLAP EAFWGLEALR ELRLGNRLS QLPTALLEPL 300
 HSLEALDLG NELSALHLPAT FHLGRRLREL SLRNNALSAL SGDIFAASPA LYRLDLGNG 360
 WTCDCRLRLG KRWMDGWHQ GRLLTVFVQC RHPPALRGKY LDYLDQOQLQ NGSCADPSPS 420
 ASLTADRRRQ PLPTAAGEEM TPPAGLAEEL PPQPQLQQQG RFLAGVAVDG AARELVGNRS 480
 ALRLSRRGPG LQQPPSPSVA AAGPAQSLD LHKKPQRGRP TRADPALAEP TPTASPGSAP 540
 SPAGDPWQRA TKHRLGTEHQ ERAAQSDGGA GLPPLVSDPC DFNKFLCNL TVEAVGADSA 600
 SVRWAVREHR SPRPLGGARF RLLFDRFGQQ PKFHRFVYLP ESSDSATLRE LRGDTPYLVC 660
 VEGVLGGRVC VPAPRDHCAG LVTLPAGSR GGVDYQLLTL ALLTVNALLV LLALAAMASR 720
 WLRRKLRRAR KGAAPVHRH MYSTRRLRS MGTGVSADFS GFQSHRPRTT VCALSEADLI 780
 EFPDCRFMDG AGGAGGSLR REDRLIQRFA D 811

70

Seq ID NO: 300 Protein Sequence
 Protein Accession #: NP_001783.2

1 11 21 31 41 51
 | | | | |
 MCRIAGALRT LLPLLAALLQ ASVEASGEIA LCKTGFPEDV YSAVLSKDVH EGQPLLVKF 60
 SNCNGKRVQ YESSPADFK VDEDMVYAV RSFPLSSEHA KFLIYAQDKE TQEKQWVAVK 120
 LSLKPTLEE SVKESAEEVE IVFPRQFSKH SGHLQQRKRD WVIPPINLPE NSRGPFPOEL 180
 VRIRSDRDN LSLRSYVTCG GADQPPGTIF IINPISGLS VTKPLDREQI ARFHLRAHAV 240
 DINGQVENP IDIVINVIDM NDNRPFLHQ VVNGTVPEGS KPGTYVMVT AIDADDPNAL 300
 NGMLRYRIVS QAPSTPSPM FTINNETGDI ITVAAGLDRE KVQYTLIIQ ATDMEGNPTY 360
 GLSNTATAVI TVTDVNDNPP EFTAMTFYGE VPENRVDIIV ANLTVTDKQ PHTPAWNAVY 420
 RISGGDPTGR FAIGTDPNNS DGLVTVVKPI DFETNRMFVL TAAENQVPL AKGIQHPQS 480
 TATVSVTVID VNEPNYPAPN PKIIRQEBGL HAGTMLTFT AQDPDRYMQ NIRYTKLSDP 540
 ANWLKIDPVN QGIIITIAVLD RESPNVKNNI YNATFLASDN GIPPMSTGT LQIYLLDIND 600
 NAOVLQPEA ETCETPDPS INITALDYDI DPNAGPFAFD LPLSPVTIKR NMTITRLNGD 660
 FAQLNLKIKF LEAGIYEVPI IITDSGNPPK SNISILRVKV QCDSNGDCT DVDRIVGAGL 720

GTGATIAILL CIIILLILVL MFVVMKRRD KERQAKQLLI DPEDDVRDNI LKYDEEGGGE 780
 EDQDYLSQL QQPDVPEPDA IKPVGIRRMED ERPIHAEPQY PVRSAAPHGP DIGDPINEGL 840
 KAADNDPTAP PYDSLIVFDY EGSGSTAGSL SSLNSSSSGG EQDYDYLNDW GPRFKKLADM 900
 YGGGDD 906

5

Seq ID NO: 301 Protein Sequence
 Protein Accession #: NP_058637.1

10 1 11 21 31 41 51 60
 | | | | |
 MVSPRMSGLL SQTIVILALIF LPQTRPAGVF ELQIHSFGPG PGPGAPRSPC SARLPCLRFF 120
 RVCLKPGLSE EAAESPCALG AALSARGPVY TEQPGAPAPD LPLPDGLLQV PFRDAWPGTF 180
 SFIIETWREE LGDQIGGPAP SLARVAGRR RLAAGGPWAR DIQRAGAWEL RFSYRACEP 240
 PAVGTACTRL CRPSAPSRC GPGLRPCAPL EDECEAPLVC RAGCSPEHGF CEQPGECRCL 300
 EGWGTPLCTV PVSTSSCLSP RGPSSATTGC LVPGPQPCDG NPCANGGSCS ETPRSFECTC 360
 PRGFYGLRCE VSGVTCADGP CFNGGLCVGG ADPDSAYICH CPPGFGGSCN EKRVDRCSLQ 420
 PCRNGLCLD LGHALRCRCR AGFAGPRCEH DLDDCAGRAC ANGCTCVGG GAHRCSCALG 480
 FGGRDCRERA DPCAARPCAH GGRCYAHFSG LVCACAPGYM GARCEFPVHP DGASALPAAP 540
 PGLRPGDPQR YLLPPALGLL VAAGVAGAAL LLVHVRRRGH SQDAGSRLLA GTPPEPSVHAL 600
 PDALNNLRTO EGSGDGPFSS VDMNRPEVD PQGIYVISAP SIYAREVATP LFPPLHTGRA 618
 GQRQHLLFPY PSSILSVK

20

Seq ID NO: 302 Protein Sequence
 Protein Accession #: fgenes prediction

25 1 11 21 31 41 51 60
 | | | | |
 MCQAFLLWVL TLWLLKNARC LQYPPEHAQ SCLISEAKQG QAQLPLGWVK WPLHLRSSLS 120
 KRLEKYPPLS LGEIEAQIC KTSSELEPSC DLVTADGSTV VTISENLPAV GFHICQQQDS 136
 HVEGMWNISK ASSQGM

30

Seq ID NO: 303 Protein Sequence
 Protein Accession #: NP_079088.1

35 1 11 21 31 41 51 60
 | | | | |
 MGCGGSRADA IEPYRYESWT RETESTWLT TDSADPPSAA APDSGPEAGG LHSGMLEDGL 120
 PSNGVPRSTA PGGIPNPEKK TNCETQCPNP QSLSSGSLTQ KQNGLQTTEA KRDAKRMPEK 145
 EVTINVTDSI QQMDRSRRIT KNCVN

40

Seq ID NO: 304 Protein Sequence
 Protein Accession #: XP_040550.1

45 1 11 21 31 41 51 60
 | | | | |
 MGADGETVVL KNMLIGINLI LLGSMIKPSE CQLEVTTERV QRQSVEEEGG IANYNTSSKE 120
 QPVVFNHVVN INVPLDNLCS SGLEASAEQE VSAEDETLAE YMGQTSDES QVTFTIRINF 180
 PKKACPCASS AQVLQELLSR IEMLEREVSV LRDQCNANCC QESAATQQLD YIPHCSGHGN 240
 FSPESCOCIC NEGWFPGKNC EPYCPLGCSS RGVCDGQCI CDSEYSGDDC SELRCPTDCS 300
 SRGLCVDEEG VCEEPYTGED CRELRCPGDC SGKGRACNGT CLCEEGYVGE DCGQRQCLNA 360
 CSGRGQCEEG LCVCEEGYQG PDCSAVAPPE DLRVAGISDR SIELEWDGPM AVTEYVISYQ 420
 PTALGGQLQ QRVPGDWSGV TITELPGLT YNISVYAVIS NILSLPITAK VATHLSTPQG 480
 LOFKTITETT VEVQNEPFSF SFDGWEISFI PKNNEGGVIA QVPSDVTSFN QTGLKPGEEY 540
 IVNVVALKEQ ARSPPTSASV STVIDGPTQI LVDRVSDTVA FVEWIPPRAK VDFILLKYGL 600
 VGGEGGRITF RLQPPPLSQYS VQALRPGSRY EVSVSAVRGT NESDSATTQF TTEIDAPKNL 660
 RVGSRATSL DLEWDNSEAE VQEKVVYST LAGEQYHEVL VPRGIGPTR ATLTLDPVGT 720
 EYGVGISAVM NSQQSVPMAT NARTELDSPR DLMVTASSET SISLIWTKAS GPIDHYRITF 780
 TPSSGIASEV TVPKORTSYT LTDLEPGAET IISVTAERGR QQSLESTVDA FTGFRPISHL 840
 HFSHVTSSSV NITWSDPSP ADRLILNYSR DEEEEMMEV SLDATKRHAV LMGLOPATEY 900
 IVNLVAHGT VTSEPIVGS ITGIDPPKDI TISNVTKDSV MVSWSPPVAS FDYRYVSYP 960
 TVQGRLDSSV VPNTVTEFTI TRLNPAETEY ISLNSVRGRE ESERICTLVH TAMDNVPDLI 1020
 ATNITPTEAL LQWAPVGEV ENYVIVLTHF AVAGETILVD GVSEEFRLVD LLPSTHYTAT 1080
 MYATNGPLTS GTISTNFTL LDPPANLTAS EVTRQSALIS WQPPRAEIN YVLTYKSTDG 1140
 SRKELIVDAE DTHIRLEGLL ENTDTYVLLQ AAQDTWSSI TSTAFTTGR VFPHPQDCAQ 1200
 HLMNGDTLSG VYPIFLNGEL SQKIQVYCDM TTDGGGWIVF QRRQNGQTD FFRKWADYRVG 1260
 FGNVEDEFWL GLDNIHRITS QGRYELRVDM RDQEEAFAS YDRFSVEDSR NLYKLIRIGSY 1320
 NGTAGDSLVS HQGRPFSTED RDNDAVTNC AMSYKGAWWY KNCHRTNLNG KYGESRHSQG 1358
 INWYHWKGHE FSIPFVEMM RPNVHRLMAG RKRQSLQF

65

Seq ID NO: 305 Protein Sequence
 Protein Accession #: NP_005874.1

70 1 11 21 31 41 51 60
 | | | | |
 MASSVAPYEQ LVRQVEALKA ENSHLRQELR DNSSHLKLE TETSGMKEVL KHLQKLEQE 120
 ARVLVSSGQT EVLEQLKALQ MDITSLYNLK FQPPITLGP EPARTPEGSPV HGSQPSKDSF 180
 GELSRATIRL LEELDRERCF LLNEIEKEEK EKLWYYSQIQ GLSKRLDELP HVETQFSQM 240
 DLIRQQLFEF AQHISLMEE RFGTSDVMQ RAQIRASRL QIDKELLEAQ DRVQOTEPQA 300
 LLAVKSVFVD EDPTEVPTH PEDGTPOPGN SKVEVFWLL SMLATRDQED TARTLLAMSS 360
 SPESCVMARR SGCLPLLLQI LHGTEAAAGG RAGAPGAPGA KDARMRANAA LHNIVFSQPD 420
 QGLARKEMRV LHVLEQIRAY CETCDWLQA RDGGPEGGGA GSAPIPIEPQ ICQATCAVMK 480
 LSFDEEYRRA MNEGLGLQAV AELLQVDYEM HKMTRDPLNL ALRRYAGMTL TNLTFGDVAN 540
 KATLCARRGC MEATVAQLAS DSEELHQVVS SILRNLWSRA DINSKKVLRE AGSVTALVQC 600
 VLRATKESTL KSVLSALWNL SAHSTENKAA ICQVDGALGF LVSTLTYSKCO SNLSLIIESG 660
 GGILRNVSLL VATREDYRQV LRDNHCLQTL LQHLTSHSLT IVSNACGTLW NLSARSARDQ 720
 ELLWDLGAVG MLRNLVSHKH XMIAMGSAAA LRNLLAHRPA KHQAAATAVS PGSCVPSLYV 780
 RKQRALEAEL DARHLAQALE HLEKQGPAA EAATKKPLPP LRHLDGLAQD YASDSGCFDD 840
 DDAPSSLAAA AATGEPASPA ALSFLGSPF LQGGALARTP PTRRGKEAE KDTSGEAAVA 900
 AKAKAKLALA VARIDQVLED ISALHTSSDD SFLSSGDPG QEAPREGRAQ SCSPCRGPEG

80

| | | | | | | | |
|----|--------------------------------------|------------|------------|-------------|------------|------------|------|
| | GRREAGSRAH | PLRLKAAHA | SLSNDSLSNG | SASDGYCPRE | HMLPCPLAAL | ASRREDPRCG | 960 |
| | QRPSPRLDLD | LPGCQAEPPA | REATSADARV | RTIKLSPTYQ | HVPLLEGASR | AGAELAGPG | 1020 |
| | ISPGARKQAW | LPADHLSKVP | EKLAAAPLSV | ASKALQKLA | QEGPLSLSRC | SSLSSLSSAG | 1080 |
| | RPGPSEGGDL | DDSDSSLEGL | EEAGPSEAE | DSTWRAPGAT | SLPVAIPAPR | RNRGRGLGVE | 1140 |
| 5 | DATPSSSEN | YVQETPLVLS | RCSSVSSLGS | FESPSSIASSI | PSEPCSQQGS | GTISPSELDP | 1200 |
| | SPGQTMPPSR | SKTPPLAPAP | QGPPEATQFS | LQWESYVKRF | LDIADCRERC | RLPSELDAQS | 1260 |
| | VRFTVEKPDE | NFSSASSLSA | LALHEHYVQQ | DVELRLLP | CPERGGGAGG | AGLHFAGHRR | 1320 |
| | REEGPAPTS | RPRGAADQEL | ELLRECLGAA | VPARLRKVAS | ALVPGRRALP | VPVYMLVPAP | 1380 |
| | APAEEDDSCT | DSAEGTFPVF | SSAASLSDET | LQGPFRDQPG | GPAGRQRPTG | RPTSARQAMG | 1440 |
| 10 | HRHKAGGAGR | SABQSRGAGK | NRAGLELPLG | RPPSAPADKD | GSKPGRTRGD | GALQSLCLTT | 1500 |
| | PTEEAIVCFY | GNDSDDEPPA | AAPTPTTHRT | SAIPRAPTRE | RPQGRKEAPA | PSKAAPAAP | 1560 |
| | PARTQPSLIA | DETPPCYSL | SSASSLSEPE | PSEPPAVHPR | GREPAVTKDP | GPGGGRDSSP | 1620 |
| | SPRAAEELQ | RCISSALPRR | RPPVSGLR | KPRATRLDER | PAEGSRERGE | EAAGSDRASD | 1680 |
| | LDSVENRAIQ | EGANSIVTWL | HQAAAATREA | SSESDSILSF | VSGLSVGSTL | QPPKHKRGQ | 1740 |
| 15 | AEGEMGSARR | PEKRGAAVSK | TSGSPRSPAG | PEKPRGTQKT | TPGVPAVLRG | RTVIYVPSPA | 1800 |
| | PRAQPKGTFG | PRATPRKVP | PCLAQPAAPA | KVPSPGQORS | RSIHRPAKTS | ELATLSQPPR | 1860 |
| | SATPPARLAK | TPSSSSSQTS | PASQPLPRKR | PPVTQAAGAL | PGPGASVPVK | TPARTLLAKQ | 1920 |
| | HKTQSPVRI | PFQRPARRG | PPPLARAVPE | PGPRGRAGTE | AGPGARGGRL | GLVRVASALS | 1980 |
| | SGSESSDRSG | FRQLTFIKE | SPGLRRRRE | LSSAESASA | PQGASPRRGR | PALPAVLCS | 2040 |
| 20 | SRCEELRAAP | RQGPAPARQR | PPAARPSGGE | RPARRTTSES | PSRLPVRAPA | ARPETVKRYA | 2100 |
| | SLPHISVARR | PGDGAAPAPA | SADAARRSSD | GEPRPLPRVA | APGTTWRRIR | DEDVPHILRS | 2160 |
| | TLPATALLPR | GSTPEDAPAG | PPRKTSDAV | VQTEEVAAPK | TNSSTSPSLE | TREPPGAPAG | 2220 |
| | GQLSLGSDV | DGPSLAKAPI | SAPFVHEGLG | VAVGGFPASR | HGSPSRARSV | PPFNYVPSPM | 2280 |
| 25 | VVAATDSAA | EKAPATASAT | LLE | | | | 2303 |
| | Seq ID NO: 306 Protein Sequence | | | | | | |
| | Protein Accession #: NP_006356.1 | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| 30 | MFLTEDLITF | NLRNLLFQL | WESSFSPGAG | GFCTTLPPSF | LRVDDRATSS | TTDSSRAPSS | 60 |
| | PRPPGSTSHC | GISTRCTERC | LCVLPLRTSQ | VPDVMAPQHD | QEFKFDLAYS | CLGKSFMSMN | 120 |
| | QDLGYSTSS | LALGLAWLSW | ETKKQNVHL | VGLDSL | | | 156 |
| | Seq ID NO: 307 Protein Sequence | | | | | | |
| | Protein Accession #: AAH32726.1 | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| 35 | MASTRSIELE | HFEERDKRPR | PGSRRGAPSS | SGGSSSSGPK | GNGLIPSPAH | SAHCSFYRTR | 60 |
| | TLQALSSEKK | AKKARFYRNG | DRYFKGLVFA | ISSDRFRSPD | ALLIELTRSL | SDNVNLPQGV | 120 |
| 40 | RTIYITDGR | KVTSLEDELE | GESYVCASNE | PFRKVDYTKN | INPNWSVNIK | GGTSRALAAA | 180 |
| | SSVKSEVKES | KDFIKPKLVT | VIRSGVKPRK | AVRILLNKKT | AHSFEQVLTD | ITEAIKLDSG | 240 |
| | VVKRLCTLDG | KQVTCIQDF | GDDDFIACG | PEKFRYAQDD | FVLHSECRV | LKSSYSRSSA | 300 |
| | VKYSGSKSPG | PSRRSKSPAS | VNGTFSSQLS | TPKSTKSSSS | SPTSPGSRFG | LKISAHGRSS | 360 |
| | SNVNGGPELD | RCISPEGVNG | NRCSESSTLL | EKYKIGKIVG | DGNFAVVKEC | IDRSTGKEFA | 420 |
| 45 | LKIIDKAKCC | GKEHLIENEV | SILRRVKHPN | IIMLVEEMET | ATELFLVME | VKGGLDFDAI | 480 |
| | TSSTKYTERD | GSAMVYNLAN | ALRYLHGLSI | VHRDIKPNEL | LVCEYPDGTK | SLKLGDFGLA | 540 |
| | TVVEGLYTV | CGTPTVAPE | IAETGYGLK | VDIWAAGVIT | YILLCGFPFP | RENNLQEDL | 600 |
| | FDQILAGLKE | FPAPYWDNIT | DSAKELISQM | LQVNVEARCT | AGQILSHPWV | SDDAQENNM | 660 |
| 50 | QAEVTGKLKQ | HFNNALPKQN | STTTGVSVM | FDLTV | | | 695 |
| | Seq ID NO: 308 Protein Sequence | | | | | | |
| | Protein Accession #: NP_055978.2 | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| 55 | MEEMEEELKC | PVCSFYREP | IILPCSHNLC | QACARNILVQ | TPESESPQSH | RAAGSGVSDY | 60 |
| | DYLDLDMKSL | YSEADSGYGS | YGGFASAPTT | PCQKSPNGVR | VFPAMPPPPA | THLSPALAPV | 120 |
| | PRNSCTICPQ | CHRSLLIDDR | GLRGFPKNRV | LEGVIDRYQQ | SKAAALKCQL | CEKAPKEATV | 180 |
| | MCEQCDVFCY | DPICRLRCHP | RGPLAKHRLV | PPAQGRVSR | LSPRKVSTCT | DHELENHSMY | 240 |
| 60 | CVQCKMPVCY | QCLEEGKHSS | HEVKALGAMW | KLHKSQLSQA | LANGLSRAKE | AKEFLVQLRN | 300 |
| | MVQIQIENSV | EFEACLVAQC | DALIDALNRR | KAQLLARVVK | EHEHKLKVVR | DQISHCTVKL | 360 |
| | RQTTLGLMEYC | LEVIKENDPS | GFLQISDALI | RRVHLTDQW | GKGTLPTRMT | TDFDLSLONS | 420 |
| | PLLQSIHQLD | FVQVKASSPV | PATPILQLEE | CCTHNSATL | SWKQPPLSTV | PADGYILELD | 480 |
| | DGNGGQFREV | YVGKETMCTV | DGLHFNSTYN | ARVKAPNKTG | VSPYSKTLVL | QTSEVAVPAF | 540 |
| | DPGSAHSDII | LSNDNLTVTC | SSYDDRVLG | KTGFSKGIHY | WELTVDRYDN | HPDPAPGVAR | 600 |
| 65 | MDVMKDVMLG | KDDKAWAMYV | DNNRSWFMGN | NSHTNRTEGG | ITKGATIGVL | LDLNRKNLTF | 660 |
| | FINDEQGGPI | AFDNEVGLFF | PAVSLNRNVQ | VTLHTGLPVP | DFYSSRASIA | | 710 |
| | Seq ID NO: 309 Protein Sequence | | | | | | |
| | Protein Accession #: NP_116025.1 | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| 70 | MEDLEEDVRF | IVDETLDFFG | LSPSDSREEE | DITVLVTPEK | PLRRGLSHRS | DPNAVAPAPQ | 60 |
| | GVRLSLGPLS | PEKLEELDE | ANRLAAQLEQ | CALQDRESAG | EGLGPRRVKP | SPRRETFVLK | 120 |
| | DSVPRDLLPT | VNSLTRSTPS | PSSLTPLRLS | NDRKGVSRL | RATSGKRPNS | MKRESPTCNL | 180 |
| 75 | FPASKSPASS | PLTRSTPPVR | GRAGPSGRAA | ASPTPIRSV | LAPQPSTNS | QRLPRPQGA | 240 |
| | AKSSSQLPIT | SAIPRPASRM | PLTSRSVPPG | RGALPPDSLS | TRKGLPRPST | AGHRVRESGH | 300 |
| | KVPVSQRLNL | PVMGATRSNL | QPPRKVAVPG | PTR | | | 333 |
| | Seq ID NO: 310 Protein Sequence | | | | | | |
| | Protein Accession #: ref XP_166946.2 | | | | | | |
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | |
| 80 | MGSDSRLPEM | EEKSGDGKAG | MSGALLAEVK | NQGLKLCWM | LVLKAEVLEW | YTSVIVGQGG | 60 |
| | HLKMDLLKE | RHRKRYLQKP | IKRCSGLMGL | NWSLRPAISS | SPLARSQEKH | HGAKNEGVMK | 120 |

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ALSFRLRLKLR KRPPTPPSQA KSWRGRTGSA ADSPGAAAMA VQAALLSTHP FVPFGFGGSP 180
 DGLGGAGFAL DKGCCPEDDE TGAPAGALLS GAEGGDVREA TRDLSFIDS ASSNIKALD 240
 KPGKSKRKVN HRNAPTVAAP AHGKAAPRRE ASQAAAAASL QSRSLAALFD SLRHVPGGAE 300
 PAGGEVAAPA AGLGGAGTGG AGGDVAGPAG ATAIPGARKV PLRARNLPSS FFTEPSRAGG 360
 GCGGPGSPDV SLGDLKGAE AVEFFELLGP DYAGTEAAV LLAAEPLDVF PAGASVLRGP 420
 PELEPGLFEP PPAVVGNNLY PEPWSVPGCS PTKKSPLTAP RGGLTINEPL SPLYPAAADS 480
 PGGEDGRGHL ASFAFFFPDC ALPPPPPPHQ VSYDYSAGYS RTAYSSLMRS DGVWEGAPGE 540
 EGAHRD 546

Seq ID NO: 311 Protein Sequence

Protein Accession #: NP_071406.1

1 11 21 31 41 51
 | | | | |
 MAPTKPSFQQ DPSRRERLQA LRKEKSRDAA RSRRGKENFE FYELAKLLPL PAATISQLDK 60
 ASIIRLTISY LKMRDFANQC DPPWNLMEG PPNTSVKGA QRRRSFALA IEVFEHLGS 120
 HILQSLDGFV FALNQEGKFL YISSETVSYL GLSQVELTGS SVFDYVHPGD HVEMAEQLGM 180
 KLPPGRGLLS QGTAEKGASS ASSSSQSETP EPVESTSPSL LTTDNTLERS FFIRMKSTLT 240
 KRGVHIKSSG YKVIHITGRL RLRSVLSHGR TVPSQIMGLV VVAHALPPPT INEVRIDCHM 300
 FVTRVMDLNL IYCNIRISD YMDLTPVDIV GKRCYHFIHA EDVEGIRHSH LDLLNKGCQV 360
 TKYYRWMQKN GGYIWIQSSA TIAINAKNAN EKNIWVNYL LSNPEYKDTF MDIAQLPHLP 420
 EKTSESSETS DSESDDKTS GITEDNENSK SDEKGNQSEN SEDPEPRKK SGNACNDNMN 480
 CNDGHSNNS PDSRSDDSF EHSDFENPKA GEDGFGALGA MQIKVERVEY SEDDLRLQNC 540
 ESLTSDSAKD SDSAGEAGAQ ASSKHQKRRK RRRKQKGSAS SRRRLSSASS PGGLDAGLVE 600
 PPRLLSSPNS ASVLKIKTEI SEPINFNDNS SIWNPYNRE ISRNESPYSM TKPPSSEHFP 660
 SPQGGGGGGG GGGGLHVAIP DSVLTTPGAD GAAARKTPG ASATAALAPV ASDPLSPPLS 720
 ASPRDKHPGN GGGGGGGGGG AGGGGPSASN SLLYTGDLEA LQRLQAGNVV LPLVHRVTGT 780
 LAATSTAAQR VYTTGTIRYA PAEVTLMQOS NLLPNAHAVN FVDVNSPGFG LDPKTPMEHL 840
 YHKVHRLNMS GPFPGAVSAA SLTQMPAGNV FTTAEGLFST LPFVVSNGI HAAQTILERKE 900
 D 901

Seq ID NO: 312 Protein Sequence

Protein Accession #: NP_005797.1

1 11 21 31 41 51
 | | | | |
 MDSASLVSS RPSSPEPDDL FLPARSKGSS GSAFTGCTVS SSTPSDCPPE LSAELRGAMG 60
 SAGAHPGDKL GSGGFKSSSS STSSSTSSAA ASSTKKDKKQ MTEPELQQLR LKINSRERKR 120
 MDDLNIAMDG LREVMPIAHG PSVRKLSKIA TLLARNYIL MLTNSLEEMK RLVSEIYGGH 180
 HAGFHPACG GLAHSAPLPA ATAHAAAAAH AAHPAVVHP ILPPAAAAAA AAAAAAVSS 240
 ASLPGSLGPS VGSIRPPHGL LKSPSAAAAA PLGGGGGGSG ASGGFQHWGG MPCPCSMQCV 300
 PPHHHVSAM GAGSLPRLTS DAK 323

Seq ID NO: 313 Protein Sequence

Protein Accession #: XP_045127.3

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 50
 55
 60
 65
 70

1 11 21 31 41 51
 | | | | |
 MTVLEESSIS LMSSVVAADF EFEEEDPQVFN TLFPSRPPIV LSSRSMEISE TSVGISAEVD 60
 MSSVTTQVP PAHGRLSVPA SLDPATAGSL VAETQVTPSS VTTAFFSVIT SILLDSFSV 120
 IANKNTPSLA VRDPSVFTPY SLVPSVSSL FSDQERSFSS EHKPRGALDF ASSFFSTPPL 180
 ELSGSISPPS EAPASLSLMP SDLSPTFSQS FSPLVETFTL FDSSDLQSSQ LSLPSSTNLE 240
 FSQIQPSSEL PLNTIMLLPS RSEVSPHSSP PSDSLEFVEA STVSLTDESA HFTSAFIETT 300
 SYLESSLISH ESAVATLVPP GSESFIDILTA GIQATSPILT VHTTPILTES SLFSTLTTPD 360
 DQISALDGHV SVLASFSKAI PTGTVLITDA YLPSGSSFVS EATPFPLPTE LTVGVPSLTP 420
 TEVPLNTSTE VSTTSTGAAT GGPLDSTLMG DAASQSPFES SAAPPLPSLR PVTAFTLEAT 480
 VDTPTLATAK PPYVCITVLA DAYLITTVLA RRAVQEIYIT AIKEVLRIHF NRAVELKVYE 540
 LFTDFTFLVT SGPFVYTAIS VINVLINSKL VRDQTLPLS VKPSFLVPES RFQVQTVLQF 600
 VPPSVDTGFC NTFQRIEKL MTALFEVRKH HQGTYNLTQV ILNITISSR VTPRRGPVNI 660
 IFAVKSTQGF LNSSEVSELL RNLSVVEFSF YLGYVVLQIA EPFQYVQLNL SOLLKSSWVR 720
 TVLLGVMEKQ LQNEVFQAEH ERKLAQLLSE VSTRRRMWR ATVAAGNSV VQVNVSRLEG 780
 DDNPVQLIYF VEDQDGERLV AVKSSDLINK MDLQRAAIL GYRIQGVIAQ PVDRVKRPS 840
 ESQSNNLWVI VGVVIVLVV MVIVVILYWK LCRTDKLDFQ PDTVANIQR QKLQIPSVKG 900
 FDFAKQLHCG HNKDDILIIH EPAPLPGLK DHTTPSENGD VPSPKSKIPS KNVHRGRVS 960
 PSDADSTVSE ESSERDAGDK TPGAVNDGRS HRAPOGPPPL PSSGNEQHSS ASIFEHVDRI 1020
 SRPPEASRRV PSKIQLIAMO PIPAPPVQRP SPADRVAESN KINKEIQTAL RHKSEIEHHR 1080
 NKIRLAKRR GHYEFPPVDD LSSGDTKERH RVYRRAQMOI DKILDPTASV PSVFIEPRKS 1140
 SRIKRSKPR RKHQVNGCPA DAEKDLITT DSDGTYRRPP GVHNSAYIGC PSDPDLPADV 1200
 QTPSSVELGR YPALPPASQ YIPPPQSIEE ARQTMHSLLD DAFALVAPSS QPASTAGVGP 1260
 GVPPGLPANS TPSQEERRAT QWGSFYSPAQ TANNPCSRYE DYGMTPTGP LPRPGFGPGL 1320
 LQSTELVPPD PQQSQASAEA PFAARGIYSE EMPVARPRP VGGTTGSQIQ HLTQVGIASR 1380
 IGAQPVEIPP SRGSQYGGGP WPSYGEDEAG RREAVPRTSG REPSAFSGNL PHRGLQGPGL 1440
 GYPTSTEDL QPGHSSASLI KAIREELLRL SQKSTVQNF HS 1482

Seq ID NO: 314 Protein Sequence

Protein Accession #: BAC04820.1

75
 80

1 11 21 31 41 51
 | | | | |
 MAPRPLGLV LALGAAAVL GSVLFILMKT YFGRGRERRR DRGEAWWGAE AARLPEWDEW 60
 DPEDEDEEP ALEEELEQREV LVLGLDGACK STFLRVLSGK PPLEGHIPTW GFNSVRLPTK 120
 DFEVDLLIEG GSONLRFYWK EFVSEVDVLV FVVDSDRLR LPWARQELHK LLDKDPDLPV 180
 VVVANKQDLS EAMSMGELQR ELGLQAIDNQ REVFLAAASI APACPTFEED GTVHIWKLLE 240
 ELLS 244

Seq ID NO: 315 Protein Sequence

Protein Accession #: NP_06563.1

1 11 21 31 41 51

| | | | | | | | | |
|----|--|----------------------------------|-------------|-------------|-------------|------------|-------------|-----|
| | | MARRAGGARM | FGSLLLFALL | AAGVAPLSWD | LPEPRSRASK | IRVHSRGNLW | ATGHFMGKKS | 60 |
| | | LEPSSPSHWG | QLPTPLPLRDQ | RLQLSHDLLG | ILLKKALGV | SLSRPAPQIQ | YRRLLVQILQ | 120 |
| 5 | | K | | | | | | 121 |
| | | Seq ID NO: 316 Protein Sequence | | | | | | |
| | | Protein Accession #: NP_002046.1 | | | | | | |
| | | 1 | 11 | 21 | 31 | 41 | 51 | |
| 10 | | MERRRITSAA | RRSYVSSGEM | MVGGLAPGRR | LQPGTRLSLA | RMPPPLPTRV | DFSLAGALNA | 60 |
| | | GFKETRASER | AEMMELNDRF | ASYIEKVRFL | EQNKALAAE | LNQLRAKEPT | KLADVYQAEI | 120 |
| | | RELRLRLDQL | TANSARLEVE | RDNLAQDLAT | VRQKLQDETN | LRLEAENNLA | AYRQEADEAT | 180 |
| | | LARLDLERKI | ESLEEEIRFL | RKIHEEEVRE | LQQLARQOV | HVELDVAKPD | LTAALKEIRT | 240 |
| 15 | | QYEMASSNM | HEAEWYRSK | FADLTDAAR | NAELLRQAGH | EANDYRRQLQ | SLTCDLESIR | 300 |
| | | GTNESLERQM | REQEERHVRE | AASYQEAAR | LEEEGQSLKD | EMARHLQEYQ | DLNVLKALD | 360 |
| | | IELATYRKL | EGEENRITIP | VQTFNSNLQIR | ETSLDTKSVS | EGHLKRNIVV | KTVEMRDGEV | 420 |
| | | IKESKQEHKD | VM | | | | | 432 |
| | | Seq ID NO: 317 Protein Sequence | | | | | | |
| | | Protein Accession #: AAA19191.1 | | | | | | |
| | | 1 | 11 | 21 | 31 | 41 | 51 | |
| 20 | | MRLSSLSGGS | SVSSDAEEYQ | PPIWKSILYQ | LQQAEPKPKR | IICPREVENR | PKYVGREFHG | 60 |
| | | IISREADEL | LGGVEGAYIL | RESQRQPGCY | TLALRFGNQT | LNRYLFHDGK | HFVGEKRFES | 120 |
| 25 | | IHDLYTDGLI | TLYIETKAAE | YISKMTTNP | YEHIGYATLL | REKVSRRLSR | SKNEPRKTNV | 180 |
| | | THEEHTAVEK | ISSLVRRRAAL | THNDNHFNYE | KTHNPKVHTF | RGPWCEYCA | NFMWGLIAQG | 240 |
| | | VRCSOGLNV | HKQCSKHVP | DCQPLKRIK | KVYCCDLTTL | VKAHNTQRP | VVDICIREIE | 300 |
| | | ARGLKSEGLY | RVSGFTEHIE | DVKMAFDRDG | EKADISANVY | PDINIITGAL | KLYFRDLPIP | 360 |
| 30 | | VITYDTYSKF | IDAAKISNAD | ERLEAVHEVL | MLLPPAHYET | LRYLMIHLKK | VTMNEKDNFM | 420 |
| | | NAENLGIVFG | PTLMRPFEDS | TLTTLHDMRY | QKLIVQILIE | NEDVLF | | 466 |
| | | Seq ID NO: 318 Protein Sequence | | | | | | |
| | | Protein Accession #: XP_113553.1 | | | | | | |
| | | 1 | 11 | 21 | 31 | 41 | 51 | |
| 35 | | MKRAHPEYSS | SDSELDETIE | VEKESADENG | NLSSALGSMS | PTTSSQILAR | KRRRGIIIEKR | 60 |
| | | RDRIRNNLS | ELRRLVPSAF | EKQGSAKLEK | AEILQMTVDH | LKMLHTAGGK | GYFDAHALAM | 120 |
| | | DYRSLGFREC | LAEVARYLSI | IEGLDASDPL | RVRLVSHLAN | YASQREASG | AHAGLGHIPW | 180 |
| 40 | | GTVPFGHPHI | AHPLLLPQNG | HGNAGTTASP | TEPHHQGRLG | SAHPEAPALR | APPSGSLGPV | 240 |
| | | LPVVTASAKL | SPPLLSVAS | LSAFFPSFGS | FHLSPNAL | PSAFTQAANL | GKPYRPMGTE | 300 |
| | | IGAF | | | | | | 304 |
| | | Seq ID NO: 319 Protein Sequence | | | | | | |
| | | Protein Accession #: NP_001927.2 | | | | | | |
| | | 1 | 11 | 21 | 31 | 41 | 51 | |
| 45 | | MTAKEPSAS | GKSVOQOEQE | LVGSNPPORN | WKGIAIALLV | ILVICSLIVT | SVILLTPAED | 60 |
| | | NSLSQKKKVT | VEDLFSEDFK | IHDPEAKWIS | DTEFIYREQK | GTVRLWNVET | NTSTVLIEGK | 120 |
| | | KIESLRIRAY | EISPDREYAL | FSYNVEPIYQ | HSYTGYYVLS | KIPHGDPQSL | DPPEVSNAKL | 180 |
| 50 | | QYAGWGPQKQ | QLIFIFENNI | YYCAHVCKQA | IRVSTGKEG | VIYNGLSDWL | YEEIEILKTHI | 240 |
| | | AHWSPDGTR | LAYAAINDSR | VPIMELPTYT | GSIIYPTVKPY | HYPKAGSENP | SISLHVIGLVN | 300 |
| | | GPTHDLNMP | DDPRRMREY | ITMVKWATST | KVAVTILNRA | QNVSILTLC | ATTGVCTKKH | 360 |
| | | EDESEAWLHR | QNEEPVFSKD | GRKFFFIIRAI | PQGGRGKFYH | ITVSSSQPNS | SNDNIQSITS | 420 |
| 55 | | GDWDVTKILA | YDEKGNKIYF | LSTEDLPRRR | QLYSANTVGN | FNRCQLSCDL | VENCTYFAS | 480 |
| | | FSHSMDFLL | KCEGPGVPMV | TVHNTDKKK | MPDLETNEHV | KKAINDRQMP | KVEYRDIEID | 540 |
| | | DYNLPMQILK | PAFTTDTTHY | PLLLVVDGTP | GSQSVAEKFE | VSWETVMVSS | HGAVVVKCDG | 600 |
| | | RSGSGFQTKL | LHEVRRRLGL | LEEKDQMEAV | RTMLKEQYID | RTRVAVFGKD | YGGYLSTYIL | 660 |
| | | PAKGENQGGT | FTCGSALSPI | TDFKLYASAF | SERYLGLHGL | DNRAYEMTKV | AHRVSALEEQ | 720 |
| 60 | | QPLIHPTAD | EKIHFQHTAE | LITQLIRGKA | NYSLIQIYPDE | SHYFTSSSLK | QHLRYRSIINF | 780 |
| | | FVECFRIQDK | LPTVTAKED | EED | | | | 803 |
| | | Seq ID NO: 320 Protein Sequence | | | | | | |
| | | Protein Accession #: XP_087461.1 | | | | | | |
| | | 1 | 11 | 21 | 31 | 41 | 51 | |
| 65 | | MLPLLAALLA | AACPLPPVRG | GAADAPGLLG | VPSNASVNAS | SAASPSPRGC | WPRRPPGPPS | 60 |
| | | ARARRRRRRR | RRLCNISVQR | QMLSSLLVRN | GRPRGFQCDL | LLFSTNAHGR | AFFAAAFHRV | 120 |
| | | GPPLLIHHLG | LAAGGAQQDL | RLCVGCGWVR | GRRTGRLRPA | AAPSAAAATA | GAPTALPAYP | 180 |
| 70 | | AAEPPGGLNL | QGEPLHFCC | DFSLEELQGE | PGWRLNRKPI | ESTLVACFMT | LVIVVWSVAA | 240 |
| | | LIWVPVPIAG | FLPNGMEQRR | TTASTTAATP | AAVPAGTTAA | AAAAAAAAAA | AVTSGVATK | 299 |
| | | Seq ID NO: 321 Protein Sequence | | | | | | |
| | | Protein Accession #: NP_036393.1 | | | | | | |
| | | 1 | 11 | 21 | 31 | 41 | 51 | |
| 75 | | MDLQGRGVPS | IDRLRVLLML | FHTMAQIMAE | QEVENLSGLS | TNPEKIDIFV | RENGTTCLMA | 60 |
| | | EFAAKFIVPV | DVWASNYVDL | ITEQADIALT | RGAEVKGRCG | HSQSELQVFW | VDRAVALKML | 120 |
| | | FVKESHNMKS | GPEATWRLSK | VQFVYDSSEK | THPKDAVSAG | KHTANSHHLS | ALVTIPAGKSY | 180 |
| 80 | | EQQAQQTISL | ASSDPQKTIV | MILSAVHIQ | PDIIISDFVMS | EEHKCPVDER | EQLEETLPLI | 240 |
| | | LGLILGLVIM | VTLAIYVHH | KMTANQVQIP | RDRSQYKHHG | | | 280 |
| | | Seq ID NO: 322 Protein Sequence | | | | | | |
| | | Protein Accession #: NP_653187 | | | | | | |
| | | 1 | 11 | 21 | 31 | 41 | 51 | |

757

PRGPHGGAAS GLNGCCRCGA RGPESRLLEF YLAMPFATPM EELARRSLA QDAPPLPVPG 120
VLLKEFTVSG NILTIRLTAA DHRQLQLSIS SCLQQLSLIM WITQCFLPVF LAQPPSQRR 180

5 Seq ID NO: 330 Protein Sequence LEK6
Protein Accession #: NP_066274

1 11 21 31 41 51
MQABGQGTGG STGDADGPGG PGIPDGPGGN AGGPGEAGAT GGRGPRGAGA ARASGPRGGA 60
10 PRGPHGGAAS AQDGRCPGCA RRPDSRLLOF RLTAADHRQL QLSISSCLQQ LSLLMWITQC 120
FLPVFLAQAP SQRR 135

15 Seq ID NO: 331 Protein Sequence
Protein Accession #: NP_008859.1

1 11 21 31 41 51
MDLVLRCLL HLAIVIGALLA VGATKVPNRQ DWLGVSRLR TKAWNRLYP EWTEAQRLLDC 60
NRGGQVSLKV SNDGPTLIGA NASFSIALNF PGSQKVLDPG QVIWVNTII NGSQVWGGQP 120
VYPQETDDAC IPFDGPGPCS GWSQKRSFV YVWKTWQYV QVLGGPVSGL SIGTGRAMLG 180
20 THTEVTVYH RRGSRYSVPL AHSSAFTIT DQVPFSVSVS QLRALDGGNK HFLRNQPLTF 240
ALQLHDPGSGY LAEADLSYTM DFGDSSGTLI SRALVVTHTY LEPGPVTAQV VLQAAIPLTS 300
CGSSPVPVGTG DGHRTAEAP NTTAGQVPTT EVVGTTPGQA PTAEPSGITS VQVPTTEVIS 360
TAPVQMPTAE STGMTPEKVP VSEVMGTTA EMSTPEATGM TPAEVSIVVL SGTAAQVTT 420
TEWVETTARE LPIPEPEGPD ASSIMSTESI TGSIGPLLDG TATLRLVKRQ VPLDCVLVRY 480
GSFSVTLDIV QGIESAEILQ AVPSGEGDAF ELTVSCQGGI PKEACMEISS PGQPPAQRLL 540
25 CQPVLPSPAC QLVHLQILKG GSGTYCLNVS LADTNSLAVV STQLIMPQGE AGLGQVPLIV 600
GILLVLMVAV LASLIYRRRL MKQDFSVPL PHSSSHWLRL PRIFCSCPIG ENSPLLSGQQ 660
V 661

30 Seq ID NO: 332 Protein Sequence
Protein Accession #: NP_001913.2

1 11 21 31 41 51
MSPLWNGPLL SCLGCKILPG AQGQFPRVCM TVDSLUNKEC CPRLGAESAN VCGSQQGRGQ 60
CTEVADTRP WSGPYILRNQ DRELWPRKF FHRTCKCTGN FAGYNCGDCK FGWTGPNCEP 120
35 KKPPVIRQNI HSLSPQEREQ FLGALDLAKK RVHPDYVITT QHNLGLLGN GTQPQFANCS 180
VYDFVWLHY YSVRDTLLGP GRPYRAIDFS HQGPAPVTHW RYHLLCLERD LQRLIGNESF 240
ALPYWNFATG RNECDVCTDQ LFGAARPDPT TLISRNSRFS SWETVCDSD DYNHLVTLN 300
GTVEGLLRN OMGRNSMKLP TLKDIRDCLS LQKFDNPPFF QNSTFSFRNA LEGFDKADGT 360
40 LDSQVMSLHN LVHSFLNGTN ALPHSAANDP IFVVLHSFTD AIFDEWMKRF NPPADAWPQE 420
LAPIGNRMV NMVPPFPPT NEELFLTSQ LGYSYALDLP VSVEETPGWP TTLVVMGTL 480
VALVGLFVLL AFLQYRRLRK GYPLMETHL SSKRYTEEA 519

45 Seq ID NO: 333 Protein Sequence
Protein Accession #: XP_059422.1

1 11 21 31 41 51
MNWHLPLFL ASVTLPISCS HFNPLSLEEL GSNTGIQVFN QIVKSRPHDN IVISPHGIAS 60
VLGMLQLGAD GRTKKQLAMV MRYGVNGVGK ILKKINKAIV SKKMKDITV ANAVFVKNAS 120
50 EIEVPVTRN KDVFQCEVRN VNFEDPASAC DSINAWVKN TRDMIDNLS PDLIDGLVLR 180
LVLVNAVYFK GLMKSRFQPE NTKKRTFVAA DGKSYQVPL AQLSVFRCS TSAPNDLWYN 240
FIELPYHGES ISMLIALPTE SSTPLSAIP HISTKTIWS MSIMVPKRVQ VILPKFTAVA 300
QTDLKEPLKV LGITDMEDSS KANFAKITRS ENLHVSHILQ KAKIEVSEDG TKASAATTAI 360
LIARSSPPWF IVDPRPLFFI RHNPTGAVLF MGQINKP 397

55 Seq ID NO: 334 Protein Sequence
Protein Accession #: XP_040512.2

1 11 21 31 41 51
MRQHDTRNGR IVLISGRRSF CSIFSVPYR DSTQVGDLLK DGRQSTGAV SLKEIIGLEG 60
60 VELGADGKTV SYTQFLLPFN AFGARRNTID STSSFSQFRN LSHRSLSIGR ASGTQGLSDT 120
GSDLGDFMDY DPNLLDDPQW PCGKHKRVLI FPSYMTTVID YVKPSDLKKD MNETFKEKFP 180
HIKLTLSKIR SLKREMRKLA QEDCGLEPT VAMAFVFEK LALKGKLNKQ NRKLCAGACV 240
LLAAKIGSDL KKEHVKHLID KLEEKFRILNR RELIAFEPPV LVALEFALHL PEHEVMPHYR 300
65 RLVSQS 306

70 Seq ID NO: 335 Protein Sequence
Protein Accession #: AAH08826

1 11 21 31 41 51
MTTLAGAVPR MMRPGPGQNY PRSGFPLEVS TPLCQGRVNO LGGVFINGRP LPNHIRHKIV 60
EMAHHGIRPC VISRLRVSH GCVSKILCRY QETGSIRPGA IGGSKPKVTT PDVEKKIEEY 120
KRENPGHFW EYRDKLLKA VCDRTVPVS SSISRIILRSK FGKGEEDAD LERKAEASE 180
75 KKAHSDIGI LSEASAPQS DEGSIDIDSEP DLPLKRRQR SRTTFTAEQL EELERAFERT 240
HYPIYITREE LAQRAKLEA RVQVWFNSRR ARWRKQAGAN QLMAFNHLIP GGFPPATMPT 300
LPTQLSETS YQTSIPQAV SDPSSTVHRP QPLPPSTVHQ STIPSNPDSS SAYCLPSTRH 360
GFSSYTDSFV PPSGSPNPMN PTIGNGLSPQ NSIRHNLSLH SKPIRVQNEG TGKSSWWMLN 420
PEGGKSGKSP RRAASMDNH SKPAKRSRA AKKASLQSG QEGAGDSPGS QFSKNPASPG 480
SHSNDPDMN STFRPRTSSN ASTISGRSLP IMTEQDDLGE GDVHSMVYPP SAAKMASTLP 540
80 SLSEISNPN MENLLDNLNL LSSPSTLTVS TQSSPGTMMQ QTPCYSPAPP NTSLSNPSPN 600
YQKYTYGQSS MSPLPQMPIQ TLQDNKSSYG GMSQYNCAPG LLKELLTSDS PPHNDIMTPV 660
DPGVAQPNR VLQGNVMMGP NSVMSTYGSQ ASHNMMNPS SHTHPGHAQQ TSAVNGRPLP 720
HTVSTMPHTS GMRNLTVQKT PVQVPLPHPM QMSALGGYSS VSSCNGYGRM GLLHQEKLP 780
DLDMGFIERL DCDMESIIRN DLMQDGLDLP NFDNVLNQS FPHSVKTTTH SWVSG 835

Seq ID NO: 336 Protein Sequence
Protein Accession #: NP_005752.1

| | | | | | | | |
|----|------------|-------------|------------|------------|------------|------------|------|
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| 5 | MEVSRKAPP | RPPRPAAPLP | LLAYLLALAA | PGRGADEPVW | RSEQAIGAIA | ASQEDGVFVA | 60 |
| | SGSCLDQLDY | SLEHSLRLY | RDQAGNCTEP | VSLAPPARPR | PGSSFSKLLL | PYREGAAGLG | 120 |
| | GLLLTGWTFD | RGACEVRPLG | NLSRNSLRNG | TEVVSCHPOG | STAGVYVRAG | RNNRWYLAVA | 180 |
| | ATYVLPEPET | ASRCNPAASD | HDTAIALKDT | EGRSLATQEL | GRLKLCGAG | SLHFVDAFLW | 240 |
| 10 | NGSIYFPYYP | YNYTSGAATG | WPSMARIAQS | TEVLFQGGAS | LDCGHGHPDG | RRLLSSSLV | 300 |
| | EALDVHAGVF | SAAAGEGQER | RSPTTALCL | FRMSEIQARA | KRVSWDFKTA | ESHCKEGDQP | 360 |
| | ERVQPIASST | LIHSDLTSVY | GTVMNRTVL | FLGTGDDQLL | KVILGENLTS | NCPEVIYEIK | 420 |
| | EETPVFYKLV | PDPVKNIYY | LTAGKEVRR | RVANCNKHS | CSECLTATDP | HCGWCHSLQR | 480 |
| | CTFGDCVHS | ENLENWLDIS | SGAKKCPKIQ | IIRSSKEKTT | VTMVGSEFSP | HSKCMVKMVD | 540 |
| 15 | SSRELQCNKS | QPNRTCTCSI | PTRATYKDV | VNVMFSGS | WNLSDRNFNT | NCSLKECPA | 600 |
| | CVETGCAMCK | SARRCIHPFT | ACDPSDYERN | QECPVAVEK | TSGGGRPKEN | KGNRTNQALQ | 660 |
| | VFYIKSIEPQ | KVSTLGKSMV | IVTGANFTRA | SNITMILKGT | STCDKDVIVQ | SHVLNDTHMK | 720 |
| | FSLPSSRKEM | KDVCIQFDGG | NCSSVGSLSY | IALPHCSLIF | PATTWISGGQ | NITMGRNFD | 780 |
| | VIDNLIISHE | LKGNINVSSEY | CVATYCGFLA | PSLKSSKVRT | NVTVKLRVQD | TYLDCGLTQY | 840 |
| 20 | REDPRFTGYR | VESEVDELE | VKIQKENDNF | NISKDDIET | LFHGENGLIN | CSFENITRNO | 900 |
| | DLTTILCKIK | GIKTASTIAN | SSKKVRVKLG | NLELYVEQES | VPSTWYFLIV | LPVLLVIVIF | 960 |
| | AAVGVTNRHS | KELSRKQSQ | LELLESELRK | EIRDGFAELQ | MDKLDVVDSP | GTVPFLDIKH | 1020 |
| | FALRTFPFES | GGFTHTIFT | MNRNDANDKN | ESLTALDALI | CNKSFLVTVI | HTLEKQKNFS | 1080 |
| | VKDRCLFASF | LTIALQTKLV | YLTSLILEVT | RDLMQCSNM | QPKMLLRTE | SVVEKLLTNW | 1140 |
| | MSVCLSGFLR | ETVGEPPYLL | VTTLNQKINK | GPVDVITCKA | LYTLNEDWLL | WQVPEPTVA | 1200 |
| 25 | LNWVFEKIPE | NESADVCNRI | SVNVLDCTI | GQAKEKIPQA | FLSKNGSPYG | LQLNEIGLEL | 1260 |
| | QMGTRQKELL | DIDSSSVILE | DGITKLNTIG | HYEISNGSTI | KVFKKIANFT | SDVEYSDHHC | 1320 |
| | HLILPDESEF | QDVQGRHRG | KHKFKVKEMY | LTKLLSTKVA | IHSVLEKLF | SIWSLPNSRA | 1380 |
| | PFAIKYFFDP | LDAQAENKNI | TDPDVVHIWK | TNSLPLRFVW | NILKNPQFVF | DIKKTPHIDG | 1440 |
| 30 | CLSVIAQAFM | DAFSLTEQQL | GKEAPTNNLL | YAKDIPTYKE | EVKSYKAIK | DLPLSSSEM | 1500 |
| | EEFLTQESKK | HENEFNEEVA | LTEIKYIYVK | YFDEILNKLE | RERGLEEAQK | QLLHVKVLFD | 1560 |
| | EKKCKNM | | | | | | 1568 |

Seq ID NO: 337 Protein Sequence
Protein Accession #: XP_063670.1

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|----|------------|------------|------------|------------|------------|------------|-----|
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| 35 | MQRILEEPAD | DCMTSTRILL | TLSEFIMSLQ | RTVYPHSEKW | RALSVPSSTY | FQELVGTQSE | 60 |
| | LALTFWHLIS | MFGFFIVSYG | FLTAFGRITL | HLDLQPNLT | PSRFDKYTGL | FIYEIEGDGL | 120 |
| | DPCFQSMVQG | ILEVLWMSKV | ESAYHTNDGD | TAGEGVNGT | SQTRGGGGA | RSRCREMEEP | 180 |
| 40 | TPEPYVDVD | KGLTLACVVF | LCLFLVVMII | RCAKVIMDPY | SAIPTSTWEE | QHLDD | 235 |

Seq ID NO: 338 Protein Sequence
Protein Accession #: FGENSEH predicted

| | | | | | | | |
|----|------------|------------|------------|------------|------------|------------|-----|
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| 45 | MEPSHSQPTM | DMGHMQERPA | ASPLKCQDGR | GSAQSPLSAA | GPQSPAPLGA | LTPAEPGLGS | 60 |
| | APRAPRARAP | RYTKRRSRSS | AVALGSAPAQ | PGPRERTGRA | SPALENNSDL | LSKASAIATG | 120 |
| | TPPCEDSTIA | RFYLPPLPTL | HPELVGTQSE | LALTFWHLIS | MFGFFIVSYG | FLTAFGRITL | 180 |
| | HLDLQPNLT | PSRFDKYTQ | LLEPLVHSKY | VLTIHWSQGL | CIWSSHPCEA | GVNGTSTQTR | 240 |
| 50 | GGGGAARSRC | REMEPTPEP | VYVDVDKGLT | LACFVFLCLF | LVMVIRCAK | VIMDPYSAIP | 300 |
| | TSTWEEQHL | D | | | | | 311 |

Seq ID NO: 339 Protein Sequence
Protein Accession #: FGENSEH predicted

| | | | | | | | |
|----|------------|------------|------------|------------|------------|------------|-----|
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| 55 | MGKDFMSKTP | KAMATQAKID | KWDLIKLSKF | CTAKETTIRV | NRQPTWEKIK | FAIYSSDEGL | 60 |
| | ISRIYNEPKQ | IYKKKTNNPI | NKWKADNRRH | FSKEDIYAAN | RHMCKSSSL | AIREMQIKTT | 120 |
| | TRCHLTPVRM | AIIKKSGNNR | TAEEQPKLRK | EAVGSIEIFR | FADGLDITLM | ILGILASLVN | 180 |
| 60 | GACPLMPLV | LGEMSDNLIS | GCLVQNTTN | YQNCQSQEK | LNEDMTLLT | YVVGIGVAAL | 240 |
| | IFGYIQISLW | IITAARQTKR | IRKQFFHSVL | AQDQGFWDSC | DIGELNTRMT | DDIDKISDGI | 300 |
| | GDKIALLFQN | MSTFSIGLAV | GLVKGWKLTL | VTLSPLIM | ASAAACSRMV | ISLTSKELSA | 360 |
| | YSKAGAVAE | VLSSIRTVIA | FRAQEKELQR | YTONLKDAD | FGIKRTIASK | VSLGAVYFFM | 420 |
| | NGTYGLAFWY | GTSILANGEP | GYTIGTVLAV | FFSVIHSSYC | IGAAVPHFET | FAIARGAAFH | 480 |
| 65 | IFQVIDKKPS | IDNFSTAGYK | PESIEGTVEF | KNVSPNYPSR | PSIKILKGLN | LRIKSGETVA | 540 |
| | LVGLWNGSGK | TVVQLQRLY | DPDDGFIMVD | ENDIRALNVR | HYRDHIGVVS | QEPVLFGTTI | 600 |
| | SNNIKYGRDD | VTDEEMERAA | REANAYDFIM | EPFNKFTLV | GEKGAQMSGG | QKQRIATARA | 660 |
| 70 | LVRNPKILIL | DEATSALDSE | SKSAVQAAL | KDTPRYSF | | | 698 |

Seq ID NO: 340 Protein Sequence
Protein Accession #: XP_166496.1

| | | | | | | | |
|----|------------|------------|------------|------------|------------|------------|-----|
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| 75 | MVDENDIRAL | NVRHYRDHIG | VVSQEPVLFG | TTISNNIKYG | RDDVTDEEME | RAAREANAYD | 60 |
| | FIMEFPNKFN | TLVGEKGAQM | SGGQKQRTAI | ARALVRNPKI | LILDEATSAL | DSEKSAVQA | 120 |
| | ALEKDTPRYS | F | | | | | 131 |

Seq ID NO: 341 Protein Sequence
Protein Accession #: XP_166305.1

| | | | | | | | |
|----|------------|------------|------------|------------|------------|------------|-----|
| | 1 | 11 | 21 | 31 | 41 | 51 | |
| 80 | MEKFRVLDL | HVGHHSALGY | GLVTLLTAGG | ERIFSAVAFQ | CPCSAAWNLP | YGLVFLVPA | 60 |
| | LALFLGYYVL | SARTWRLLTG | CCSSARASCG | SALRGSVCT | QISAAAALAP | LTWVAALLG | 120 |
| | GAFYECAATG | SAFAQRLCL | GRNRSAAEL | PLVPCNQA | SDVQDLLKLD | KAQSQVLGWI | 180 |

LIADVIIILL IFTSVTRCLS PVSFLQLKFW KIYLEQEQQI LKSKATEHAT ELAKENIKCF 240
 FEGSHPKYEN TFSMKWQQI SSLYTFNPKG QYYSMLHKYV NRKETHSIR STEGDTVIPV 300
 LGFVDSSGIN STPEL 315

5

Seq ID NO: 342 Protein Sequence
 Protein Accession #: NP_115587.5

1 11 21 31 41 51
 | | | | |
 MARSPPATLF LFLLLGQPP PSRPQSLGTT KLRLVGPESK PEEGRLEVLH QGQWGTVCDD 60
 NFAIQEATVA CRQLGFEEAL TWAHSAKYGQ GEGPIWLDNV QCVGTESSLD QCGSNGWGV 120
 DCSHSEVDGV ICHPRRRHGY LSETVSNALG PQGRRLEEV LKPIILASAKQ HSPVTEGAVE 180
 VKYEGHWRQV CDQGWMTMNS RVVCGMLGFP SEVPVDSHY RYKVDLKMMD PKSRKLSLTN 240
 KNSFWIHQVT CLGTEPHMAN CQVQVAPARG KLRPACPGGM HAVVSCVAGP HFRPPKTKPQ 300
 RKGSAWAEPR VRLRSGAVG EGRVEVLAMR QWGTVCDFRW NLISASVVCRL QLGPGSAREA 360
 LFGARLGGGL GPIHLESEVR RGYERTLSDC PALEGSQNGC QHENAASVRC NVPNMGFQNG 420
 VRLAGGRIP ELLLEVQVEV NGVPRWGSVC SENWGLTEAM VACRQLGLGF AIHAYKETWF 480
 WSGTPRAQEV VMSGVRCST ELALQQCQRH GPVCHSHGGG RFLAGVSCMD SAPDLVMNAQ 540
 LVQETAYLED RPLSQLYCAH EENCLSKSAD HMDWPYGYRR LLRFSTQIYN LGRTDFRPKT 600
 GRDSWVWQC HRHYHSIEVF THYDLLTLNG SKVAEGHKAS FCLEDTNCP GLQRRYACAN 660
 FGEQGVTVGC WDTYRHDIDC QWVDITDVG GNYIFQVIVN PHYEVAESDF SNMMLQCRCK 720
 YDGHVRVWLN CHTGNSYPAN AELSLEQEQR LRNNLI 756

25

Seq ID NO: 343 Protein Sequence
 Protein Accession #: NP_001789.2

1 11 21 31 41 51
 | | | | |
 MENFQKVEKI GEGTYGVVYK ARNKLTGEVV ALKKIRLDTE TEGVPSTAIR EISLLKELNH 60
 PNIVKLLDVI HTENKLYLVF EFLHQDLKKF MDASALTGIP LPLIKSYLFQ LLQGLAFCHS 120
 HRVLHRDLKP QNLLINTEGA IKLADFLAR AFGVPVRYT HEVVTWLYRA PEILLGCKYK 180
 STAVDIWSLG CIPAEVTR ALFPGDSEID QLFRIPTLG TPDEVVWPGV TSMFDYKPSF 240
 PKWARQDFSK VVPPLEDGR SLLSQMLHYD PNKRISAKAA LAHPFFQDVT KVPVHLRL 298

35

Seq ID NO: 344 Protein Sequence
 Protein Accession #: NP_439892.1

1 11 21 31 41 51
 | | | | |
 MENFQKVEKI GEGTYGVVYK ARNKLTGEVV ALKKIRLDTE TEGVPSTAIR EISLLKELNH 60
 PNIVKLLDVI HTENKLYLVF EFLHQDLKKF MDASALTGIP LPLIKSYLFQ LLQGLAFCHS 120
 HRVLHRDLKP QNLLINTEGA IKLADFLAR AFGVPVRYT HEVTRRALFP GDSEIDQLFR 180
 IFRTLTPTDE VVWPGVTSMP DYKPSFPKWA RQDFSKVVP LDEDGRSLLS QMLHYDPYKR 240
 ISAKAALAH FFDVTKVPV HLRL 264

45

Seq ID NO: 345 Protein Sequence
 Protein Accession #: NP_116127.1

1 11 21 31 41 51
 | | | | |
 MKLGCVLMAV ALYLSLGLV VAQMLLAASF ETLQCEGPVC TEESCHTED DLTAREAGF 60
 QVKAYTFSEP FHLIVSYDWL ILQGPAPKVF EGDLLVLRQ AWQDWPLTQV TFYRDGSALG 120
 PPGPNRFPST TVVQKADSGH YHCSGIFQSP GPGIPETASV VAITVQELFP APILRAVPSA 180
 EPOAGSPMTL SCQTKLPLQR SAARLLFSFY KDGRIVQSRG LSSEFQIPTA SEDHSGSYWC 240
 EAATEDNQVW QSPQLEIRV QGASSAAPP TLNPAQKSA AFGTAPEEAP GPLPPPTPS 300
 SEDPGFSSPL GMPDPHLYHQ MGLLLKHMMD VRVLLGHLLM ELRELSGHQK PGTTKATAE 359

55

Seq ID NO: 346 Protein Sequence
 Protein Accession #: NP_002337.1

1 11 21 31 41 51
 | | | | |
 MKIFLPLVLA ALLGVERASS LMCFSCLNOK SNLYCLKPTI CSDQDNYCVT VSASAGIGNL 60
 VTFGHSLSKT CSPACPIPEG VNVGVASMG I SCCQSFLCNF SAADGGLRAS VTLILAGLLL 120
 SLLPALLRFP P 131

65

Seq ID NO: 347 Protein Sequence
 Protein Accession #: XP_113526.2

1 11 21 31 41 51
 | | | | |
 MEDLGENTMV LSTLRSLNMF ISQRVEGGSG LDISTSAPGS LQMYYQSMQ LEERAQIIRS 60
 KSHLIQVERE KMQMELSHKR ARVELERAAS TSARNYEREV DRNQELLTRI RQLQEREAGA 120
 EEMQEQQLER NRQCCQNLD AASKRLREKED SLAQAGETIN ALKGRISELQ HSMVDQEMRV 180
 KRLESEKQEL QEQLDLQHKK QCEANQKIQE LQASQEARAD HEQQIKDLEQ KLSLQEQDAA 240
 IVKNMKSELV RLPRLRELK QLRRESAHLR EMRETNGLLQ EELEGLQKRL GRQEKMQETL 300
 VGLELENERL LAKLQSWERL DQTMGLSIRT PEDLSRFVVE LQRELEALD KNSAVTSSAR 360
 GLEKARQQIQ EELRQVSGQL LEERKKRETH EALARRLQKR VLLLTKERDG MRAILGSYDS 420
 ELTPAIESPO LTRRMREAEAD MVQKVHSHA EMEAQLSQAL EELGGQKQRA DMLEMLKML 480
 KSQSSAEDQS FLFSREAEAD LRLKVEELEG ERSRLSEER MLEAQLERRA LQGDYDQSR 540
 KVLHMSLNPT SVARQLRED HSQLAECER LRGLLRAMER GGTVPADLEA AAASLPSSKE 600
 VAEKKQVES AELKNQRLKE VFQTKIQEFR KACYTLTGQY IDITTENQYR LTSLYAEHPG 660
 DCLIFKATSP SGSKMQLLET EFSHTVGELI EVHLRRQDSI PAFLLSSLTLE LFSRQTVA 718

80

Seq ID NO: 348 Protein Sequence
 Protein Accession #: NP_000264.1

1 11 21 31 41 51
 | | | | |
 MTQAGRRGPG TPEPRPTQP MASPRLGTF CPTRDAATQL VLSFQPRAPH ALCLSGGLR 60
 LALGLLQLLP GRRPAGPGSP ATSPASVRI LRAAAACDLL GCLGMVIRST VWLGFNPFVD 120

5
SVSDMNHTEI WPAAFVCVGS MWIQLLYSAC FWWLFCYAVD AYLVIRRSAG LSTILLYHIM 180
AMGLATLLCV EGAAMLYYPS VSRCEGLDH AIPHYVTMYL PLLLVLVANP ILFOKTVTAV 240
ASLLKRGQGI YTENERRMGA VIKIRFFKIM LVLIICWLSN IINESLLFYL EMQTDINGGS 300
LKPVRTAAKT TWFMIGILNP AQGFLLSLAF YGWTCCSLGF QSPRKEIQWE SLTTSAAEGA 360
HPSPLMPHEN PASGKVSQVG GQTSDEALSM LSEGSDASTI EIHTASESCN KNEGDPALPT 420
HGDLL 424

10
Seq ID NO: 349 Protein Sequence
Protein Accession #: NP_647478.1
1 11 21 31 41 51
| | | | |
MGPKDSAKCL HRGPQPSHWA AGDGPTQERC GPRSLGSPVL GLDTCRAWDH VDGQILGQLR 60
PLTEEEEEEAG AGATLSRGPA FPGMGSEELR LASFYDWPLT AEVPPPELLAA AGFFHTGHQD 120
KVRCCFCYCG LQSWKRGDDP WTEHAKWFPS CQFLLRSGKR DFVHSVQETH SOLLGSDWPW 180
15
EPEDAAPVA PSVPASGYPE LPTPRREVQS ESAQEPGGVS PAEAQRAHWV LEPPGARDVE 240
AQLRRQEER TCKVCLDRAV SIVFVPCGHL VCAECAPGLQ LCPICRAPVR SRVRTFLS 298

20
Seq ID NO: 350 Protein Sequence
Protein Accession #: NP_071444.1
1 11 21 31 41 51
| | | | |
MGPKDSAKCL HRGPQPSHWA AGDGPTQERC GPRSLGSPVL GLDTCRAWDH VDGQILGQLR 60
PLTEEEEEEAG AGATLSRGPA FPGMGSEELR LASFYDWPLT AEVPPPELLAA AGFFHTGHQD 120
KVRCCFCYCG LQSWKRGDDP WTEHAKWFPS CQFLLRSGKR DFVHSVQETH SOLLGSDWPW 180
25
EPEDAAPVA PSVPASGYPE LPTPRREVQS ESAQEPGARD VEAQLRRQE ERTCKVCLDR 240
AVSIVFVPCG HLVCACAPG LQLCPICRAP VRSRVRTFLS 280

30
Seq ID NO: 351 Protein Sequence
Protein Accession #: NP_066300.1
1 11 21 31 41 51
| | | | |
MGSVSSLISG HSFHSHKCR A SQYKLRKSSH LKKLNRYSDG LLRPGFSQDS GHGKSSSKMG 60
KSEDFFYIKV SQKARGSHHP DYTALSSGDL GGQAGVDFDP STPPKLMPPS NQLEMSEK 120
AVRPTAFKPV LPRSGAILHS SPESASHQLH PAPPDKPKEQ ELKPGLCGSA LSDSGRNSMS 180
35
SLPTHSTSSS YQLDPLVTPV GPTSRRFGGSA HNITQGVIVL DSNMMSLKAL SPSDGGSKLG 240
HSNKADKGPS CVRSPISTDE CSIQELEQKL LEREGALQKL QRSFEEKELA SSLAYEERPR 300
RCRDELEGPE PKGGNKLKQA SQKSQRAQOV LHLQVLQLOQ EKRLRQLELE SLMKEQDLLE 360
TKLRSYEREK TSFGPALLET QWEVCQKSGE ISLLKQQLKE SQTEVNAKAS EILGLKAQLK 420
40
DTRGLEGLE LRTQDLEGAL RTKGLELEVC ENELQRKQNE AELLREKYNL LBQELQELRA 480
QAALARDMGP PTFPEDVPAL QRELERLRAE LREERQGHQD MSSGPOHERL VWKEEKEKVI 540
QYKQQLQSSY VAMYQRNQLR EKALQQLARG DSAGEPLEVD LEGADIPYED IIAETEI 596

45
Seq ID NO: 352 Protein Sequence
Protein Accession #: AAG41361.1
1 11 21 31 41 51
| | | | |
MPKNSKVVKR ELDDDVTEVS KDLLSNEDAA DDAFKTSELI VDGQEEKOTD VEEGSEVEDE 60
RPAWNSKLQY ILAQVGFVSG LGNVWRFPYL CQKNGGGAYL LPYLILLMVI GIPLFFLELS 120
VQQRIRRGSI GVMNYISPKL GGIGFASCVV CYFVALYVNV IIGWSLFYFS QSFQQLPMD 180
50
QCPLVKNASH TFVEPECEQS SATTYWYRE ALNISSISE SGLNWKMTI CLLAHVVMVC 240
LAMIKGIQSS GKIIYFSSLF PYVVLICFLI RAFLNGSID GIRHMTFPLK EIMLEPKVNR 300
EAATQVFFAL GLGFGGVIAF SSYNKRDNNC HFDVAVLSFI NFFTSLVATL VVFAVLGFKA 360
NVINEKCITQ NSETIMFLK MGNISQDIIP HHINLSTVTA EDYHLVYDII QKVKEEFPA 420
55
LHLNSCKIEE ELNKAUVGTG LAFIAFTEAM THFPASPFWV VMFFLMLVNL GLGSMFGTIE 480
GIVTPIVDTF KVRKEILTIV CCLLAFICGL IFVQRSGNYF VTMFDDYSAT LPLLIVVILE 540
NIAVCFVYGI DKFMEDLKM LGFAPSRYYY YMKYISPLM LLSLLIASV NMGLSPPGYN 600
ANIEDKASEE FLSYPTWGLV VCVSLVVFAL LPVPVVFIVR RFNLIIDSSG NIASVYTKRG 660
60
RVLKEPVNLE GDDTSLINGK IPSEMPSPNF GKNIYRKQSG SPTLDTAPNG RYIGLYLMD 720
IMPDMPESDL 730

65
Seq ID NO: 353 Protein Sequence
Protein Accession #: NP_005594.1
1 11 21 31 41 51
| | | | |
MEGERSPLLL SQETAGQKPL SVHRPPTSGC LGPVREDQA EAWGSCCPCP ETKHQALSQT 60
PKKGPAPELS PGSSCVKYLI FLNFPFSL LLLALAIGLW GLAVKGLSGS DLGGPLPTDP 120
MLGLALGLLV VSAASLAGCL GALCENTCLL RGFSGGILAF LVLEAVAGAL VVALWGLPLQ 180
70
SLEHTLRVAI AHYQDDPDLR FLDDQVQLGL RCCGAASYQD WQONLYFNCS SPGVQACSLP 240
ASCCIDPREG GASVNDQCGF GVLRLDADA QRVVYLEGCG PPLRRWLRAN LAASGGYATA 300
VLLQGAELL LAARLLGALA ARSGAAYGPG AHGEDRAGPQ SPSPGAPPAA KPARG 355

75
Seq ID NO: 354 Protein Sequence
Protein Accession #: AAL84622.1
1 11 21 31 41 51
| | | | |
MADPEVVVSS CSSHEENRC NFNQQTSPSE ELLLEDQMRK KLKFFFMNCP EKFWARGRKP 60
WKLAIQILKI AMVTIQLVLF GLSNQMVVAF KEENTIAFKH LFLKGYMDRM DDYAVVYTS 120
DVEDQLIFAV NQYLQLVNVV VGNHAYENKG TKQSAMAICQ HPYKRGNIYP GNDTFIDPE 180
80
IETECFFVEP DEPHIGTPA ENKLNLTLDL HRLLTVELQF KLKAINLQTV RHQELPDQYD 240
FTLITFDNK AHSGRKISL DNDISIRECK DMHVSQSIQK NTHYMMIFDA FVILTCLVSL 300
ILCRSVIRG LQLQEEFVNF FLLHYKKEVS VSDQMEFVNG WYIMIIISDI LTIIGSILKM 360
EIQAKSLTSY DVCSILIGTS TMLVNLGVIR YLGFFAKYNL LILTQAAALF NVIRFCCCAA 420
MIYLYGFCFG WIVLGPYHDK FRSLNMVSEC LFSLINGDDM FATFAKMQQK SYLVWLFSLR 480
YLYSFISLFI YMILSLFIAL ITDTYETIKQ YQDGFPETE LRTFISECKD LPNSGKYRLE 540

| | | |
|----------------------------------|--|-----|
| DDPPVSLFCC CKK | | 553 |
| Seq ID NO: 355 Protein Sequence | | |
| Protein Accession #: NP_000105.1 | | |
| 5 | 1 11 21 31 41 51 | |
| | | |
| | MEPGLWLLFG LTVTSAAGFV PCSQSGDAGR RGVSAQPTAA RSEGDCEETV AGPGEETVAG | 60 |
| | PGEPTVAPTA LQGPSPGSPG QEQAABGAPE HHRSRRTCTF TYKDKECVY CHLDIWIINT | 120 |
| 10 | PEQTVPYGLS NYRGSFRGKR SAGPLPGNLQ LSHRPHLRCA CVGRYDKACL HFCTQTLDVS | 180 |
| | SNRRTAEKTD KEEEGKVEVK DQSKQALDL HHPKLMPSG LALAPSTCPR CLFQEGAP | 238 |
| Seq ID NO: 356 Protein Sequence | | |
| Protein Accession #: NP_005347.2 | | |
| 15 | 1 11 21 31 41 51 | |
| | | |
| | MGGCCSSHPE DDWMENIDVC ENCHYPIVPL DGKGTLLIRN GSEVRDPLVT YEGSNPPASP | 60 |
| | LQDNLVIALH SYEPSHDGDL GFEKGEPLRI LEQSGEWWKA QSLTTGQEGF IPFNFAKAN | 120 |
| | SLEPEPWFFK NLGRKDAERQ LLAPGNTHGS FLIRESESTA GSFSLSVRDF DQNGQEVVXH | 180 |
| 20 | YKIRNLNNGG FYISPRITFP GLHELVRHYT NASDGLCTRL SRPCQTQKPQ KPWWEDWEV | 240 |
| | PRETLKLVLR LGAGQPGFVW MGYNGHTKV AVKSLKQGS SPDAFLAEAN LMKQLQHQL | 300 |
| | VRLYAVVTQE PIYIITEYME NGSLVDFLKT PSGIKLTINK LLDMAAQIAE GMAFIEERNY | 360 |
| | IHRDLRAANI LVSDTLCKI ADPLGLARIE DNEYTAREGA KFPKMTAPE AINYGTFIK | 420 |
| | SDVMSGILL TEIVTHGRIP YPGMTNFEVI QNLERGVRMV RPDNCPPELY QLMRLCWKER | 480 |
| 25 | PEDRPTFDYL RSVLEDFFTA TEGGYQPQP | 509 |
| Seq ID NO: 357 Protein Sequence | | |
| Protein Accession #: NP_055469.1 | | |
| 30 | 1 11 21 31 41 51 | |
| | | |
| | MAIAYLGSSC PSQPPSSAL SLSPTPSDFE QESGIETAMR FSPDVALAVS TTPAVLPTTN | 60 |
| | IQPVGTFFEE LPSEPTLEP ATSPLVVTEV PEEPSQRATT VSTTMATTAA TSTGDPVTAT | 120 |
| | VPATVATATP STPAAPPFTA TTAVIRTTGV RRLPLPLTT VATARATTPE APSPTTAAV | 180 |
| | LDTEAPTREL VSTATSPRA LPRPATTEP DIPERSTLPL GTTAPGPTEV AQTPTPETFL | 240 |
| 35 | TTIRDEPEVP VSGGSGDFE LPEEETTQPD TANEVAVVG AAKASSPPG TLPKARGPGP | 300 |
| | GLLDNAIDSG SAAQLPQKS ILERKEVLVA VIVGVVVGAL FAFVLVTLI YRMKKKDEGS | 360 |
| | YTLLEPKQAS VTQKPKQKE EFYA | 384 |
| Seq ID NO: 358 Protein Sequence | | |
| Protein Accession #: NP_008848.1 | | |
| 40 | 1 11 21 31 41 51 | |
| | | |
| | MYGNYSHFMK PPAGYGGSPG HTGSTMSPS AALSTGKPMO SHPSYTDTPV SAPRTLSAVG | 60 |
| | TPLNALGSPY RVITSAMGPP SGALAAPPGI NLVAPPSSQL NVVNSVSSE DIKPLPGLPG | 120 |
| 45 | IQNMNYPSTS PGLSVKHICA ICGDRSSGKH YGVYSCGCK GFFKRTIRKD LIYTCRDNKO | 180 |
| | CLIDKRQNR CQYCRQKCL VMGMKREAVQ EERQSRERA ESEAECATSG HEDMPVERIL | 240 |
| | EAELEVEPT ESYGDMNMEN STNDPVTNIC HAADKQLFTL VEWAKRIPHF SDLTLEDQVI | 300 |
| | LLRAGWNELL IASFSHRVS VQDGILLATG LHVHRSSAHS AGVGSIFDRV LTELVSQMKD | 360 |
| | MQMDKSELGC LRAIVLFND AKGLSNPSEV ETLREKVYAT LEAYTKQKYP EQPGRFAKLL | 420 |
| 50 | LRLPALRSIG LKCLEHLFFF KLIGDTPIDT FLMEMLETPL QIT | 463 |
| Seq ID NO: 359 Protein Sequence | | |
| Protein Accession #: NP_002176.1 | | |
| 55 | 1 11 21 31 41 51 | |
| | | |
| | MTILGTTFGM VFSLLQVVGSG ESGYAQNGDL EDAELDDYSF SCYSQLEVNG SQHSLTCAFE | 60 |
| | DPOVNTTNLE FEICGALVEV KCLNFRKLQE IYFIETKKFL LIGKSNICVK VGEKSLTCKK | 120 |
| | IDLTTIVKPE APFDLSVIYR EGANDFVVT NTSHLQKKYV KVLMDVAYR QEKDENKWT | 180 |
| | VNLSSTKLTL LQKRLQPAAM YEIKVRSIPD HYFKGFSEW SPSYFRTPE INNSSGEMDP | 240 |
| 60 | ILLTISILSF FSVALLVILA CVLWKKRIKP IVWPSLPDHK KTLHLCKKP RKNLNVSFNP | 300 |
| | ESFLDQIHR VDDIQARDEV EGFLQDTFPQ QLEESEKORL GGDVQSPNCP SEDVVVPES | 360 |
| | FGRDSSLTCL AGNVACDAP ILSSRSRLDC RESGKNGPHV YQDLLLSLGT TNSTLPPFFS | 420 |
| | LQSGITLNP VAQQPILTS LGSNQEEAYV TMSSFYQNG | 459 |
| Seq ID NO: 360 Protein Sequence | | |
| Protein Accession #: NP_006263.1 | | |
| 65 | 1 11 21 31 41 51 | |
| | | |
| | MSELEKAMVA LIDVFHQYSG REGDKHKLK SELKELINNE LSHFLEEIKE QEVVDKVMET | 60 |
| 70 | LDNDGDECD QEFMAFVAM VTTACHEFFE HE | 92 |
| Seq ID NO: 361 Protein Sequence | | |
| Protein Accession #: NP_006148.1 | | |
| 75 | 1 11 21 31 41 51 | |
| | | |
| | MPMDLILVW FCVCTARTV GFGMDPDLQ DIVTELDLVN TILGVAQVSG MHNASKAFLF | 60 |
| | QDIEREIHAA PHVSEKLIQL FQNKSEFTIL ATVQQKPSTS GVILSIRELE HSYFELESSG | 120 |
| | LRDEIRYHYI HNGKPRTEAL PYRMADGQWH KVALSVSASH LLLHVDNRI YERVIDPPDT | 180 |
| 80 | NLPFGNLWL GQRNQKHGLF KGIIQDGKII FMPNGYITQC PNLNHTCPTC SDFLSLVQGI | 240 |
| | MDLQELLAKM TAKLYNAETR LSQLENCHCE KTCQVSGLLY RDQDSWVDGD HCRNCTCKSG | 300 |
| | AVECRMSCP PLNCSPDSL VHIAGQCKV CRPKCIYGGK VLAEGQRILT KSCRECRGGV | 360 |
| | LVKITEMCPP LNCSEKDHIL PENQCCRVCR GHNFCAEGPK CGENSECKNW NTKATCECKS | 420 |
| | GYISVQGDSA YCEDIECAA KMHYCHANTV CVNLPGLYRC DCPVGYIRVD DFSCTEHDEC | 480 |

| | | | | | | | | |
|----|-----|----------------------------------|------------|------------|------------|-------------|-------------|------------|
| 5 | 540 | GSQGHNCDE | AICTNTVQGH | SCTCKPGYVG | NGTICRAFCE | EGCRYGGTCV | APNKCVCPSG | 540 |
| | 600 | FTGSHCEKDI | DECSGEGIEC | HNHSRCVNL | P | GWYHCECRSG | FHDDGTYSLS | GESCIDIDEC |
| | 660 | ALRTHTCWMD | SACINLAGGF | DCLCPSPGSC | | SGDCPHEGGL | KHNGQVWTLK | EDRCSVCSCK |
| | 720 | DGKIFCRRTA | CDQNPASDL | FCCPECDTRV | TSQCLDQNGH | KLYRSGDNWT | HSCQCCRCLE | 720 |
| | 780 | GEVDCWPLTC | PNLSCEYTAI | LEGECCPRCV | SDPCLADNIT | YDIRKTC LDS | YGVSRLSGSV | 780 |
| | 810 | WTMAGSPCTT | CKCKNGRVCC | SVDFECLQNN | | | | 810 |
| 10 | | Seq ID NO: 362 Protein Sequence | | | | | | |
| | | Protein Accession #: NP_057264.1 | | | | | | |
| | | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | | |
| | | MGSNSQAGR | HIYKSLADDO | PFDSEVPPKR | PTSRLIMHSM | AMFGREFCYA | VEAAYVTPVL | 60 |
| | | LSVGLPSSLY | SIWFLSPIL | GFLLPVVG | ASDHCRSRWG | RRRPYILTIG | VMMLVGMALY | 120 |
| 15 | | LNGATVVAAL | IANPRRLVM | AISVTMIGVV | LFDFAAFDID | GPIKAYLFDV | CSHQDKEKGL | 180 |
| | | HYHALFTGFG | GALGYLLGAI | DWAHLELGR | LGTEFQVMFF | FSALVLTLCF | TVHLCSISEA | 240 |
| | | PLTEVAKGIP | PQQTPODPPL | SSDGMVEYGS | IEKVNGYVN | PELAMQGAKN | KNHAEQTRRA | 300 |
| | | MTLKSLLRAL | VMPPPHYRYL | CISHLIGWTA | FLSNMLPFTD | FMGQIVYRGD | PYSAHNSTEF | 360 |
| | | LIYERGVEVG | CWGFINSVF | SSLYSYFQKV | LVSYIGLKGL | YFTGYLLFGL | GTGFIGLFPN | 420 |
| 20 | | VYSTLVLCSL | FGVMSSTLYT | VPFNLITEYH | REEEKERQQA | PGGDPDNVSR | GKGMDCATLT | 480 |
| | | CMVQLAQILV | GGGLGFLVNT | AGTVVVVVIT | ASAVALIGCC | FVALFVRYVD | | 530 |
| | | Seq ID NO: 363 Protein Sequence | | | | | | |
| | | Protein Accession #: NP_036532.1 | | | | | | |
| 25 | | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | | |
| | | MELALLQGLV | VMAGVPIIQG | GILNLNKMVK | QVTGKMPILS | YWPYGCHCGL | GGRGQPKDAT | 60 |
| | | DWCQTHDCC | YDHLKTQCCS | IYKDYRYNPF | SQGNIHCSDK | GSWCEQQLCA | CDKEVAFCLK | 120 |
| | | RNLDTYQKRL | RFYWRPHCRG | QTPGC | | | | 145 |
| 30 | | Seq ID NO: 364 Protein Sequence | | | | | | |
| | | Protein Accession #: NP_061313.1 | | | | | | |
| | | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | | |
| | | MRLPDLRPWT | SLLLVDAALL | WLLQGPLGTL | LPQGLPGLWL | EGTLRLGGLW | GLLKLRLGLL | 60 |
| 35 | | FVGTLLPLC | LATPLTVSLR | ALVAGASRAP | PARVASAPWS | WLLVGYGAG | LSWSLWAVLS | 120 |
| | | PPGAQEKEQD | QVNNKVLMMR | LLKLSRPDLP | LLVAAFFFLV | LAVLGETLIP | HYSGRVIDIL | 180 |
| | | GGDFDPHAF | SAIFFMCLFS | FGSSLSAGCR | GGCFTYTMSR | INLRIREQLF | SSLLRQDLGF | 240 |
| | | FQETKTGELN | SRLSSDTTLM | SNWLPLNANV | LLRSLVKVVG | LYGFMLSISP | RLTLLSLHLM | 300 |
| 40 | | PFTIAAEKVY | NTRHQEVLRE | IQDAVARAQ | VVREAVGGLQ | TVRSFGAEH | EVCRYKEALE | 360 |
| | | QCRQLYWRD | LERALYLLIR | RVLHLGVQML | MLSCGLQQMQ | DGELTQGSLL | SFMIYQESVG | 420 |
| | | SVYQTLVYIY | GDMLSNVGAA | EKVFSYMDRQ | PNLPSPGTLA | PTTLQGVVVF | QDVSFAYPNR | 480 |
| | | PDRPVLKGLT | FTLRPGEVTA | LVGPNSSGKS | TVAALLQNLV | QPTGGQVLLD | EKPISQYEHC | 540 |
| | | YLHSQVSVG | QEPVLFSGSV | RNNIAYGLQS | CEDDKVMAAA | QAAHADDIFIQ | EMEHGIYTDV | 600 |
| 45 | | GEKGSQLAAG | QKQRLAARA | LVRDPRVLIL | | | | 630 |
| | | Seq ID NO: 365 Protein Sequence | | | | | | |
| | | Protein Accession #: NP_002407 | | | | | | |
| | | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | | |
| 50 | | MKSGSVLFL | GIILLVLIGV | QGTFFVRKGR | CSCISTNQGT | IHLQSLKDLK | QFAPSPPSCEK | 60 |
| | | IEIIATLKNG | VQTCNLNPSA | DVKELIKKWE | KQVSQKKKQK | NGKGHQKKKV | LKVRKSQSR | 120 |
| | | QKKTT | | | | | | |
| 55 | | Seq ID NO: 366 Protein Sequence | | | | | | |
| | | Protein Accession #: NP_006524.1 | | | | | | |
| | | 1 | 11 | 21 | 31 | 41 | 51 | |
| | | | | | | | | |
| | | MARSLVCLGV | IILLSAFSGP | GVRGGPMPKL | ADRLCADQE | CSHPISMAVA | LQDYMAPDCR | 60 |
| | | FLTIHRGQVV | YVFSKLKGRG | RLFWGGSVQG | DYYGDLAARL | GYFPSSIVRE | DQTLKPGKVD | 120 |
| 60 | | VKTRKWDIFYC | Q | | | | | 131 |

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

- 1 1. A method for determining the presence or absence of a pathological cell in a
2 patient, said method comprising detecting a nucleic acid comprising a sequence at least 80%
3 identical to a sequence as described in Tables 2A-68 in a biological sample from said patient,
4 thereby determining the presence or absence of said pathological cell.
- 1 2. The method of Claim 1, wherein:
2 a) said pathology is described in Table 1, including a cancer; and/or
3 b) said biological sample comprises isolated nucleic acids.
- 1 3. The method of Claim 1, wherein said biological sample is tissue from an organ
2 which is affected by said pathology of Table 1, including a cancer.
- 1 4. The method of Claim 2, wherein said nucleic acids are mRNA
- 1 5. The method of Claim 2:
2 a) further comprising a step of amplifying nucleic acids before said step of detecting
3 said nucleic acid; or
4 b) where said detecting is of a protein encoded by said nucleic acid.
- 1 6. The method of Claim 1, wherein said nucleic acid comprises a sequence as
2 described in Tables 2A-68.
- 1 7. The method of Claim 2, wherein:
2 a) said detecting step is carried out by:
3 i) using a labeled nucleic acid probe;
4 ii) utilizing a biochip comprising a sequence at least 80% identical to a sequence
5 as described in Tables 2A-68; or
6 iii) detecting a polypeptide encoded by said nucleic acid; or
7 b) said patient is:
8 i) undergoing a therapeutic regimen to treat said pathology of Table 1; or
9 ii) is suspected of having said pathology or cancer.
- 1 8. An isolated nucleic acid molecule comprising a sequence as described in
2 Tables 2A-68.

- 1 9. The nucleic acid molecule of Claim 8, which is labeled.
- 1 10. An expression vector comprising the nucleic acid of Claim 8.
- 1 11. A host cell comprising the expression vector of Claim 10.
- 1 12. An isolated polypeptide which is encoded by a nucleic acid molecule
2 comprising a sequence as described in Tables 2A-68.
- 1 13. An antibody that specifically binds a polypeptide of Claim 12.
- 1 14. The antibody of Claim 13:
2 a) conjugated to an effector component;
3 b) conjugated to a detectable label, including a fluorescent label, a radioisotope, or a
4 cytotoxic chemical;
5 c) which is an antibody fragment; or
6 d) which is a humanized antibody.
- 1 15. A method for specifically targeting a compound to a pathological cell in a
2 patient, said method comprising administering to said patient an antibody of Claim 13,
3 thereby providing said targetting.
- 1 16. A method for determining the presence or absence of a pathological cell in a
2 patient, said method comprising contacting a biological sample with an antibody of Claim 13.
- 1 17. The method of Claim 16, wherein:
2 a) said antibody is conjugated to:
3 i) an effector component; or
4 ii) a fluorescent label; or
5 b) said biological sample is a blood, serum, urine, or stool sample.
- 1 18. A method for identifying a compound that modulates a pathology-associated
2 polypeptide, said method comprising the steps of:

- a) contacting said compound with a pathology-associated polypeptide, said polypeptide encoded by a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-68; and
- b) determining the functional effect of said compound upon said polypeptide.

19. A drug screening assay comprising the steps of:

- a) administering a test compound to a mammal having a pathology of Table 1 or a cell isolated therefrom; and
- b) comparing the level of gene expression of a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as described in Tables 2A-68 in a treated cell or mammal with the level of gene expression of said polynucleotide in a control cell or mammal, wherein a test compound that modulates said level of expression of the polynucleotide is a candidate for the treatment of said pathology.

(19) World Intellectual Property Organization
International Bureau



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— of inventorship (Rule 4.17(iv)) for US only

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WO 03/025138 A3

(54) Title: METHODS OF DIAGNOSIS OF CANCER COMPOSITIONS AND METHODS OF SCREENING FOR MODULATORS OF CANCER

(57) Abstract: Described herein are genes whose expression are up-regulated or down-regulated in specific cancers. Related methods and compositions that can be used for diagnosis and treatment of those cancers are disclosed. Also described herein are methods that can be used to identify modulators of selected cancers.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/29560

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12Q 1/68

US CL : 435/6

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6, 7.1, 287.2; 436/63, 64

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Please See Continuation Sheet

C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category * | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|-----------------|---|-----------------------|
| X,P — Y,P | US 6,426,186 B1 (JONES et al.) 30 July 2002 (30.07.2002), see especially Detailed Description of the Invention and Sequence 62. | 1-6 7 |
| X — Y | US 6,194,158 B1 (KROES et al.) 27 February 2001 (27.02.2001), see especially Background of the Invention and Detailed Description of the Invention. | 2-5 1, 6, 7 |
| X,P — Y,P | US 6,440,676 B1 (KROES et al.) 27 August 2002 (27.08.2002), see especially Background of the Invention and Detailed Description of the Invention. | 2-5 1, 6, 7 |
| Y,P | US 6,500,938 B1 (AU-YOUNG et al.) 31 December 2002 (31.12.2002), see especially Summary of the Invention and Description of the Invention. | 1-7 |
| Y | SMYTH TEMPLETON et al. Cloning and Characterization of Human Tumor Cell Interstitial Collagenase. September 1990, Volume 50, Number 17, pages 5431-5437, especially Figure 2. | 1-7 |

☐ Further documents are listed in the continuation of Box C.

☐ See patent family annex.

| | | | |
|--|---|----|--|
| * Special categories of cited documents: | | *T | later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention |
| "A" | document defining the general state of the art which is not considered to be of particular relevance | *X | document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone |
| "E" | earlier application or patent published on or after the international filing date | *Y | document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art |
| "L" | document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified) | *& | document member of the same patent family |
| "O" | document referring to an oral disclosure, use, exhibition or other means | | |
| "P" | document published prior to the international filing date but later than the priority date claimed | | |

Date of the actual completion of the international search

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/29560

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet x

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; It is covered by claims Nos.: 1-7 for Specie A(hemangiomas) and B (SEQ ID NO: 1)

Remark on Protest ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/29560

This application contains the following inventions or groups of inventions, which are not so linked as to form a single general inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional examination fees must be paid.

Groups 1-104,648, claim(s) 1-7, drawn to a method for determining the presence or absence of a pathological (Specie A) cell in a patient via detection of polynucleotides that are at least 80% identical to listed sequences (Specie B). If electing from this Group Set, Applicants are asked to elect one species from A and B. Species A has 254 possibilities (see Table 1). Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions in this Group Set including all possible combinations of Species A and B is 104,648.

Groups 104,649-105,060, claim(s) 8-12, drawn to an isolated nucleic acid molecules from Tables 2A-68, expression vectors, host cells, and polypeptides encoded by nucleic acid molecules with listed sequences from Tables 2A-68 (Species B). If electing from this Group Set, Applicants are asked to elect one species from Species B. Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions possible in this Group Set with Specie B is 412.

Groups 105,061-105,472, claim(s) 13-14, drawn to an antibody that binds to a polypeptide encoded by a polynucleotide with sequences from Tables 2A-68 (Species B). If electing from this Group Set, Applicants are asked to elect one species from Species B. Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions possible in this Group Set with Specie B is 412.

Groups 105,473-105,884, claim(s) 15, drawn to a method for targeting a compound to a pathological cell in a patient via administering an antibody that binds to a polypeptide encoded by a polynucleotide from Tables 2A-68 (Species B). If electing from this Group Set, Applicants are asked to elect one species from Species B. Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions possible in this Group Set with Specie B is 412.

Groups 105,885-106,296, claim(s) 16-17, drawn to a method for determining the presence or absence of a pathological cell in a patient via contacting the sample with an antibody that binds to a polypeptide encoded by a polynucleotide from Tables 2A-68 (Species B). If electing from this Group Set, Applicants are asked to elect one species from Species B. Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions possible in this Group Set with Specie B is 412.

Groups 106,297-106,708, claim(s) 18, drawn to a method for identifying a compound that modulates a pathology-associated polypeptide encoded by a polynucleotide that hybridizes to a sequence in Tables 2A-68 (Species B). If electing from this Group Set, Applicants are asked to elect one species from Species B. Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions possible in this Group Set with Specie B is 412.

Groups 106,709-211,356, claim(s) 19, drawn to drug screening assay by administering a compound to a mammal or cell having a pathology (of Table 1) and comparing the level of gene expression of a polynucleotide that hybridizes to a sequence that is 80% identical to sequences as described in Tables 2A-68 (Species B) to gene expression in control cells or mammals. If electing from this Group Set, Applicants are asked to elect one species from A and B. Species A has 254 possibilities (see Table 1). Please note that the sequences in Tables 2A-68 are unsearchable as they are not included in the Sequence Listing. Applicants have supplied 412 nucleic acid sequences from which a selection can be made for Specie B. The total number of individual inventions in this Group Set including all possible combinations of Species A and B is 104,648.

This International Searching Authority considers that the international application does not comply with the requirements of unity of invention (Rules 13.1, 13.2, and 13.3) for the reasons indicated below:

The inventions listed as all Group Sets (Groups 1-211,356) do not relate to a single general inventive concept under PCT Rule 13.1, because under PCT Rule 13.2 they lack the same or corresponding special technical features for the following reasons:

Groups 1-104,648 and Groups 105,472-211,356 are directed to methods or assays which vary in one or more of the following: reactants, steps, and/or goals which are not coextensive and which do not share the same technical feature. Groups 104,649-105,472 have two separate special technical features, a nucleic acid and an antibody, respectively. These are directed to different chemical entity types regarding the critical limitations featuring different structures and functions. The antibodies undergo recognition and binding reactions

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/29560

wherein what is bound is different from what is bound by the compositions including the nucleic acids. Thus, in summary, each Group is directed to a different special technical feature and thus supports this lack of unity.

This application contains claims directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single general inventive concept under PCT Rule 13.1.

In order for more than one species to be examined, the appropriate additional examination fees must be paid. The species are as follows:

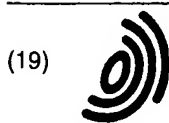
The claims in the Groups 1-104,648 and 106,709-211,356 include a series of species A directed to different pathologies which are listed in Table 1. Each of these types of pathologies are separate entities which affect patients differently, meaning each has its own special technical feature.

The claims in all Groups (1-211,356) include a series of species B directed to nucleic acid sequence listed (412 possibilities) which are considered separate as each defines its own special technical feature.

The first listed pathology (Specie A) and SEQ ID NO: 1 (Species B) will be automatically searched. For each additional Group with a specie combination elected, the fee is an additional \$210.00.

Continuation of B. FIELDS SEARCHED Item 3:

WEST, PUBMED, BIOSIS, CAPLUS, MEDLINE, SCISEARCH, EMBASE searching terms: diagnosis, cancer, screen, modulator, pathological cell, patient, nucleic acid, tissue, mRNA, detect, probe, biochip, array, therapeutic



Europäisches Patentamt
European Patent Office
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(54) **Means and methods for diagnosing and treating affective disorders**

(57) The present invention relates to nucleic acid molecules, preferably genomic sequences, encoding an ATP-gated ion channel P2X7R which contain a mutation in the 5'UTR or 3'UTR regions, a mutation in exon 3, 5, 6, 8 or 13 or in introns 1, 3, 4, 5, 6, 7, 9, 11 or 12 or a deletion in exon 13, which allow to diagnose affective disorders. The invention further relates to polypeptides encoded by said nucleic acid molecules vectors and host cells comprising said nucleic acid molecules as well as to methods for producing polypeptides encoded by said nucleic acid molecules. The present invention also provides antibodies specifically directed to polypeptides encoded by said nucleic acid molecules and aptamers specifically binding said nucleic acid molecules.

Additionally, primers for selectively amplifying said nucleic acid molecules are provided in the present invention as well as kits, compositions, particularly pharmaceutical and diagnostic compositions comprising said nucleic acid molecules, vectors, polypeptides, aptamers, antibodies and/or primers. Moreover, the

present invention relates to methods for diagnosing affective disorders associated with a non-functional P2X7R protein, an altered ATP-gating of the P2X7R protein, an over- or underexpression of the P2X7R protein or associated with the presence of any one of the aforementioned nucleic acid molecules or polypeptides encoded thereby. Additionally, the present invention relates to uses and methods for treating affective disorders employing a functional or non-functional ATP-gated ion-channel P2X7R.

The present invention also relates to uses of modulators of P2X7R activity for treating affective diseases.

Furthermore, the present invention also relates to methods for identifying and characterizing compounds which are capable of specifically interacting with or altering the characteristics of the polypeptides of the present invention as well as to methods for the production of pharmaceutical compositions.

EP 1 469 072 A2

Description

[0001] The present invention relates to nucleic acid molecules, preferably genomic sequences, encoding an ATP-gated ion channel P2X7R which contain a mutation in the 5'UTR or 3'UTR regions, a mutation in exon 3, 5, 6, 8 or 13 or in introns 1, 3, 4, 5, 6, 7, 9, 11 or 12 or a deletion in exon 13, which allow to diagnose affective disorders. The invention further relates to polypeptides encoded by said nucleic acid molecules vectors and host cells comprising said nucleic acid molecules as well as to methods for producing polypeptides encoded by said nucleic acid molecules. The present invention also provides antibodies specifically directed to polypeptides encoded by said nucleic acid molecules and aptamers specifically binding said nucleic acid molecules.

Additionally, primers for selectively amplifying said nucleic acid molecules are provided in the present invention as well as kits, compositions, particularly pharmaceutical and diagnostic compositions comprising said nucleic acid molecules, vectors, polypeptides, aptamers, antibodies and/or primers. Moreover, the present invention relates to methods for diagnosing affective disorders associated with a non-functional P2X7R protein, an altered ATP-gating of the P2X7R protein, an over- or underexpression of the P2X7R protein or associated with the presence of any one of the aforementioned nucleic acid molecules or polypeptides encoded thereby. Additionally, the present invention relates to uses and methods for treating affective disorders employing a functional or non-functional ATP-gated ion-channel P2X7R. The present invention also relates to uses of modulators of P2X7R activity for treating affective diseases. Furthermore, the present invention also relates to methods for identifying and characterizing compounds which are capable of specifically interacting with or altering the characteristics of the polypeptides of the present invention as well as to methods for the production of pharmaceutical compositions.

[0002] Up to 10% of persons visiting a physician are afflicted with an affective disorder (also known as behavioural disorder, mood disorder). Nonetheless, most cases remain undiagnosed or inadequately treated. Affective disorders include among others, depression, anxiety, and bipolar disorder. These diseases are well described in the literature; see, for example, Diagnostic and Statistical Manual of Mental Disorders-4th Edition Text Revision (DMS-IV-TR), American Psychiatric Press, 2000.

Depression, also known as unipolar affective disorder, is characterized by a combination of symptoms such as lowered mood, loss of energy, loss of interest, feeling of physical illness, poor concentration, altered appetite, altered sleep and a slowing down of physical and mental functions resulting in a relentless feeling of hopelessness, helplessness, guilt, and anxiety. The primary subtypes of this disease are major depression, dysthymia (milder depression), and atypical depression. Other important forms of depression are premenstrual dysphoric disorder and seasonal affective disorder. Present treatment of depression consists of psychotherapy, antidepressant drugs, or a combination of both. Most antidepressive drugs target the transport of the neurotransmitters serotonin and/or norepinephrine, or the activity of the enzyme monoamine oxidase. They include: Selective serotonin-reuptake inhibitors (e.g., fluoxetine, paroxetine, sertraline, fluvoxamine), tricyclic antidepressants (e.g., amitriptyline, imipramine, desipramine, nortriptyline), monoamine oxidase inhibitors (e.g., phenelzine, isocarboxazid, tranylcypromine), and designer antidepressants such as mirtazapine, reboxetine, nefazodone. However, all existing antidepressive drugs possess shortcomings such as long latency until response, high degree of non-responders and undesirable side effects (Holsboer, Biol. Psychol. 57 (2001), 47-65). Therefore, a need exists in the medical community for new antidepressive drugs with improved pharmacological profile (Baldwin, Hum. Psychopharmacol. Clin. Exp. 16 (2001), S93-S99).

Anxiety disorders are defined by an excessive or inappropriate aroused state characterized by feelings of apprehension, uncertainty, or fear. They are classified according to the severity and duration of their symptoms and specific affective characteristics. Categories include: (1) Generalized anxiety disorder, (2) panic disorder, (3) phobias, (4) obsessive-compulsive disorder, (5) post-traumatic stress disorder, and (6) separation anxiety disorder. The standard treatment for most anxiety disorders is a combination of cognitive-behavioural therapy with antidepressant medication. Additional medications include benzodiazepines and buspirone.

[0003] Bipolar disorder, also known as manic-depression, is characterized by mood swings between periods of mania (i.e. mood elevation including exaggerated euphoria, irritability) and periods of depression. Bipolar disorder is classified according to the severity of the symptoms. Patients diagnosed with bipolar disorder type I suffer from manic or mixed episodes with or without major depression. In Bipolar Disorder type II, patients have episodes of hypomania and episodes of major depression. With hypomania the symptoms of mania (euphoria or irritability) appear in milder forms and are of shorter duration. The current drugs used to treat bipolar disorders are lithium, valproate and lamotrigine, which stimulates the release of the neurotransmitter glutamate. As with antidepressive drugs, they take weeks to become effective and can result in undesirable side effects, for example, high levels of lithium in the blood can be fatal. Compelling evidence suggest that affective disorders are biological diseases. However, there are no laboratory tests or other procedures that a common physician can use to make a definitive diagnosis. Instead, a specially trained physician or psychiatrist must diagnose the illness based on a group of symptoms that occur together. This process is often time consuming and laborious requiring several visits for the physician to perform a careful history of the symptoms that the patient is currently experiencing as well as any symptoms he or she has had in the past. Therefore,

an easy and effective method for the accurate diagnosis of affective disorders is of high interest to the medical community (Wittchen et al., J. Clin. Psychiatry 62, suppl. 26 (2001), 23-28).

Most patients afflicted with affective disorders have family antecedents and identical twins studies suggest a strong genetic component. For example, genetic mapping on an isolated population of the central valley of Costa Rica suggests a locus for severe bipolar disorder at chromosome 18q22-q23 (Freimer et al., Nature Genetics 12 (1996), 436-441). Moreover, genetic studies performed on the Old Order Amish population suggest that genes on chromosomes 6, 13, and 15 may contribute to the susceptibility of bipolar affective disorder (Ginns et al., Nature Genetics 12 (1996), 431-435). Recently, a genome-wide search in a homogenous population found in the Saguenay/Lac-St-Jean region of Quebec suggests the presence of a major locus for bipolar disorder on chromosome 12q23-q24 (Morissette et al., Am. J. Med. Genet. (Neuropsychiatr. Genet.) 88 (1999), 567-587). Susceptibility loci on chromosomes 5 and 21 were also found in this study. Other groups report minimal evidence for linkage in the region of 12q23 (Kelsoe et al., Proc. Natl. Acad. Sci. USA 98 (2001), 585-590; Sklar, Annu. Rev. Genomics Hum. Genet. 3 (2002), 371-413). Given the various loci mentioned in the above studies (e.g., links to chromosomes 5, 6, 12, 13, 15, 18, 21), a definite genetic link for affective diseases remains to be found.

[0004] Thus, although several genes have been assumed to be linked with affective disorders as mentioned hereinabove, however, no clear correlation has so far been shown. Since no well-suited medication nor diagnosis on a molecular level for affective disorders is available, there is a need for identifying a gene whose mutations cause the whole spectrum of affective disorders as well as for providing medicaments and methods for diagnosis and treatment of affective disorders.

[0005] Thus, the technical problem underlying the present invention is to provide means and methods for diagnosis and treating affective disorders.

[0006] The solution to said technical problem is achieved by providing the embodiments characterized in the claims.

[0007] Accordingly, the present invention relates to a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of:

(a) a genomic nucleotide sequence encoding an ATP-gated ion channel P2X7R and which contains a mutation in the 5'UTR region corresponding to positions 362, 532, 1100, 1122, 1171 or 1702 of the genomic sequence of the wild-type ATP-gated ion channel P2X7R as depicted in SEQ ID NO: 1, wherein at said position said nucleotide is replaced by another nucleotide;

(b) a nucleic acid sequence encoding a polypeptide which has an amino acid sequence of the ATP-gated ion channel P2X7R, wherein in the exon as indicated in column "Exon" of the following Table A the amino acid residue as indicated in column "Amino acid residue" of Table A corresponding to the position as indicated in column "Position in wild-type" of Table A of the wild-type ATP-gated ion channel P2X7R amino acid sequence as depicted in SEQ ID NO: 3 or 4 is replaced by another amino acid residue

Table A

| Exon | Amino acid residue | Position in wild-type |
|---------|--------------------|-----------------------|
| exon 3 | R (Arg) | 117 |
| exon 5 | G (Gly) | 150 |
| exon 6 | E (Glu) | 186 |
| exon 6 | L (Leu) | 191 |
| exon 8 | R (Arg) | 270 |
| exon 13 | I (Ile) | 568 |
| exon 13 | R (Arg) | 578 |

(c) a nucleotide sequence encoding an ATP-gated ion channel P2X7R and which contains a mutation in exon 5 or 8 corresponding to position 32548 or position 37633 of the wild-type ATP-gated ion channel P2X7R nucleotide sequence as depicted in SEQ ID NO: 1, wherein at said position said nucleotide is replaced by another nucleotide

(d) a nucleic acid sequence encoding a polypeptide which has an amino acid sequence of an ATP-gated ion channel P2X7R, wherein amino acids corresponding to positions 488 to 494 of the wild-type ATP-gated ion channel P2X7R as depicted in SEQ ID NO: 3 or 4 are deleted;

(e) a genomic nucleotide sequence encoding an ATP-gated ion channel P2X7R, wherein in the intron as indicated in column "Intron" of the following Table B the nucleotide as indicated in column "Replaced nucleotide" of Table B

corresponding to the position as indicated in column "Position in wild-type" of Table B of the wild-type ATP-gated ion channel P2X7R nucleotide sequence as depicted in SEQ ID NO: 1 is replaced by another nucleotide

Table B

| Intron | REPLACED NUCLEOTIDE | Position in wild-type |
|-----------|---------------------|-----------------------|
| intron 1 | G | 3166 |
| intron 1 | C | 24778 |
| intron 1 | C | 24830 |
| intron 3 | A | 26308 |
| intron 3 | G | 26422 |
| intron 4 | G | 32394 |
| intron 4 | T | 32434 |
| intron 5 | A | 32783 |
| intron 6 | G | 35641 |
| intron 6 | A | 35725 |
| intron 6 | T | 36001 |
| intron 7 | G | 36378 |
| intron 7 | T | 36387 |
| intron 7 | G | 36398 |
| intron 9 | C | 47214 |
| intron 11 | T | 47563 |
| intron 12 | C | 54307 |
| intron 12 | G | 54308 |

(f) a genomic nucleotide sequence encoding an ATP-gated ion channel P2X7R and which contains a mutation in the 3'UTR region corresponding to position 55169, 55170, 55171, 55917 or 54925 of the wild-type ATP-gated ion channel P2X7R nucleotide sequence as depicted in SEQ ID NO: 1, wherein at said position said nucleotide is replaced by another nucleotide;

(g) a nucleotide sequence comprising at least 20 or 21 nucleotides and comprising the mutations or deletions as defined in any one of (a) to (f);

(h) a nucleic acid sequence comprising a nucleotide sequence as shown in any one of SEQ ID NOs: 13 to 51;

(i) a nucleic acid sequence encoding a polypeptide comprising the amino acid sequence of SEQ ID NOs: 5 to 12;

(j) a nucleotide sequence which hybridizes to a nucleotide sequence defined in any one of (a) to (g) or to the nucleotide sequence of (h) and having a mutation as defined in any one of (a) to (f); and

(k) a nucleic acid sequence being degenerate as a result of the genetic code to the nucleic acid sequence as defined in (j).

[0008] It has surprisingly been found that mutations in the P2X7R gene which encodes the ATP-gated ion channel P2X7R can cause the whole spectrum of affective disorders. Six different mutations in the 5'UTR of the P2X7R gene, seven different mutations in exons 3, 5, 6, 8 and 13 of the P2X7R gene leading to an amino acid replacement of the corresponding amino acid in the wild-type sequence of P2X7R depicted in SEQ ID NO: 3 or 4 and two mutations in exons 5 and 8 of said gene, respectively, leading to a replacement of a nucleotide by another nucleotide, a deletion of nucleotides in exon 13 of said gene, 18 mutations in introns 1, 3, 4, 5, 6, 7, 9, 11 and 12 and 5 mutations in the 3'UTR of the P2X7R gene have been identified to co-segregate with the affection status in 41 unrelated families affected with affective disorders. The term "affective disorder" when used in the context of the present invention means to include, but is not limited to, depression, anxiety, unipolar disorder, bipolar disorder type I, bipolar disorder type II, mania, attention deficit hyperactive disorder, substance abuse, and any other disorders affecting the normal behaviour, or mood of an individual.

Each mutation causes alterations that can explain affective disorders as shown in the Examples hereinbelow.

[0009] P2X7R is an ATP-gated ion channel belonging to the P2X ionotropic channel family. The gene was first isolated from rat brain (Surprenant et al., (1996), 272, 735-738; Genbank accession number NM_019256) and subsequently from a human monocyte library (Rassendren et al., J. Biol. Chem. 272 (1997), 5482-5486; Genbank accession numbers NM_002562, Y09561) by virtue of its sequence homology with the other members of the P2X family. It was later found that P2X7R corresponded to the unidentified P2Z receptor which mediates the permeabilising action of ATP on mast cells and macrophages (Dahlgvist and Diamant, Acta Physiol. Scand. 34 (1974), 368-384; Steinberg and Silverstein, J. Biol. Chem. 262 (1987), 3118-3122; Gordon, Biochem. J. 233 (1986), 309-319). The P2X7R has two hydrophobic membrane-spanning domains, an extracellular loop, and forms transmembrane ion channels. P2X7 receptors seem to function only in homooligomeric form and bear a pharmacological profile markedly different from other P2X homo- or heteromers (North and Surprenant, Annual Rev. Pharmacology Toxicology 40 (2000), 563-580). P2X7R requires levels of ATP in excess of 1 mM to achieve activation, whereas other P2X receptors activate at ATP concentrations of $\leq 100 \mu\text{M}$ (Steinberg et al., J. Biol. Chem. 262 (1987), 8884-8888; Greenberg et al., J. Biol. Chem. 263 (1988), 10337-10343) 32). While all P2X receptors demonstrate non-selective channel-like properties following ligation, the channels formed by the P2X7R can rapidly transform into pores that can allow the passage of molecules of up to 900 Dalton (Virginio et al., J. Physiol. 519 (1999), 335-346).

P2X7R is expressed in hematopoietic cells, mast cells and macrophages (Surprenant et al., Science 272 (1996), 3118-3122), where it is organized in tetrameric or hexameric form (Kim et al., J. Biol. Chem. 276 (2001), 23262-23267). P2X7R is *inter alia* involved in the regulation of the immune function and inflammatory response.

[0010] Activation of P2X7R by ATP in macrophages is associated with mitogenic stimulation of T cells (Baricordi et al., Blood 87 (1996), 682-690), the release of cytokines such as interleukin- 1β (Griffiths et al., J. Immunol. 154 (1995), 2821-2828), and formation of macrophage polykaryons (Falzoni et al., J. Clin. Invest. 95 (1995), 1207-1216). Stimulation of the P2X7R with ATP can also result in cell death by triggering massive transmembrane ion fluxes (particularly influx of Ca^{2+} and Na^{+} , and efflux of K^{+}) and the formation of non-selective plasma membrane pores (Di Virgilio et al., Cell Death Differ. 5 (1998), 191-199).

In the brain, P2X7R was originally thought to be restricted to microglia (resident macrophage of the brain) and ependymal cells rather than neurons (Collo et al., Neuropharmacology 36 (1997), 1277-1283) suggesting a role of P2X7R in neurodegeneration. However, P2X7R has since been found in neurons of the rat retina (Brandle et al., Brain Research Molecular Brain Res. 62 (1998), 106-109), cochlear ganglion cells (Brandle et al., Neuroscience Letters 273 (1999), 105-108), and presynaptic terminals of neurons throughout the brainstem and spinal cord (Deuchards et al., J. Neurosci. 21 (2001), 7143-7152). Subsequent studies also suggest that P2X7R regulates the release of neurotransmitters such as glutamate and GABA in neurons of the hippocampus (Armstrong et al., J. Neuroscience 22 (2002), 5938-5945, Sperlagh et al., J. Neurochem. 81 (2002), 1196-1211). Organisation of P2X7R in glial cells and astrocytes of the brain appears monomeric (Kim et al., J. Biol. Chem. 276 (2001), 23262-23267).

Several agonists and antagonists of P2X7R have been identified. Brilliant Blue (Jiang et al., Mol. Pharmacol. 58 (2000), 82-88), the isoquinolines 1-[N,O-Bis(5-isoquinolinesulfonyl)-N-methyl-L-tyrosyl]-4-phenylpiperazine and N-[1-[N-methyl-p-(5-isoquinolinesulfonyl)benzyl]-2-(4-phenylpiperazine)ethyl]-5-isoquinolinesulfonamide (Humphreys et al., Mol. Pharmacol., 54 (1998), 22-32), adamantane derivatives (WO 99/29660, WO 99/29661, WO 00/61569, WO 01/42194, WO 01/44170, WO 01/44213), substituted phenyl compounds (WO 00/71529), piperidine and piperazine derivatives (WO 01/46200) are antagonists of P2X7R while Oxidized ATP (oATP) acts as an irreversible inhibitor of the receptor (Chen et al., J. Biol. Chem., 268 (1993), 8199-8203). Some of these antagonists are presently being evaluated for the treatment of inflammatory, immune, and cardiovascular diseases. BzATP (2'-3'-O-(4-Benzoylbenzoyl)adenosine 5'-triphosphate ($\text{C}_{24}\text{H}_{24}\text{N}_5\text{O}_{15}\text{P}_3$)) acts as agonist of P2X7R (North and Surprenant, Annu. Rev. Pharmacol. Toxicol. 40 (2000), 563-580). WO 99/55901 describes a method for identifying compounds that modulate the activity of a mammalian purinoreceptor selected from the group consisting of P2X2, P2X3, P2X4, P2X5, P2X6 and P2X7 and suggests a role of said purinoreceptors in therapy of behavioural disorders such as epilepsy, depression and aging-associated degenerative diseases.

[0011] Mutant mice lacking P2X7R are healthy, fertile and demonstrate no overt phenotype. However, in contrast to their wild-type counterparts, LPS-activated peritoneal macrophages from *P2X7R*^{-/-} animals fail to generate mature interleukin- 1β (IL- 1β) when challenged with ATP suggesting an inability of peritoneal macrophages to release IL-1 in response to ATP (Solle et al., J. Biol. Chem. 276 (2001), 125-132). A detailed behavioural study of the *P2X7R*^{-/-} mice was not performed. In humans, a Glu-496 to Ala polymorphism leads to the loss of P2X7 function (Gu et al., J. Biol. Chem. 276 (2001), 11135-11142) and is associated with B-cell chronic lymphocytic leukaemia (Thunberg, et al, The Lancet 360 (2002), 1935-1939). Additional polymorphs in the putative P2X7R promoter region, and coding region have been reported (Li et al., FEBS Lett. 531 (2002), 127-131; EP 1199372).

Despite the abundant literature concerning P2X7R, a role in affective disorders has never been suggested or alluded to in the prior art.

[0012] Before the present invention is described in detail, it is to be understood that this invention is not limited to

the particular methodology, protocols, cell lines, vectors, and reagents described herein as these may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims. Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art.

Preferably, the terms used herein are defined as described in "A multilingual glossary of biotechnological terms: (IUPAC Recommendations)", Leuenberger, H.G.W, Nagel, B. and Kölbl, H. eds. (1995), Helvetica Chimica Acta, CH-4010 Basel, Switzerland).

[0013] Throughout this specification and the claims which follow, unless the context requires otherwise, the word "comprise", and variations such as "comprises" and "comprising", will be understood to imply the inclusion of a stated integer or step or group of integers or steps but not the exclusion of any other integer or step or group of integer or step. Several documents are cited throughout the text of this specification. Each of the documents cited herein (including all patents, patent applications, scientific publications, manufacturer's specifications, instructions, etc.), whether supra or infra, are hereby incorporated by reference in their entirety. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

It must be noted that as used herein and in the appended claims, the singular forms "a", "an", and "the", include plural referents unless the context clearly indicates otherwise. Thus, for example, reference to "a reagent" includes one or more of such different reagents, and reference to "the method" includes reference to equivalent steps and methods known to those of ordinary skill in the art that could be modified or substituted for the methods described herein.

[0014] In accordance with the present invention, the term "nucleic acid sequence" means the sequence of bases comprising purine- and pyrimidine bases which are comprised by nucleic acid molecules, whereby said bases represent the primary structure of a nucleic acid molecule. Nucleic acid sequences include DNA, cDNA, genomic DNA, RNA, synthetic forms and mixed polymers, both sense and antisense strands, or may contain non-natural or derivatized nucleotide bases, as will be readily appreciated by those skilled in the art.

[0015] When used herein, the term "polypeptide" means a peptide, a protein, or a polypeptide which encompasses amino acid chains of a given length, wherein the amino acid residues are linked by covalent peptide bonds. However, peptidomimetics of such proteins/polypeptides wherein amino acid(s) and/or peptide bond(s) have been replaced by functional analogs are also encompassed by the invention as well as other than the 20 gene-encoded amino acids, such as selenocysteine. Peptides, oligopeptides and proteins may be termed polypeptides. The terms polypeptide and protein are often used interchangeably herein. The term polypeptide also refers to, and does not exclude, modifications of the polypeptide, e.g., glycosylation, acetylation, phosphorylation and the like. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature.

[0016] The term "position" used in accordance with the present invention means the position of either an amino acid within an amino acid sequence depicted herein or the position of a nucleotide within a nucleic acid sequence depicted herein.

[0017] The term "ATP-gated ion channel P2X7R", in accordance with this invention, denotes a polypeptide which can be classified as a member of the P2X ionotropic receptor family. They are also known as purinergic receptors. P2X receptors are ligand-gated ion channels. The ligand for these receptors may be ATP and/or another natural nucleotide such as ADP, UTP and UDP, or a synthetic nucleotide such as 2-methylthioATP. The criteria for the classification are: (1) a sequence homology that is higher than 39% across the family or different species; (2) signal transduction mechanism involving ion conductance (Khakh et al., Pharmacol Rev. 253 (2001), 107-18). Accordingly, the term "ATP-gated ion channel P2X7R" is interchangeable with the terms "ionotropic receptor" or "purinergic receptor". Preferably, the term "ATP-gated ion channel P2X7R" denotes a polypeptide which can be classified as an ATP-gated ion channel P2X7R on the basis of one or more structural and/or functional characteristics, preferably those described above. Structural characteristics refer to certain structural features which allow to classify a polypeptide as being a P2X7R protein. One such feature is the amino acid sequence. In the context of the present invention a polypeptide is classified as an ATP-gated ion channel P2X7R if it shows a certain degree of sequence identity over its own length to the amino acid sequence of the human P2X7R protein depicted in SEQ ID NO: 3 or 4. This degree of sequence identity is at least 40%, more preferably at least 50%, even more preferably at least 60%, at least 70%, at least 80%, at least 90% or at least 95%. It is particularly preferred that the degree of sequence identity is at least 65%.

[0018] Moreover, structural characteristics of P2X7R proteins are two hydrophobic membrane-spanning domains, an extra cellular loop which could be analyzed by using the program TMPRED (Hofmann Biol. Chem. 347 (1993), 166) or TMHMM (Krogh J. Mol. Bio. 305 (2001), 567-580). Additionally, P2X7R may exist as a single polypeptide, as dimer, tetramer or the like.

[0019] Thus, in the context of the present invention a protein is preferably classified as a P2X7R protein if it displays at least one of the above-mentioned structural characteristics. Functional characteristics refer to properties related to the biological activity of the P2X7R protein. In particular, P2X7R is an ATP-gated ion channel which allows calcium and sodium ions to pass from extracellular solution to intracellular solution, and allows potassium ions to pass from

intracellular to extracellular solution. Moreover, the ATP-gated ion channel P2X7R forms naturally a homooligomeric form. The characteristics of P2X7R receptor proteins can be determined as mentioned hereinbelow. The term "ATP-gated ion channels P2X7R" comprises functional and non-functional forms of the ATP-gated ion channels P2X7R. A functional ATP-gated ion channel P2X7R is understood to be a P2X7R protein which has at least one of the above-mentioned functional characteristics which can be measured by methods known in the art. A non-functional ATP-gated ion channel P2X7R is a protein which can be classified as a P2X7R protein due to structural characteristics as described above but which has lost at least one, preferably all, functional characteristics of a P2X7R protein as described above. Non-functionality of the P2X7R protein can, e.g., be determined by measuring whether calcium and sodium ions can flow into cells or whether potassium ions can exit from cells. Thus, it is possible to determine the occurrence of a mutation in the ATP-gated ion channel P2X7R by measuring either calcium and/or sodium influx or efflux of cells. Cells harbouring a mutation in the P2X7R gene show an altered ion influx and/or efflux in comparison to cells harbouring a wild-type P2X7R protein.

Additionally, there are different methods that could be used to determine whether the P2X7R is functional or non-functional, for example, altered. One method consists of measuring the rate of ATP-induced incorporation of ethidium into cells, e.g. cells isolated from an individual. Ethidium is incorporated into the cells through P2X7R pores, when the pore formation is activated by ATP. Cells are then incubated with or without ATP in the presence of ethidium, then they are analyzed by flow cytometry. Ethidium fluorescence is measured and compared in the presence or absence of ATP. If the P2X7R has lower activity, the ethidium fluorescence induced by ATP will be lower than in control cells. Such a method was used to verify P2X7R activity in isolated B-lymphocytes and T-lymphocytes from leukaemia patients (Wiley et al., *Lancet* 359 (2002), 1114-1119). Briefly, isolated cells are incubated in 1 ml of Hepes buffered potassium chloride at 37°C with continuous stirring. Ethidium is then added at a concentration of 25 mol/l, followed 40 seconds later by the addition of 10 µl of 100 mmol/l ATP stock. Cells are analyzed at 1,000 events/s by flow cytometry using a Coulter Elite flow cytometer (Coulter, Hialeah, FL) with argon laser excitation at 488 nm. Fluorescent emission was collected using a 590-nm long-pass filter. The linear mean channel fluorescence intensity for each gated subpopulation over successive 5-s intervals was analyzed with the use of Win-MDI software (Joseph Trotter, version 2.7) and plotted against time.

Another method of determining P2X7R activity is to measure calcium entry into isolated cells incubated with fluorescent dyes that emit only upon binding to calcium. The cells have to be loaded with the dye and then the calcium entry has to be stimulated. Examples of such dyes include Fura-2, Calcium green, calcium orange, calcium crimson (all available from Molecular Probes). Methods of measuring calcium transport are well known in the art; see for example, Takahashi et al., *Physiol Rev.* 79 (1999), 1089-1125. Furthermore, calcium entry into the cells produces changes in the membrane electric potential. This changes can be measured by electrophysiology (patch clamp) or by using dyes which are sensitive to voltage change. Such methods are also well known in the art, see for example, Gonzalez et al., *DDT* 4 (1999), 431-439; González and Tsien, *Chemistry & Biology* 4 (1997), 269-277; González and Tsien, *Biophysical Journal* 69 (1995), 1272-1280.

Yet another method is to measure uptake of ¹³³Ba²¹. Ba²¹ is a good surrogate for Ca²¹ and once inside the cell is neither pumped nor sequestered by transport ATPases. Ba²¹ uptake can be measured over 60 s using ¹³³BaCl₂ (final concentration, 0.2 mM). At time 0, a prewarmed stock solution of ¹³³Ba²¹ (0.4 mM and 1 µCi/ml) is added in equal volumes to prewarmed isolated cells in 150 mM KCl with HEPES (pH 7.4) at 37°C. ATP (1 mM) is added either 10 minutes before or simultaneously with the ¹³³Ba²¹ isotope. Aliquots of 0.8 ml are taken at time points between 0 and 60 s and are immediately mixed with 0.2 ml of ice-cold 50 mM MgCl₂ (in KCl-HEPES medium) that had been previously layered over 250 µl of oil mixture (di-n-butyl phthalate and di-iso-octyl phthalate, 7:3 vol/vol) and then centrifuged at 8,000 g for 30 s. The supernatants and the oil are aspirated, and the cell pellets are counted in a Wallac Wizard 3 automatic gamma-counter or in any other suitable gamma measuring unit.

[0020] The present invention is based on the finding that mutations of different kinds in the P2X7R gene are linked to the occurrence of affective disorders. The first type of mutations are mutations in the 5'UTR. Examples of such mutations are single nucleotide replacements at positions corresponding to positions 362, 532, 1100, 1122, 1171 or 1702 of the genomic sequence of the wild-type ATP-gated ion channel P2X7R as described in SEQ ID NO: 1.

[0021] The position with respect to nucleotide sequences mentioned herein refer to the sequence shown in SEQ ID NO: 1. This sequence represents the nucleic acid sequence of the P2X7R gene encoding the ATP-gated ion channel P2X7R. It is possible for the skilled person to identify the position in the genomic sequence corresponding to a position in SEQ ID NO: 1 by aligning the sequences. Moreover, the exact locations of the exons and introns are indicated in SEQ ID NO: 1 hereinbelow. Additionally, the person skilled in the art is able to identify exons and introns of the P2X7R gene by comparing SEQ ID NO: 1 with SEQ ID NO: 2 which shows the cDNA sequence of the P2X7R gene.

[0022] Preferably, at position 362 in the 5'UTR of the genomic sequence of the P2X7R gene depicted in SEQ ID NO: 1 a thymine (T) is replaced by another nucleotide, preferably a purine base. More preferably, at said position said thymidine is replaced by a pyrimidine base. Particularly preferred, said thymine is replaced by a cytosine (C).

[0023] At position 532 in the 5'UTR of the genomic sequence of the P2X7R gene depicted in SEQ ID NO: 1 a thymine

(T) is preferably replaced by another nucleotide, preferably a pyrimidine base. More preferably, at said position said thymine is replaced by a purine base. Particularly preferred, said thymine is replaced by a guanine (G).

[0024] The adenine (A) residues at positions 1100 and 1122, respectively, in the 5'UTR of the genomic sequence of the P2X7R gene is preferably replaced by a pyrimidine base. More preferably, said adenine is replaced by a purine base and particularly preferred said adenine is replaced by a guanine (G).

[0025] At position 1171 in the 5'UTR of the genomic sequence of the P2X7R gene depicted in SEQ ID NO: 1 a cytidine (C) is replaced by another nucleotide, preferably by a pyrimidine base. More preferably, said cytidine is replaced by a purine base and even more preferred, said cytidine is replaced by a guanine (G).

[0026] The guanine at position 1702 in the 5'UTR of the genomic sequence of the gene P2X7R depicted in SEQ ID NO: 1 is replaced by another nucleotide, preferably by a pyrimidine base. More preferably, said guanine is replaced by a purine base and particularly preferred it is replaced by an adenine (A).

[0027] A second type of mutation found in the P2X7R gene are mutations in exons which lead to amino acid substitutions in the corresponding amino acid sequence. These are the mutations listed under item (b), supra. In this context, the term "an amino acid residue as indicated in column 'Amino acid residue' of Table A corresponding to position X of the wild-type ATP-gated ion channel P2X7R as depicted in column 'Position in wild-type' "has the following meaning: The amino acid residue in question would be located at position X in the sequence of SEQ ID NO: 3 or 4 if the sequence in which said amino acid residue occurs is compared and aligned with the amino acid sequence of SEQ ID NO: 3 or 4. The amino acid sequence shown in SEQ ID NO: 3 or 4 is the amino acid sequence of the human P2X7R gene and is used as a reference sequence in the present invention.

In order to determine whether an amino acid residue or nucleotide residue in a given P2X7R sequence corresponds to a certain position in the amino acid sequence or nucleotide sequence of SEQ ID NO: 1, 3 or 4, the skilled person can use means and methods well-known in the art, e.g., alignments, either manually or by using computer programs such as those mentioned further down below in connection with the definition of the term "hybridization" and degrees of homology.

[0028] For example, BLAST2.0, which stands for Basic Local Alignment Search Tool (Altschul, Nucl. Acids Res. 25 (1997), 3389-3402; Altschul, J. Mol. Biol. 215 (1990), 403-410), can be used to search for local sequence alignments. BLAST produces alignments of both nucleotide and amino acid sequences to determine sequence similarity. Because of the local nature of the alignments, BLAST is especially useful in determining exact matches or in identifying similar sequences. The fundamental unit of BLAST algorithm output is the High-scoring Segment Pair (HSP). An HSP consists of two sequence fragments of arbitrary but equal lengths whose alignment is locally maximal and for which the alignment score meets or exceeds a threshold or cutoff score set by the user. The BLAST approach is to look for HSPs between a query sequence and a database sequence, to evaluate the statistical significance of any matches found, and to report only those matches which satisfy the user-selected threshold of significance. The parameter E establishes the statistically significant threshold for reporting database sequence matches. E is interpreted as the upper bound of the expected frequency of chance occurrence of an HSP (or set of HSPs) within the context of the entire database search. Any database sequence whose match satisfies E is reported in the program output.

Analogous computer techniques using BLAST (Altschul (1997), loc. cit.; Altschul (1993), loc. cit.; Altschul (1990), loc. cit.) are used to search for identical or related molecules in nucleotide databases such as GenBank or EMBL. This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is categorized as exact or similar. The basis of the search is the product score which is defined as:

$$\frac{\% \text{sequence identity} \times \% \text{maximum BLAST score}}{100}$$

and it takes into account both the degree of similarity between two sequences and the length of the sequence match. For example, with a product score of 40, the match will be exact within a 1-2% error; and at 70, the match will be exact. Similar molecules are usually identified by selecting those which show product scores between 15 and 40, although lower scores may identify related molecules.

[0029] As mentioned above, the second group of mutations identified in the P2X7R gene are mutations in the exons of the P2X7R gene which lead to amino acid substitutions. In this respect SEQ ID NO 2 shows the cDNA sequence of the P2X7R gene. In exon 3 at position 117 of the corresponding wild-type amino acid sequence of P2X7R depicted in SEQ ID NO: 3 or 4 an arginine (R) residue is replaced by another amino acid residue, preferably by an aliphatic, acidic or basic amino acid residue. More preferably, by an aromatic amino acid residue which is particularly preferred to be a tryptophane (W). The resulting polypeptide is shown in SEQ ID NO: 5.

[0030] In exon 5 at position 150 of the wild-type amino acid sequence of P2X7R depicted in SEQ ID NO: 3 or 4 a glycine (G) residue is replaced by another amino acid residue, preferably by an aliphatic, aromatic or acidic amino acid

residue. More preferably, by a basic amino acid residue and particularly preferred by an arginine (R). The resulting polypeptide is shown in SEQ ID NO: 6.

[0031] At position 186 in exon 6 of the wild-type amino acid sequence of P2X7R depicted in SEQ ID NO: 3 or 4 a glutamate residue (E) is replaced by another amino acid residue, preferably by an aliphatic, aromatic or acidic amino acid residue. More preferably, said glutamate is replaced by a basic amino acid residue which is particularly preferred a lysine (K). The resulting polypeptide is shown in SEQ ID NO: 7.

[0032] In exon 6 of the wild-type amino acid sequence of P2X7R depicted in SEQ ID NO: 3 or 4 at position 191 a leucine residue (L) is replaced by another amino acid residue. Said amino acid residue is preferably an aliphatic, acidic or basic amino acid residue. More preferably, said amino acid residue is an aromatic amino acid residue which is particularly preferred to be a proline (P). The resulting polypeptide is shown in SEQ ID NO: 8.

[0033] In exon 8 of the wild-type amino acid sequence of P2X7R depicted in SEQ ID NO: 3 or 4 at position 270 an arginine residue (R) is replaced by another amino acid residue. Said amino acid residue is preferably an aromatic, acidic or basic amino acid residue. More preferably, said amino acid residue is an aliphatic amino acid residue which is particularly preferred to be a cysteine (C). The resulting polypeptide is shown in SEQ ID NO: 9.

[0034] At position 568 in exon 13 of the wild-type amino acid residue of P2X7R depicted in SEQ ID NO: 3 or 4 an isoleucine (I) residue is replaced by another amino acid residue. More preferably, said isoleucine is replaced by an aromatic, basic or acidic amino acid residue. Even more preferred, said isoleucine is replaced by an aliphatic amino acid residue which is particularly preferred to be an asparagine (N). The resulting polypeptide is shown in SEQ ID NO: 10.

[0035] In exon 13 at position 578 in the wild-type amino acid sequence of P2X7R depicted in SEQ ID NO: 3 or 4 an arginine residue (R) is replaced by another amino acid residue. Said amino acid residue is preferably an aromatic, acidic or basic amino acid residue. More preferably, it is an aliphatic amino acid residue and particularly preferred it is a glutamine (Q) residue. The resulting polypeptide is shown in SEQ ID NO: 12.

[0036] It is envisaged that the above-mentioned mutations in the exons of the P2X7R gene occur due to point mutations caused by, e.g. chemical and/or physical means or inaccuracy of the replication complex followed by a failure of the reparation machinery of a cell, can result in a change of a single codon. Possible types of point mutations are transitions, i.e. change of a purine or pyrimidine base for another purine or pyrimidine base, e.g. adenine to guanine or thymidine to cytosine or transversions, i.e. change of a purine or pyrimidine base for another pyrimidine or purine base, e.g., adenine to thymidine or guanine to cytosine. Additionally a point mutation can also be caused by insertion or deletion of one or more nucleotides.

[0037] The mutations leading to the replacement of the amino acids as mentioned hereinabove and hereinbelow are indicated in Table 1 hereinbelow.

[0038] The third group of mutations in the P2X7R gene has been identified to be in exons 5 and 8 of the P2X7R gene depicted in SEQ ID NO: 1 and to be silent, i.e. they do not lead to amino acid changes. In particular, at position 32548 in exon 5 of the wild-type genomic sequence P2X7R gene depicted in SEQ ID NO: 1 a cytidine residue is replaced by another nucleotide. Said nucleotide is preferably a pyrimidine base and particularly preferred a thymine. The exchange of the cytidine residue at position 32548 in exon 5 of the P2X7R gene by another nucleotide preferably does not lead to the replacement of the amino acid cysteine by another amino acid residue.

[0039] In exon 8 of the wild-type P2X7R gene depicted in SEQ ID NO: 1 at position 37633 a cytidine residue is replaced by another nucleotide residue. Said nucleotide residue is preferably a pyrimidine base and particularly preferred thymine. Due to this replacement the amino acid aspartate (D) encoded by the respective codon in which at position 37633 a replacement has taken place is preferably not replaced by another amino acid residue.

The above-mentioned mutations in exons 5 and 8 at positions 32548 and 37633, respectively; of the wild-type P2X7R gene depicted in SEQ ID NO: 1 are mutations at the third position of a triplet codon, i.e. at the wobble base, which lead to so-called silent mutations. Silent mutations do normally not lead to a change of the amino acid due to the degeneracy of the genetic code, i.e. 64 triplets encode at all 20 naturally occurring amino acids. However, said silent mutations lead to a change in the codon encoding its respective amino acids insofar that the newly generated codon may not fit so well into the codon usage of an organism. Namely, the newly generated codon is not translated by the ribosome with the same efficiency as the "old" codon. This may lead to insufficient amounts of the corresponding polypeptide causing an distinct phenotype.

[0040] The fourth group of mutations in the P2X7R gene described hereinabove in item (d) is a deletion of 7 amino acids corresponding to positions 488 to 494 of the wild-type P2X7R amino acid sequence as depicted in SEQ ID NO: 3 or 4. Thus, the present invention also relates to nucleic acid sequences encoding a P2X7R protein in which amino acids corresponding to positions 488 to 494 of the wild-type ATP-gated ion channel P2X7R as depicted in SEQ ID NO: 3 or 4 are deleted. This means, according to the present invention, that a fragment encompassing amino acid positions 488 to 494 of the corresponding wild-type amino acid sequence depicted in SEQ ID NO: 3 or 4 is deleted which results in a shortened polypeptide. An example for such a shortened polypeptide is depicted in SEQ ID NO: 11. This type of mutation as described herein preferably encodes a non-functional ATP-gated ion channel P2X7R. In the present in-

vention the deletion of a fragment encompassing amino acids 488 to 494 of the wild-type amino acid sequence depicted in SEQ ID NO: 3 or 4 is the result of a deletion in exon 13. The resulting protein depicted in SEQ ID NO: 11 lacks amino acids 488 to 494 of the corresponding wild type amino acid sequence depicted in SEQ ID NO: 3 or 4 such that amino acid position 494 of the deleted polypeptide depicted in SEQ ID NO: 11 corresponds to amino acid position 502 of the wild-type amino acid sequence depicted in SEQ ID NO: 3 or 4. Preferably, the nucleic acid sequence of the invention encodes a P2X7R polypeptide in which exactly amino acids corresponding to positions 488 to 494 of SEQ ID NO: 3 or 4 are deleted. However, also mutants are comprised in which either more or less amino acids within the P2X7R amino acid sequence set forth in SEQ ID NO: 3 or 4 may be deleted due to, for example, atypical splicing or deletion of nucleotides of the nucleic acid molecule encoding P2X7R or wrong posttranslational processes, as long as the P2X7R ATP-gated ion channel is non-functional. For example, it is also possible that further amino acids preceding amino acid position 488 or amino acids succeeding amino acid position 494 may be deleted or that less amino acids are deleted.

Preferably at least one, more preferably at least two, even more preferably at least three and most preferably at least 5 amino acid residues are further deleted upstream from the position corresponding to amino acid residue 488 and/or downstream of the position corresponding to amino acid residue 494 of SEQ ID NO: 3 or 4.

However, it is preferred that not more than 20, preferably not more than 15, even more preferably not more than 10 and most preferably not more than 7 amino acid residues are further deleted upstream of the position corresponding to amino acid residue 488 of SEQ ID NO: 3 or 4 or downstream of the position corresponding to amino acid residue 494 of SEQ ID NO: 3 or 4.

[0041] Another group of mutation (mentioned in item (e), supra) resides in introns 1, 3, 4, 5, 6, 7, 9, 11 or 12 of the wild-type genomic sequence of P2X7R depicted in SEQ ID NO: 1. Said mutations in said introns are point mutations as shown in Table B hereinabove and in Table 1, hereinbelow.

[0042] At the respective position indicated in the column "Position in wild-type" in Table B or indicated in the column "Polymorphism" in Table 1 the position of the nucleotide residue in the respective intron which is replaced by another nucleotide residue is shown. Accordingly, the term "a nucleotide as indicated in column "Intron" of the Table B corresponding to the position as indicated in column "Replaced nucleotide" of Table B corresponding to the position as indicated in column "Position in wild-type" of Table B is replaced by another nucleotide means that a nucleotide residue in a P2X7R encoding sequence would be located at position Y in SEQ ID NO: 1 when the P2X7R sequence is compared and aligned with the sequence of SEQ ID NO: 1.

If the nucleotide at the respective position is a purine base such as adenine or guanine it is preferred that due to a transition it is replaced by another purine base.

For example, an adenine is replaced by a guanine or a guanine is replaced by an adenine. If the nucleotide at the respective position is a pyrimidine base it is preferred that due to a transition it is replaced by another pyrimidine base. For example, thymine is replaced by a cytidine and a cytidine is replaced by a thymine.

[0043] It is also preferred that due to a transversion a purine base is replaced by a pyrimidine base or vice versa. For example, an adenine is replaced by a thymine and a guanine is replaced by a cytidine. Particularly preferred, said nucleotide in introns 1, 3, 4, 5, 6, 7, 9, 11 or 12 of the P2X7R gene depicted in SEQ ID NO: 1 is replaced by the nucleotide depicted in column "Polymorphism" of Table 1, hereinbelow.

[0044] A last group of mutations that has been identified relates to mutations which reside in the 3'UTR of the wild-type P2X7R gene depicted in SEQ ID NO: 1. The mutations were found at positions 54925, 55169, 55170, 55171 or 55917 respectively, of the wild-type P2X7R gene depicted in SEQ ID NO: 1.

[0045] At position 54925 a guanine residue was found to be replaced by another nucleotide. Preferably, said guanine residue is replaced by a pyrimidine base, more preferably by a purine base and particularly preferred by an adenine.

[0046] At position 55169 a cytidine residue is replaced by another nucleotide, preferably by a pyrimidine base. More preferably, it is replaced by a purine base and particularly preferred, it is replaced by an adenine.

At positions 55170 and 55171 an adenine residue is replaced by another nucleotide residue, preferably by a purine base. More preferably, said adenine residue is replaced by a pyrimidine base and particularly preferred said adenine residue is replaced by a cytidine residue. It was also found that at position 55917 a cytidine residue is replaced by another nucleotide. Preferably, said nucleotide residue is a purine base, more preferably a pyrimidine base and particularly preferable a thymine.

[0047] As is evident from the above, not all identified mutations are located in exons or lead to a change in the amino acid sequence. Some of the mutations are located in the 5'UTR, the 3'UTR or in introns.

[0048] It is known that polymorphisms in promoter and enhancer regions can affect gene function by modulating transcription, particularly if they are situated at recognition sites for DNA binding proteins (Fishman et al., J. Clin. Invest. 102 (1998), 1369-1376). The term "polymorphism" which is used in the present invention means single nucleotide substitution, nucleotide insertion and nucleotide deletion which in the case of insertion and deletion includes insertion or deletion of one or more nucleotides at a position of a gene and corresponding alterations in expressed proteins. Polymorphisms in the 5' untranslated region (5'UTR) of genes can affect the efficiency with which proteins are trans-

lated. A representative example of this is in the c-myc gene where a C-G SNP that creates an internal ribosome entry site is associated with increased efficiency of c-myc translation and myeloma (Chappell et al., *Oncogene* 19 (2000), 4437-4440). Polymorphisms in the 3'UTR can affect gene function by altering the secondary structure of RNA and efficiency of translation or by affecting motifs in the RNA that bind proteins which regulate RNA degradation. Polymorphisms within introns can affect gene function by affecting RNA splicing resulting in aberrant polypeptides. Another way in which intronic polymorphisms can affect gene function is when they affect regulatory motifs within introns. Examples are the Sp1 binding site polymorphism within intron 1 of the COLIA1 gene (Mann et al., *J. Clin. Invest* 107 (2001), 899-907) and a repeat polymorphisms within the IL-1Ra gene (Keen et al., *Bone* 23 (1998), 367-371). Further examples between intronic SNPs and gene function are described in Caceres and Komblitt, *Trends Genet.* 4 (2002), 186-93. Example 4 on page 52, line 30 to page 53, line 51 of the text describes potential alternative splicing events and aberrant protein production associated with three SNPs disclosed in the application.

[0049] The nucleic acid sequences described hereinabove may comprise at least 56580 nucleotides, preferably at least 10000 nucleotides, at least 5000 nucleotides, at least 1000 nucleotides, at least 500 nucleotides, at least 100 nucleotides. More preferably, said nucleic acid sequences comprise at least 50 nucleotides and particularly preferred they comprise at least 20 or 21 nucleotides comprising the mutations or deletions as described hereinabove. Most preferably such a nucleic acid sequence has a sequence as depicted in any one of SEQ ID NOs: 13 to 51.

[0050] The nucleic acid sequences described hereinabove which comprise mutations in exons leading to a replacement of the corresponding amino acid sequence of the P2X7R wild-type polypeptide depicted in SEQ ID NO: 3 or 4 encode polypeptides shown in SEQ ID NOs: 5 to 10 and 12

Additionally, the nucleic acid sequences described hereinabove which comprise a deletion leading to a truncated polypeptide in comparison to the full-length polypeptide of the wild-type P2X7R polypeptide shown in SEQ ID NO: 3 or 4 is shown in SEQ ID NO: 11.

[0051] The present invention also relates to nucleic acid molecules which hybridize to one of the above described nucleic acid molecules and which shows a mutation as described hereinabove.

The term "hybridizes" as used in accordance with the present invention may relate to hybridizations under stringent or non-stringent conditions. If not further specified, the conditions are preferably non-stringent. Said hybridization conditions may be established according to conventional protocols described, for example, in Sambrook, Russell "Molecular Cloning, A Laboratory Manual", Cold Spring Harbor Laboratory, N.Y. (2001); Ausubel, "Current Protocols in Molecular Biology", Green Publishing Associates and Wiley Interscience, N.Y. (1989), or Higgins and Hames (Eds.) "Nucleic acid hybridization, a practical approach" IRL Press Oxford, Washington DC, (1985). The setting of conditions is well within the skill of the artisan and can be determined according to protocols described in the art. Thus, the detection of only specifically hybridizing sequences will usually require stringent hybridization and washing conditions such as 0.1xSSC, 0.1% SDS at 65°C. Non-stringent hybridization conditions for the detection of homologous or not exactly complementary sequences may be set at 6xSSC, 1% SDS at 65°C. As is well known, the length of the probe and the composition of the nucleic acid to be determined constitute further parameters of the hybridization conditions. Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility. Hybridizing nucleic acid molecules also comprise fragments of the above described molecules. Such fragments may represent nucleic acid sequences which code for a non-functional ATP-gated ion channel P2X7R or a non-functional fragment thereof, and which have a length of at least 12 nucleotides, preferably at least 15, more preferably at least 18, more preferably of at least 21 nucleotides, more preferably at least 30 nucleotides, even more preferably at least 40 nucleotides and most preferably at least 60 nucleotides. Furthermore, nucleic acid molecules which hybridize with any of the aforementioned nucleic acid molecules also include complementary fragments, derivatives and allelic variants of these molecules. Additionally, a hybridization complex refers to a complex between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary G and C bases and between complementary A and T bases; these hydrogen bonds may be further stabilized by base stacking interactions. The two complementary nucleic acid sequences hydrogen bond in an antiparallel configuration. A hybridization complex may be formed in solution (e.g., Cot or Rot analysis) or between one nucleic acid sequence present in solution and another nucleic acid sequence immobilized on a solid support (e.g., membranes, filters, chips, pins or glass slides to which, e.g., cells have been fixed). The terms complementary or complementarity refer to the natural binding of polynucleotides under permissive salt and temperature conditions by base-pairing. For example, the sequence "A-G-T" binds to the complementary sequence "T-C-A". Complementarity between two single-stranded molecules may be "partial", in which only some of the nucleic acids bind, or it may be complete when total complementarity exists between single-stranded molecules. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of hybridization between nucleic acid strands. This is of particular importance in amplification reactions, which depend upon binding between nucleic acids strands.

The term "hybridizing sequences" preferably refers to sequences which display a sequence identity of at least 40%, preferably at least 50%, more preferably at least 60%, even more preferably at least 70%, particularly preferred at least 80%, more particularly preferred at least 90%, even more particularly preferred at least 95% and most preferably at least 97% identity with a nucleic acid sequence as described above encoding a P2X7R protein having a described mutation. Moreover, the term "hybridizing sequences" preferably refers to sequences encoding a P2X7R protein having a sequence identity of at least 40%, preferably at least 50%, more preferably at least 60%, even more preferably at least 70%, particularly preferred at least 80%, more particularly preferred at least 90%, even more particularly preferred at least 95% and most preferably at least 97% identity with an amino acid sequence of a P2X7R mutant as described herein above.

In accordance with the present invention, the term "identical" or "percent identity" in the context of two or more nucleic acid or amino acid sequences, refers to two or more sequences or subsequences that are the same, or that have a specified percentage of amino acid residues or nucleotides that are the same (e.g., 60% or 65% identity, preferably, 70-95% identity, more preferably at least 95% identity), when compared and aligned for maximum correspondence over a window of comparison, or over a designated region as measured using a sequence comparison algorithm as known in the art, or by manual alignment and visual inspection. Sequences having, for example, 60% to 95% or greater sequence identity are considered to be substantially identical. Such a definition also applies to the complement of a test sequence. Preferably the described identity exists over a region that is at least about 15 to 25 amino acids or nucleotides in length, more preferably, over a region that is about 50 to 100 amino acids or nucleotides in length. Those having skill in the art will know how to determine percent identity between/among sequences using, for example, algorithms such as those based on CLUSTALW computer program (Thompson Nucl. Acids Res. 2 (1994), 4673-4680) or FASTDB (Brutlag Comp. App. Biosci. 6 (1990), 237-245), as known in the art.

Although the FASTDB algorithm typically does not consider internal non-matching deletions or additions in sequences, i.e., gaps, in its calculation, this can be corrected manually to avoid an overestimation of the % identity. CLUSTALW, however, does take sequence gaps into account in its identity calculations. Also available to those having skill in this art are the BLAST and BLAST 2.0 algorithms (Altschul Nucl. Acids Res. 25 (1977), 3389-3402). The BLASTN program for nucleic acid sequences uses as defaults a word length (W) of 11, an expectation (E) of 10, M=5, N=4, and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength (W) of 3, and an expectation (E) of 10. The BLOSUM62 scoring matrix (Henikoff Proc. Natl. Acad. Sci., USA, 89, (1989), 10915) uses alignments (B) of 50, expectation (E) of 10, M=5, N=4, and a comparison of both strands.

[0052] Moreover, the present invention also relates to nucleic acid molecules the sequence of which is degenerate in comparison with the sequence of an above-described hybridizing molecule. When used in accordance with the present invention the term "being degenerate as a result of the genetic code" means that due to the redundancy of the genetic code different nucleotide sequences code for the same amino acid.

[0053] The present invention also related to nucleic acid molecules which comprise one or more of the above-described mutations or deletions.

[0054] The nucleic acid molecules according to the invention may be derived from any organism encoding corresponding P2X7R ATP-gated ion channels. For example, P2X7R ATP-gated ion channels have been reported in various organisms, for example, rat (see, Suprenant (1996), loc. cit.), mouse (Genbank Accession No. AJ 489297), xenopus (Genbank Accession No. AJ 345114), chicken (Genbank Accession No. BM 491404) or Bos Taurus (Genbank Accession No. AF 083073). In a preferred embodiment the nucleic acid molecule of the invention is derived from a vertebrate, preferably from a mammal, even more preferably the nucleic acid molecule is derived from rabbit or guinea pig, and most preferably the nucleic acid is derived from mouse, rat or human.

[0055] The nucleic acid molecule according to the invention may be any type of nucleic acid, e.g. DNA, RNA or PNA (peptide nucleic acid).

For the purposes of the present invention, a peptide nucleic acid (PNA) is a polyamide type of DNA analog and the monomeric units for adenine, guanine, thymine and cytosine are available commercially (Perceptive Biosystems). Certain components of DNA, such as phosphorus, phosphorus oxides, or deoxyribose derivatives, are not present in PNAs. As disclosed by Nielsen et al., Science 254:1497 (1991); and Egholm et al., Nature 365:666 (1993), PNAs bind specifically and tightly to complementary DNA strands and are not degraded by nucleases. In fact, PNA binds more strongly to DNA than DNA itself does. This is probably because there is no electrostatic repulsion between the two strands, and also the polyamide backbone is more flexible. Because of this, PNA/DNA duplexes bind under a wider range of stringency conditions than DNA/DNA duplexes, making it easier to perform multiplex hybridization. Smaller probes can be used than with DNA due to the strong binding. In addition, it is more likely that single base mismatches can be determined with PNA/DNA hybridization because a single mismatch in a PNA/DNA 15-mer lowers the melting point (T.sub.m) by 8°-20° C, vs. 4°-16° C for the DNA/DNA 15-mer duplex. Also, the absence of charge groups in PNA means that hybridization can be done at low ionic strengths and reduce possible interference by salt during the analysis.

[0056] The DNA may, for example, be cDNA. In a preferred embodiment it is a genomic DNA. The RNA may be, e.g., mRNA. The nucleic acid molecule may be natural, synthetic or semisynthetic or it may be a derivative, such as

peptide nucleic acid (Nielsen, Science 254 (1991), 1497-1500) or phosphorothioates. Furthermore, the nucleic acid molecule may be a recombinantly produced chimeric nucleic acid molecule comprising any of the aforementioned nucleic acid molecules either alone or in combination.

[0057] Preferably, the nucleic acid molecule of the present invention is part of a vector. Therefore, the present invention relates in another embodiment to a vector comprising the nucleic acid molecule of this invention. Such a vector may be, e.g., a plasmid, cosmid, virus, bacteriophage or another vector used e.g. conventionally in genetic engineering, and may comprise further genes such as marker genes which allow for the selection of said vector in a suitable host cell and under suitable conditions.

[0058] The nucleic acid molecules of the present invention may be inserted into several commercially available vectors. Nonlimiting examples include plasmid vectors compatible with mammalian cells, such as pUC, pBluescript (Stratagene), pET (Novagen), pREP (Invitrogen), pCRTopo (Invitrogen), pcDNA3 (Invitrogen), pCEP4 (Invitrogen), pMC1 neo (Stratagene), pXT1 (Stratagene), pSG5 (Stratagene), EBO-pSV2neo, pBPV-1, pDBPVMNTneo, pRSvgpt, pRS-Vneo, pSV2-dhfr, pUCTag, pIZD35, pLXIN and pSIR (Clontech) and pIRES-EGFP (Clontech). Baculovirus vectors such as pBlueBac, BacPacz Baculovirus Expression System (CLONTECH), and MaxBac™ Baculovirus Expression System, insect cells and protocols (Invitrogen) are available commercially and may also be used to produce high yields of biologically active protein. (see also, Miller (1993), Curr. Op. Genet. Dev., 3, 9; O'Reilly, Baculovirus Expression Vectors: A Laboratory Manual, p. 127). In addition, prokaryotic vectors such as pcDNA2; and yeast vectors such as pYes2 are nonlimiting examples of other vectors suitable for use with the present invention. For vector modification techniques, see Sambrook and Russel (2001), loc. cit. Vectors can contain one or more replication and inheritance systems for cloning or expression, one or more markers for selection in the host, e. g., antibiotic resistance, and one or more expression cassettes.

The coding sequences inserted in the vector can be synthesized by standard methods, isolated from natural sources, or prepared as hybrids. Ligation of the coding sequences to transcriptional regulatory elements (e. g., promoters, enhancers, and/or insulators) and/or to other amino acid encoding sequences can be carried out using established methods.

[0059] Furthermore, the vectors may, in addition to the nucleic acid sequences of the invention, comprise expression control elements, allowing proper expression of the coding regions in suitable hosts. Such control elements are known to the artisan and may include a promoter, translation initiation codon, translation and insertion site or internal ribosomal entry sites (IRES) (Owens, Proc. Natl. Acad. Sci. USA 98 (2001), 1471-1476) for introducing an insert into the vector. Preferably, the nucleic acid molecule of the invention is operatively linked to said expression control sequences allowing expression in eukaryotic or prokaryotic cells. Particularly preferred are in this context control sequences which allow for correct expression in neuronal cells and/or cells derived from nervous tissue.

Control elements ensuring expression in eukaryotic and prokaryotic cells are well known to those skilled in the art. As mentioned above, they usually comprise regulatory sequences ensuring initiation of transcription and optionally poly-A signals ensuring termination of transcription and stabilization of the transcript. Additional regulatory elements may include transcriptional as well as translational enhancers, and/or naturally-associated or heterologous promoter regions. Possible regulatory elements permitting expression in for example mammalian host cells comprise the CMV-HSV thymidine kinase promoter, SV40, RSV-promoter (Rous sarcome virus), human elongation factor 1 α -promoter, CMV enhancer, CaM-kinase promoter or SV40-enhancer.

For the expression for example in nervous tissue and/or cells derived therefrom, several regulatory sequences are well known in the art, like the minimal promoter sequence of human neurofilament L (Charron, J. Biol. Chem. 270 (1995), 25739-25745). For the expression in prokaryotic cells, a multitude of promoters including, for example, the tac-lac-promoter, the lacUV5 or the trp promoter, has been described. Beside elements which are responsible for the initiation of transcription such regulatory elements may also comprise transcription termination signals, such as SV40-poly-A site or the tk-poly-A site, downstream of the polynucleotide. In this context, suitable expression vectors are known in the art such as Okayama-Berg cDNA expression vector pcDV1 (Pharmacia), pRc/CMV, pcDNA1, pcDNA3 (Invitrogen, as used, inter alia in the appended examples), pSPORT1 (GIBCO BRL) or pGEMHE (Promega), or prokaryotic expression vectors, such as lambda gt11.

[0060] An expression vector according to this invention is at least capable of directing the replication, and preferably the expression, of the nucleic acids and protein of this invention. Suitable origins of replication include, for example, the Col E1, the SV40 viral and the M 13 origins of replication. Suitable promoters include, for example, the cytomegalovirus (CMV) promoter, the iacZ promoter, the gai10 promoter and the Autographa californica multiple nuclear polyhedrosis virus (AcMNPV) polyhedral promoter. Suitable termination sequences include, for example, the bovine growth hormone, SV40, iacZ and AcMNPV polyhedral polyadenylation signals. Examples of selectable markers include neomycin, ampicillin, and hygromycin resistance and the like. Specifically-designed vectors allow the shuttling of DNA between different host cells, such as bacteria-yeast, or bacteria-animal cells, or bacteria-fungal cells, or bacteria invertebrate cells.

Beside the nucleic acid molecules of the present invention, the vector may further comprise nucleic acid sequences

encoding for secretion signals. Such sequences are well known to the person skilled in the art. Furthermore, depending on the expression system used leader sequences capable of directing the expressed polypeptide to a cellular compartment may be added to the coding sequence of the nucleic acid molecules of the invention and are well known in the art. The leader sequence(s) is (are) assembled in appropriate phase with translation, initiation and termination sequences, and preferably, a leader sequence capable of directing secretion of translated protein, or a part thereof, into, inter alia, the extracellular membrane. Optionally, the heterologous sequence can encode a fusion protein including an C- or N-terminal identification peptide imparting desired characteristics, e.g., stabilization or simplified purification of expressed recombinant product. Once the vector has been incorporated into the appropriate host, the host is maintained under conditions suitable for high level expression of the nucleotide sequences, and, as desired, the collection and purification of the proteins, antigenic fragments or fusion proteins of the invention may follow. Of course, the vector can also comprise regulatory regions from pathogenic organisms.

Furthermore, said vector may also be, besides an expression vector, a gene transfer and/or gene targeting vector. Gene therapy, which is based on introducing therapeutic genes (for example for vaccination) into cells by ex-vivo or in-vivo techniques is one of the most important applications of gene transfer. Suitable vectors, vector systems and methods for in-vitro or in-vivo gene therapy are described in the literature and are known to the person skilled in the art; see, e.g., Giordano, Nature Medicine 2 (1996), 534-539; Schaper, Circ. Res. 79 (1996), 911-919; Anderson, Science 256 (1992), 808-813, Isner, Lancet 348 (1996), 370-374; Muhlhauser, Circ. Res. 77 (1995), 1077-1086; Wang, Nature Medicine 2 (1996), 714-716; WO 94/29469; WO 97/00957; Schaper, Current Opinion in Biotechnology 7 (1996), 635-640 or Verma, Nature 389 (1997), 239-242 and references cited therein.

The nucleic acid molecules of the invention and vectors as described herein above may be designed for direct introduction or for introduction via liposomes, or viral vectors (e.g. adenoviral, retroviral) into the cell. Additionally, baculoviral systems or systems based on vaccinia virus or Semliki Forest Virus can be used as eukaryotic expression system for the nucleic acid molecules of the invention. In addition to recombinant production, fragments of the protein, the fusion protein or antigenic fragments of the invention may be produced by direct peptide synthesis using solid-phase techniques (cf Stewart et al. (1969) Solid Phase Peptide Synthesis; Freeman Co., San Francisco; Merrifield, J. Am. Chem. Soc. 85 (1963), 2149-2154). In vitro protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Perkin Elmer, Foster City CA) in accordance with the instructions provided by the manufacturer. Various fragments may be chemically synthesized separately and combined using chemical methods to produce the full length molecule.

[0061] The present invention in addition relates to a host transformed with a vector of the present invention or to a host comprising the nucleic acid molecule of the invention. Said host may be produced by introducing said vector or nucleotide sequence into a host cell which upon its presence in the cell mediates the expression of a protein encoded by the nucleotide sequence of the invention or comprising a nucleotide sequence or a vector according to the invention wherein the nucleotide sequence and/or the encoded polypeptide is foreign to the host cell.

By "foreign" it is meant that the nucleotide sequence and/or the encoded polypeptide is either heterologous with respect to the host, this means derived from a cell or organism with a different genomic background, or is homologous with respect to the host but located in a different genomic environment than the naturally occurring counterpart of said nucleotide sequence. This means that, if the nucleotide sequence is homologous with respect to the host, it is not located in its natural location in the genome of said host, in particular it is surrounded by different genes. In this case the nucleotide sequence may be either under the control of its own promoter or under the control of a heterologous promoter. The location of the introduced nucleic acid molecule or the vector can be determined by the skilled person by using methods well-known to the person skilled in the art, e.g., Southern Blotting. The vector or nucleotide sequence according to the invention which is present in the host may either be integrated into the genome of the host or it may be maintained in some form extrachromosomally. In this respect, it is also to be understood that the nucleotide sequence of the invention can be used to restore or create a mutant gene via homologous recombination.

[0062] Said host may be any prokaryotic or eukaryotic cell. Suitable prokaryotic/bacterial cells are those generally used for cloning like *E. coli*, *Salmonella typhimurium*, *Serratia marcescens* or *Bacillus subtilis*. Said eukaryotic host may be a mammalian cell, an amphibian cell, a fish cell, an insect cell, a fungal cell, a plant cell or a bacterial cell (e.g., *E. coli* strains HB101, DH5a, XL1 Blue, Y1090 and JM101). Eukaryotic recombinant host cells are preferred. Examples of eukaryotic host cells include, but are not limited to, yeast, e.g., *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces lactis* or *Pichia pastoris* cells, cell lines of human, bovine, porcine, monkey, and rodent origin, as well as insect cells, including but not limited to, *Spodoptera frugiperda* insect cells and *Drosophila*-derived insect cells as well as zebra fish cells. Mammalian species-derived cell lines suitable for use and commercially available include, but are not limited to, L cells, CV-1 cells, COS-1 cells (ATCC CRL 1650), COS-7 cells (ATCC CRL 1651), HeLa cells (ATCC CCL 2), C1271 (ATCC CRL 1616), BS-C-1 (ATCC CCL 26) and MRC-5 (ATCC CCL 171).

[0063] In a particularly preferred embodiment said mammalian cell is a neuronal cell and/or a cultured cell like, inter alia, a HEK 293 (human embryonic kidney) cell, a CHO, HeLa, NIH3T3, BHK, PC12 cell or a neuronal stem cell preferably derived from a mammal and more preferably from a human.

In another more preferred embodiment said amphibian cell is an oocyte. In an even more preferred embodiment said oocyte is a frog oocyte, particularly preferred a *Xenopus laevis* oocyte.

[0064] In a more preferred embodiment, the host according to the invention is a non-human transgenic organism. Said non-human organism may be a mammal, amphibian, a fish, an insect, a fungus or a plant. Particularly preferred non-human transgenic animals are *Drosophila* species, *Caenorhabditis elegans*, *Xenopus* species, zebra fish, *Spodoptera frugiperda*, *Autographa californica*, mice and rats. Transgenic plants comprise, but are not limited to, wheat, tobacco, parsley and *Arabidopsis*. Transgenic fungi are also well known in the art and comprise, inter alia, yeasts, like *S. pombe* or *S. cerevisiae*, or *Aspergillus*, *Neurospora* or *Ustilago* species or *Pichia* species.

[0065] In another embodiment, the present invention relates to a method for producing the polypeptide encoded by a nucleic acid molecule of the invention comprising culturing/raising the host of the invention and isolating the produced polypeptide.

A large number of suitable methods exist in the art to produce polypeptides in appropriate hosts. If the host is a unicellular organism or a mammalian or insect cell, the person skilled in the art can revert to a variety of culture conditions that can be further optimized without an undue burden of work. Conveniently, the produced protein is harvested from the culture medium or from isolated (biological) membranes by established techniques. Furthermore, the produced polypeptide may be directly isolated from the host cell. Said host cell may be part of or derived from a part of a host organism, for example said host cell may be part of the CNS of an animal or the harvestable part of a plant. Additionally, the produced polypeptide may be isolated from fluids derived from said host, like blood, milk or cerebrospinal fluid.

[0066] Additionally the present invention relates to polypeptides depicted in SEQ ID NOs: 5 to 12 which are encoded by the nucleic acid molecules of the invention or produced by the method of the invention. The polypeptide of the invention may accordingly be produced by microbiological methods or by transgenic mammals. It is also envisaged that the polypeptide of the invention is recovered from transgenic plants. Alternatively, the polypeptide of the invention may be produced synthetically or semi-synthetically.

For example, chemical synthesis, such as the solid phase procedure described by Houghton Proc. Natl. Acad. Sci. USA (82) (1985), 5131-5135, can be used. Another method is in vitro translation of mRNA. A preferred method involves the recombinant production of protein in host cells as described above. For example, nucleotide acid sequences comprising all or a portion of any one of the nucleotide sequences according to the invention can be synthesized by PCR, inserted into an expression vector, and a host cell transformed with the expression vector. Thereafter, the host cell is cultured to produce the desired polypeptide, which is isolated and purified. Protein isolation and purification can be achieved by any one of several known techniques; for example and without limitation, ion exchange chromatography, gel filtration chromatography and affinity chromatography, high pressure liquid chromatography (HPLC), reversed phase HPLC, preparative disc gel electrophoresis. In addition, cell-free translation systems can be used to produce the polypeptides of the present invention. Suitable cell-free expression systems for use in accordance with the present invention include rabbit reticulocyte lysate, wheat germ extract, canine pancreatic microsomal membranes, *E. coli* S30 extract, and coupled transcription/translation systems such as the TNT-system (Promega). These systems allow the expression of recombinant polypeptides or peptides upon the addition of cloning vectors, DNA fragments, or RNA sequences containing coding regions and appropriate promoter elements. As mentioned supra, protein isolation/purification techniques may require modification of the proteins of the present invention using conventional methods. For example, a histidine tag can be added to the protein to allow purification on a nickel column. Other modifications may cause higher or lower activity, permit higher levels of protein production, or simplify purification of the protein.

[0067] In a further embodiment, the present invention relates to an antibody specifically directed to a polypeptide of the invention, wherein said antibody specifically reacts with an epitope generated and/or formed by the mutation in the ATP-gated ion channel P2X7R selected from the group consisting of:

(i) an epitope specifically presented by a polypeptide which has an amino acid sequence of an ATP-gated ion channel P2X7R, wherein the R (Arg), G (Gly), E (Glu), L (Leu), R (Arg), I (Ile) or R (Arg) residue corresponding to position 117, 150, 186, 191, 270, 568 or 578 of the wild-type ATP-gated ion channel P2X7R as depicted in SEQ ID NO: 3 or 4 is replaced by another amino acid residue; and

(ii) an epitope specifically presented by a polypeptide which has an amino acid sequence of an ATP-gated ion channel P2X7R, wherein amino acids corresponding to positions 488 to 494 of the wild-type ATP-gated ion channel P2X7R as depicted in SEQ ID NO: 3 or 4 are deleted.

[0068] With respect to preferred embodiments of (i) and (ii) the same applies as described above in connection with the nucleic acid molecules. The term "specifically" in this context means that the antibody reacts with the mutant P2X7R protein but not with a wild-type P2X7R protein. Preferably this term also means that such an antibody does not bind to other mutant forms of the P2X7R protein, in particular those described herein. Whether the antibody specifically reacts as defined herein above can easily be tested, inter alia, by comparing the reaction of said antibody with a wild-type ATP-gated ion channel P2X7R (or a subunit or a fragment thereof) with the reaction of said antibody with a mutant

P2X7R polypeptide of the invention.

The antibody of the present invention can be, for example, polyclonal or monoclonal. The term "antibody" also comprises derivatives or fragments thereof which still retain the binding specificity. Techniques for the production of antibodies are well known in the art and described, e.g. in Harlow and Lane "Antibodies, A Laboratory Manual", CSH Press, Cold Spring Harbor, 1988. These antibodies can be used, for example, for the immunoprecipitation and immunolocalization of the polypeptides of the invention as well as for the monitoring of the presence of such polypeptides, for example, in recombinant organisms or in diagnosis. They can also be used for the identification of compounds interacting with the proteins according to the invention (as mentioned herein below). For example, surface plasmon resonance as employed in the BIAcore system can be used to increase the efficiency of phage antibodies which bind to an epitope of the polypeptide of the invention (Schier, Human Antibodies Hybridomas 7 (1996), 97-105; Malmberg, J. Immunol. Methods 183 (1995), 7-13).

The present invention furthermore includes chimeric, single chain and humanized antibodies, as well as antibody fragments, like, inter alia, Fab fragments. Antibody fragments or derivatives further comprise F(ab')₂, Fv or scFv fragments; see, for example, Harlow and Lane, loc. cit.. Various procedures are known in the art and may be used for the production of such antibodies and/or fragments. Thus, the (antibody) derivatives can be produced by peptidomimetics. Further, techniques described for the production of single chain antibodies (see, inter alia, US Patent 4,946,778) can be adapted to produce single chain antibodies to polypeptide(s) of this invention. Also, transgenic animals may be used to express humanized antibodies to polypeptides of this invention. Most preferably, the antibody of this invention is a monoclonal antibody. For the preparation of monoclonal antibodies, any technique which provides antibodies produced by continuous cell line cultures can be used. Examples for such techniques include the hybridoma technique (Köhler and Milstein Nature 256 (1975), 495-497), the trioma technique, the human B-cell hybridoma technique (Kozbor, Immunology Today 4 (1983), 72) and the EBV-hybridoma technique to produce human monoclonal antibodies (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc. (1985), 77-96). Techniques describing the production of single chain antibodies (e.g., US Patent 4,946,778) can be adapted to produce single chain antibodies to immunogenic polypeptides as described above. Furthermore, transgenic mice may be used to express humanized antibodies directed against said immunogenic polypeptides. It is in particular preferred that the antibodies/antibody constructs as well as antibody fragments or derivatives to be employed in accordance with this invention or capable to be expressed in a cell. This may, inter alia, be achieved by direct injection of the corresponding proteinaceous molecules or by injection of nucleic acid molecules encoding the same. Furthermore, gene therapy approaches are envisaged. Accordingly, in context of the present invention, the term "antibody molecule" relates to full immunoglobulin molecules as well as to parts of such immunoglobulin molecules. Furthermore, the term relates, as discussed above, to modified and/or altered antibody molecules, like chimeric and humanized antibodies. The term also relates to monoclonal or polyclonal antibodies as well as to recombinantly or synthetically generated/synthesized antibodies. The term also relates to intact antibodies as well as to antibody fragments thereof, like, separated light and heavy chains, Fab, Fab/c, Fv, Fab', F(ab')₂. The term "antibody molecule" also comprises bifunctional antibodies and antibody constructs, like single chain Fvs (scFv) or antibody-fusion proteins. It is also envisaged in context of this invention that the term "antibody" comprises antibody constructs which may be expressed in cells, e.g. antibody constructs which may be transfected and/or transduced via, inter alia, viruses or vectors. It is in particular envisaged that such antibody constructs specifically recognize the polypeptides of the present invention. It is, furthermore, envisaged that said antibody construct is employed in gene therapy approaches.

[0069] The present invention relates also to an aptamer specifically binding to a polypeptide according to the invention wherein said aptamer reacts with an epitope of a polypeptide of the present invention. The present invention furthermore relates to an aptamer specifically directed to a corresponding nucleic acid molecule according to the invention.

In accordance with the present invention, the term "aptamer" means nucleic acid molecules that can bind to target molecules. Aptamers commonly comprise RNA, single stranded DNA, modified RNA or modified DNA molecules. The preparation of aptamers is well known in the art and may involve, inter alia, the use of combinatorial RNA libraries to identify binding sides (Gold, Ann. Rev. Biochem. 64 (1995), 763-797).

[0070] Furthermore, the present invention relates to a primer or pair of primers capable of specifically amplifying the nucleic acid molecules of the present invention. The term "primer" when used in the present invention means a single-stranded nucleic acid molecule capable of annealing the nucleic acid molecule of the present application and thereby being capable of serving as a starting point for amplification. Said term also comprises oligoribo- or deoxyribonucleotides which are complementary to a region of one of the strands of a nucleic acid molecule of the present invention. According to the present invention the term "pair of primers" means a pair of primers that are with respect to a complementary region of a nucleic acid molecule directed in the opposite direction towards each other to enable, for example, amplification by polymerase chain reaction (PCR).

The term "amplifying" refers to repeated copying of a specified sequence of nucleotides resulting in an increase in the amount of said specified sequence of nucleotides. and allows the generation of a multitude of identical or essentially identical (i.e. at least 95% more preferred at least 98%, even more preferred at least 99% and most preferred at least

99.5% such as 99.9% identical) nucleic acid molecules or parts thereof. Such methods are well established in the art; see Sambrook et al. "Molecular Cloning, A Laboratory Manual", 2nd edition 1989, CSH Press, Cold Spring Harbor. They include polymerase chain reaction (PCR) and modifications thereof, ligase chain reaction (LCR) to name some preferred amplification methods.

When used in the context of primers the term "specifically" means that only the nucleic acid molecules as described herein above are amplified and nucleic acid molecules encoding the wild-type P2X7R ATP-gated receptor as depicted in SEQ ID NO: 1 are not amplified. Thus, a primer according to the invention is preferably a primer which binds to a region of a nucleic acid molecule of the invention which is unique for this molecule and which is not present in the wild-type P2X7R encoding sequence, i.e. the primer binds in a region in which one of the above described mutations occur. In connection with a pair of primers according to the invention it is possible that one of the primers of the pair is specific in the above described meaning or both of the primers of the pair are specific. In both cases, the use of such a pair of primers would allow to specifically amplify a mutant of the invention as described herein-above but not the wild-type P2X7R encoding sequence.

The 3'-OH end of a primer is used by a polymerase to be extended by successive incorporation of nucleotides. The primer or pair of primers of the present invention can be used, for example, in primer extension experiments on template RNA according to methods known by the person skilled in the art. Preferably, the primer or pair of primers of the present invention are used for amplification reactions on template RNA or template DNA, preferably cDNA or genomic DNA. The terms "template DNA" or "template RNA" refers to DNA or RNA molecules or fragments thereof of any source or nucleotide composition, that comprise a target nucleotide sequence as defined above. The primer or pair of primers can also be used for hybridization experiments as known in the art. Preferably, the primer or pair of primers are used in polymerase chain reactions to amplify sequences corresponding to a sequence of the nucleic acid molecule of the present invention. It is known that the length of a primer results from different parameters (Gillam, Gene 8 (1979), 81-97; Innis, PCR Protocols: A guide to methods and applications, Academic Press, San Diego, USA (1990)). Preferably, the primer should only hybridize or bind to a specific region of a target nucleotide sequence. The length of a primer that statistically hybridizes only to one region of a target nucleotide sequence can be calculated by the following formula: $(\frac{1}{4})^x$ (whereby x is the length of the primer). For example a hepta- or octanucleotide would be sufficient to bind statistically only once on a sequence of 37 kb. However, it is known that a primer exactly matching to a complementary template strand must be at least 9 base pairs in length, otherwise no stable-double strand can be generated (Goulian, Biochemistry 12 (1973), 2893-2901). It is also envisaged that computer-based algorithms can be used to design primers capable of amplifying the nucleic acid molecules of the invention. Preferably, the primers of the invention are at least 10 nucleotides in length, more preferred at least 12 nucleotides in length, even more preferred at least 15 nucleotides in length, particularly preferred at least 18 nucleotides in length, even more particularly preferred at least 20 nucleotides in length and most preferably at least 25 nucleotides in length. The invention, however, can also be carried out with primers which are shorter or longer.

It is also envisaged that the primer or pair of primers is labeled. The label may, for example, be a radioactive label, such as ³²P, ³³P or ³⁵S. In a preferred embodiment of the invention, the label is a non-radioactive label, for example, digoxigenin, biotin and fluorescence dye or a dye.

In another preferred embodiment said primers are selected from the group consisting of SEQ ID NOs: 52 to 111.

[0071] In yet another embodiment, the present invention relates to a composition comprising a nucleic acid molecule, a vector, a polypeptide, an antibody, an aptamer and/or a primer or pair of primers of the invention.

The term "composition", as used in accordance with the present invention, relates to compositions which comprise at least one nucleic acid molecule, vector, polypeptide, an antibody and/or primer or pair of primers of this invention. It may, optionally, comprise further molecules capable of altering the characteristics of the component of the invention thereby, for example, suppressing, blocking, modulating and/or activating their function which have neuroprotective, nootropic, antidepressive and/or cell-protective properties as will also be described herein below. The composition may be in solid, liquid or gaseous form and may be, inter alia, in the form of (a) powder(s), (a) tablet(s), (a) solution(s) or (an) aerosol(s).

[0072] In a preferred embodiment the composition according to the invention is a diagnostic composition, optionally further comprising suitable means for detection. As described above, the present invention is based on the surprising finding that mutations in the P2X7R protein are connected with affective disorders. Thus, this knowledge now allows to diagnose affective disorders in an easy way. The diagnostic composition comprises at least one of the aforementioned compounds of the invention. The diagnostic composition may be used, inter alia, for methods for determining the presence and/or expression of the nucleic acids and/or polypeptides of the invention. This may be effected by detecting, e.g., the presence of a corresponding gene in the genetic material of an individual or the presence of the corresponding mRNA which comprises isolation of DNA or RNA from a cell derived from said individual, contacting the DNA or RNA so obtained with a nucleic acid probe as described above under hybridizing conditions, and detecting the presence of mRNAs hybridized to the probe. Alternatively, the diagnostic composition may also be used for detecting the presence of a nucleic acid molecule of the invention by PCR. Furthermore, polypeptides of the invention can be

detected with methods known in the art, which comprise, inter alia, immunological methods, like, RIA, FIA, ELISA, FACS or Western blotting.

Furthermore, the diagnostic composition of the invention may be useful, inter alia, in detecting the prevalence, the onset or the progress of a disease related to the expression of a polypeptide of the invention. Accordingly, the diagnostic composition of the invention may be used, inter alia, for assessing the prevalence, the onset and/or the disease status of affective disorders, as defined herein above. It is also contemplated that the diagnostic composition of the invention may be useful in discriminating (the) stage(s) of a disease.

[0073] The diagnostic composition optionally comprises suitable means for detection. The nucleic acid molecule(s), vector(s), host(s), antibody(ies), aptamer(s), polypeptide(s) described above are, for example, suitable for use in immunoassays in which they can be utilized in liquid phase or bound to a solid phase carrier. Examples of well-known carriers include glass, polystyrene, polyvinyl ion, polypropylene, polyethylene, polycarbonate, dextran, nylon, amyloses, natural and modified celluloses, polyacrylamides, agaroses, and magnetite. The nature of the carrier can be either soluble or insoluble for the purposes of the invention.

Solid phase carriers are known to those in the art and may comprise polystyrene beads, latex beads, magnetic beads, colloid metal particles, glass and/or silicon chips and surfaces, nitrocellulose strips, membranes, sheets, duracytes and the walls of wells of a reaction tray, plastic tubes or other test tubes. Suitable methods of immobilizing nucleic acid molecule(s), vector(s), host(s), antibody(ies), aptamer(s), polypeptide(s), etc. on solid phases include but are not limited to ionic, hydrophobic, covalent interactions or (chemical) crosslinking and the like. Examples of immunoassays which can utilize said compounds of the invention are competitive and non-competitive immunoassays in either a direct or indirect format. Commonly used detection assays can comprise radioisotopic or non-radioisotopic methods. Examples of such immunoassays are the radioimmunoassay (RIA), the sandwich (immunometric assay) and the Northern or Southern blot assay. Furthermore, these detection methods comprise, inter alia, IRMA (Immune Radioimmunometric Assay), EIA (Enzyme Immuno Assay), ELISA (Enzyme Linked Immuno Assay), FIA (Fluorescent Immuno Assay), and CLIA (Chemiluminescent Immune Assay). Furthermore, the diagnostic compounds of the present invention may be

are employed in techniques like FRET (Fluorescence Resonance Energy Transfer) assays. Appropriate labels and methods for labeling are known to those of ordinary skill in the art. Examples of the types of labels which can be used in the present invention include inter alia, fluorochromes (like fluorescein, rhodamine, Texas Red, etc.), enzymes (like horse radish peroxidase, β -galactosidase, alkaline phosphatase), radioactive isotopes (like ^{32}P , ^{33}P , ^{35}S or ^{125}I), biotin, digoxigenin, colloidal metals, chemi- or bioluminescent compounds (like dioxetanes, luminol or acridiniums).

[0074] A variety of techniques are available for labeling biomolecules, are well known to the person skilled in the art and are considered to be within the scope of the present invention and comprise, inter alia, covalent coupling of enzymes or biotinyl groups, phosphorylations, biotinylations, random priming, nick-translations, tailing (using terminal transferases). Such techniques are, e.g., described in Tijssen, "Practice and theory of enzyme immunoassays", Burden and von Knippenburg (Eds), Volume 15 (1985); "Basic methods in molecular biology", Davis LG, Diber MD, Battey Elsevier (1990); Mayer, (Eds) "Immunochemical methods in cell and molecular biology" Academic Press, London (1987); or in the series "Methods in Enzymology", Academic Press, Inc. Detection methods comprise, but are not limited to, autoradiography, fluorescence microscopy, direct and indirect enzymatic reactions, etc.

Said diagnostic composition may be used for methods for detecting the presence and/or abundance of a nucleic acid molecule of the invention in a biological and/or medical sample and/or for detecting expression of such a nucleic acid molecule (e.g. by determining the mRNA or the expressed polypeptide). Furthermore, said diagnostic composition may also be used in methods of the present invention, inter alia, for the detection of specific antagonists or agonists for P2X7R ATP-gated ion channels (see herein below).

[0075] In a further embodiment the present invention provides a method of diagnosing an affective disorder or a susceptibility to an affective disorder comprising the step of determining in a sample obtained from an individual whether the P2X7R protein expressed in the cells of said individual is non-functional, shows an altered ATP-gating in comparison to the wild-type P2X7R protein or is over- or under-expressed in comparison to the P2X7R protein level of an unaffected individual.

The term "over- or under-expressed in comparison to the P2X7R protein level" in the context of the present invention means that the P2X7R protein level is higher or lower than the P2X7R level of a healthy individual, i.e. an individual not affected with an affective disorder. The over-expression may result, e.g. from an increased amount of P2X7R mRNA caused by enhanced transcription rates due to increased activity of the RNA-polymerase II. The amount of mRNA may accordingly lead to an increased translation and, thus, to a higher protein level of P2X7R. It may also be possible that a higher amount of P2X7R protein is caused by increased stability of the protein. An under-expression of P2X7R protein may be caused by low transcription rates of the P2X7R gene and, thus, insufficient amounts of P2X7R mRNA give only rise to a low P2X7R protein amount. Another reason may be that the P2X7R protein is unstable and, thus, is not present in amounts comparable to the wild-type protein level.

The under- or over-expression of P2X7R protein may be determined by methods well-known to the person skilled in the art. These include, but are not limited, to methods for determining the amount of mRNA or the amount and/or activity of the protein. Examples are Northern Blot analysis or immuno based techniques, such as Western Blotting.

"Non-functional" means that the P2X7R protein has lost at least one functional property displayed by the wild-type P2X7R protein as described herein above. Preferably, "non-functional" means that the P2X7R protein does no longer function as a channel. Non-functionality may, e.g., be caused by the fact that one allele occurring in an individual codes for a P2X7R protein which leads to non-functional dimers (dominant negative mutation). Whether a P2X7R protein in an individual is functional or non-functional can be determined by the methods described herein above and in the examples.

The term "altered ATP-gating" means that the respective P2X7R protein reacts in a different way to ATP than the wild-type P2X7R protein. This can be determined as described in the appended examples or as described hereinabove.

In the context of diagnosis, not only the activity of the P2X7R could be of diagnostic value but also the amount of expression. For example, if a polymorphism affects RNA stability or translation efficiency, this could lead to lower expression of the P2X7 protein not only in the hippocampus but also in the blood. Therefore, one could speculate that a lower amount of P2X7 detected by western blot in blood cells could be related to depression.

[0076] Another aspect of the present invention is a method for diagnosing an affective disorder or a susceptibility to an affective disorder comprising the step of determining in a sample obtained from an individual whether the P2X7R gene sequence or encoded protein thereof comprises a mutation in comparison to the wild-type P2X7R sequence.

[0077] A preferred embodiment of the present invention is a method, wherein a mutation is a mutation in a P2X7R sequence as defined hereinabove and/or a nucleotide replacement or deletion selected from the following Table C indicating in column "Region of P2X7R" the region of the P2X7R genomic nucleotide sequence in which the replacement or deletion occurs, in column "Nucleotide" of Table C the nucleotide which is replaced by another nucleotide or the nucleotides which are deleted and in column "Position in wild-type" of Table C the corresponding position in the nucleotide sequence of the wild-type ATP-gated ion channel P2X7R as depicted in SEQ ID NO: 1

Table C

| Region of P2X7R | Nucleotide | Position in wild-type |
|-----------------|------------|-----------------------|
| 5'UTR | T | 362 |
| 5'UTR | T | 532 |
| 5'UTR | A | 1100 |
| 5'UTR | A | 1122 |
| 5'UTR | C | 1171 |
| 5'UTR | T | 1351 |
| 5'UTR | G | 1702 |
| 5'UTR | T | 1731 |
| 5'UTR | C | 1860 |
| 5'UTR | C | 2162 |
| 5'UTR | C | 2238 |
| 5'UTR | A | 2373 |
| 5'UTR | G | 2569 |
| 5'UTR | G | 2702 |
| intron 1 | G | 3166 |
| intron 1 | C | 24778 |
| intron 1 | C | 24830 |
| exon 2 | T | 24942 |
| exon 3 | C | 26188 |
| exon 3 | A | 26308 |

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Table C (continued)

| | Region of P2X7R | Nucleotide | Position in wild-type |
|----|-----------------|------------------|-----------------------|
| 5 | exon 3 | G | 26422 |
| | intron 4 | G | 32394 |
| | intron 4 | T | 32434 |
| | exon 5 | G | 32493 |
| 10 | exon 5 | G | 32506 |
| | exon 5 | C | 32507 |
| | exon 5 | C | 32548 |
| 15 | intron 5 | A | 32783 |
| | intron 5 | T | 35309 |
| | intron 5 | C | 35374 |
| | intron 5 | A | 35378 |
| 20 | exon 6 | G | 35438 |
| | exon 6 | T | 35454 |
| | intron 6 | T | 35549 |
| 25 | intron 6 | G | 35641 |
| | intron 6 | A | 35725 |
| | intron 6 | T | 36001 |
| | intron 6 | A | 36064 |
| 30 | intron 6 | deletion of GTTT | 36091 to 36094 |
| | intron 6 | C | 36108 |
| | intron 7 | C | 36374 |
| 35 | intron 7 | G | 36378 |
| | intron 7 | T | 36387 |
| | intron 7 | G | 36398 |
| | intron 7 | C | 37439 |
| 40 | intron 7 | T | 37513 |
| | exon 8 | C | 37604 |
| | exon 8 | G | 37605 |
| 45 | exon 8 | G | 37623 |
| | exon 8 | C | 37633 |
| | intron 9 | C | 47214 |
| | exon 11 | G | 47383 |
| 50 | exon 11 | C | 47411 |
| | intron 11 | T | 47563 |
| | intron 12 | C | 54307 |
| 55 | intron 12 | G | 54308 |
| | exon 13 | C | 54399 |

Table C (continued)

| Region of P2X7R | Nucleotide | Position in wild-type |
|-----------------|-----------------------------------|-----------------------|
| exon 13 | A | 54480 |
| exon 13 | C | 54523 |
| exon 13 | deletion of CCCTGAGAGCCACAGGTGCCT | 54562 to 54582 |
| exon 13 | A | 54588 |
| exon 13 | C | 54664 |
| exon 13 | G | 54703 |
| exon 13 | A | 54804 |
| exon 13 | G | 54834 |
| exon 13 | G | 54847 |
| 3'UTR | G | 54925 |
| 3'UTR | C | 55169 |
| 3'UTR | A | 55170 |
| 3'UTR | A | 55171 |
| 3'UTR | C | 55917 |

[0078] As indicated hereinabove, if the respective nucleotide which is replaced by another nucleotide is a purine base, it is preferred to be replaced by another purine base. If it is a pyrimidine base, it is preferred to be replaced by another pyrimidine base. It is also preferred that a purine base is replaced by a pyrimidine base and that a pyrimidine base is replaced by a purine base. Most preferably, the nucleotides indicated in Table C are replaced by the nucleotides indicated at the respective position in Table 12 hereinbelow (see Example 3).

[0079] In a preferred embodiment the present invention relates to diagnostic composition designed for use in a method in which the occurrence of the mutation in the ATP-gated ion channel P2X7R gene is determined by PCR, immunological methods and/or electrophysiological methods as described herein below and in the appended Examples. Additionally, it is possible to determine the occurrence of a mutation in the ATP-gated ion channel P2X7R as described hereinabove.

[0080] In yet another aspect the present invention relates to the use of a nucleic acid molecule, a vector, a polypeptide, an antibody, aptamer and/or a primer or pair of primers of the present invention for the preparation of a diagnostic composition for the detection of an affective disorder.

[0081] It is also envisaged that the present invention relates to methods of diagnosing an affective disorder of an individual comprising:

- (a) isolating DNA from cells obtained from an individual;
- (b) determining all or part of the nucleotide composition of the P2X7R gene; and
- (c) analyzing said nucleotide composition of P2X7R for the presence of one or more polymorphism, mutation or allelic variation.

[0082] The term "gene" means a nucleotide sequence associated with the production of a protein, including promoter sequences, enhancer sequences, intron sequences, exon sequences, coding regions, 5' untranslated region (5'UTR), 3' untranslated region (3'UTR), and splice variants.

[0083] In a preferred embodiment of the described method the individual is a mammal and more preferably human. Moreover, the cells are preferably derived from skin, blood, urine or cerebral spinal fluid.

[0084] The method of the present invention allows for the diagnosis of an affective disorder according to the composition of a genetic marker corresponding to the P2X7R gene. As is demonstrated by the appended examples, polymorphisms in the P2X7R are genetically linked to patients suffering from an affective disorder.

[0085] In accordance with this embodiment of the present invention, the diagnosis of an affective disorder can, e.g., be effected by isolating cells from an individual, and isolating the genomic DNA of said cells. Such cells can be collected from body fluids, skin, hair, biopsies and other sources. Collection and analysis of cells from bodily fluids such as blood,

urine and cerebrospinal fluid is well known to the art; see for example, Rodak, "Haematology: Clinical Principles & Applications" second ed., WB Saunders Co, 2002; Brunzel, "Fundamentals of Urine and Body Fluids Analysis", WB Saunders Co, 1994; Herndon and Brumback (Ed.), "Cerebrospinal Fluid", Kluwer Academic Pub., 1989. In addition, methods for DNA isolation are well described in the art; see, for example, Sambrook et al., "Molecular Cloning: A Laboratory Manual", 3rd edition, Cold Spring Harbor Laboratory, 2001.

[0086] Once DNA has been isolated, various oligonucleotide primers spanning the P2X7R locus may be designed in order to amplify the genetic material by Polymerase Chain Reaction (PCR). Conventional methods for designing, synthesizing, producing said oligonucleotide primers and performing PCR amplification may be found in standard textbooks, see, for example Agrawal (Ed.), "Protocols for Oligonucleotides and Analogs: Synthesis and Properties (Methods in Molecular Biology, 20)", Humana Press, 1993; Innis et al. (Ed.), "PCR Applications: Protocols for Functional Genomics", Academic Press, 1999; Chen and Janes (Ed.), "PCR Cloning Protocols: From Molecular Cloning to Genetic", 2nd edition, Humana Press, 2002. Primers for the detection of P2X7R polymorphisms are also given in, but not limited to, SEQ ID NO: 52 to SEQ ID NO: 111. Once DNA has been amplified, nucleotide structure can be analysed by sequencing methods and compared to normal P2X7R DNA.

[0087] Sequencing may be performed manually by any molecular biologist of ordinary skills or by an automated sequencing apparatus. These procedures are common in the art, see, for example, Adams et al. (Ed.), "Automated DNA Sequencing and Analysis", Academic Press, 1994; Alphey, "DNA Sequencing: From Experimental Methods to Bioinformatics", Springer Verlag Publishing, 1997.

[0088] Detection and analysis of polymorphisms in P2X7R can also be performed using amplification refractory mutation system (ARMSTM), amplification refractory mutation system linear extension (ALEXTM), single-strand conformation polymorphism (SSCP), heteroduplex analysis, PCR-SSCP, fluorescent SSCP in an automated DNA sequencer, denaturing gradient gel electrophoresis, RNase protection assays, detection of mutations by sequence specific oligonucleotide hybridization, chemical cleavage methods, enzyme mismatch cleavage methods, cleavage fragment length methods, allele-specific oligonucleotide hybridization on DNA chips, and other such methods known in the art, see, for example Nollau et al, Clin. Chem. 43 (1997), 1114-1128; Burczak and Mardis (Ed.), "Polymorphism Detection & Analysis Techniques", Eaton Pub Co, 2000; Cotton et al. (Ed.), "Mutation Detection: A Practical Approach", Irl Press, 1998; Taylor (Ed.), "Laboratory Methods for the Detection of Mutations and Polymorphisms in DNA", CRC Press, 1997.

[0089] The present invention also relates to a method of diagnosing an affective disorder in an individual comprising:

- (a) isolating RNA from cells obtained from an individual;
- (b) converting the RNA into cDNA;
- (c) determining all or part of the nucleotide composition of the cDNA so obtained; and
- (c) analyzing said nucleotide composition for the presence of one or more polymorphism(s) or allelic variation.

[0090] With respect to the preferred embodiments the same applies as already described above.

[0091] Detection and analysis of polymorphisms in the P2X7R RNA can be performed according to the methods described above.

[0092] The present invention also relates to a method for diagnosing an affective disorder in an individual comprising:

- (a) isolating RNA or proteins from cells obtained from an individual;
- (b) determining the levels of P2X7R RNA or protein; and
- (c) comparing the levels of P2X7R RNA or protein with the corresponding levels from a normal individual not afflicted with an affective disorder.

[0093] With respect to the preferred embodiments the same applies as already described above.

[0094] As is demonstrated by the appended examples, a relationship exists between the expression, or protein level of P2X7R and an affective disorder. This and other embodiments of the present invention will readily occur to those of ordinary skill in the art in view of the disclosure herein.

[0095] According to another aspect on the invention, there is provided a polynucleotide comprising at least 20 bases of the human P2X7R gene and comprising a mutation or polymorphism selected from any of the following:

Table 1:

| Novel polymorphisms in the human P2X7R | | |
|--|--|--------------------------------------|
| Region in P2X7 | Polymorphism | Protein Modification |
| 5'UTR | 362 T-C | |
| 5'UTR | 532 T-G | |
| 5'UTR | 1100 A-G | |
| 5'UTR | 1122 A-G | |
| 5'UTR | 1171 C-G | |
| 5'UTR | 1702 G-A | |
| Intron01 | 3166 G-C | |
| Intron01 | 24778 C-T | |
| Intron01 | 24830 6C-T | |
| Exon03 | 26188 C-T | Arg117Trp |
| Intron03 | 26308 A-G | |
| Intron03 | 26422 G-A | |
| Intron04 | 32394 G-A | |
| Intron04 | 32434 T-C | |
| Exon05 | 32493 G-A | Gly150Arg |
| Exon05 | 32548 C-T | Silent Cys168 |
| Intron05 | 32783 A-C | |
| Exon06 | 35438 G-A | Glu186Lys |
| Exon06 | 35454 T-C | Leu191Pro |
| Intron06 | 35641 G-C | |
| Intron06 | 35725 A-C | |
| Intron06 | 36001 T-G | |
| Intron07 | 36378 G-A | |
| Intron07 | 36387 T-A | |
| Intron07 | 36398 G-C | |
| Exon08 | 37604 C-T | Arg270Cys |
| Exon08 | 37633 C-T | Silent Asp279 |
| Intron09 | 47214 C-T | |
| Intron11 | 47563 T-C | |
| Intron12 | 54307 C-T | |
| Intron12 | 54308 G-A | |
| Exon 13 | 54562-54582 deletion of CCCTGAGA GCCACAGGTGCCT | deletion of 7aa 488 to 494 (PESHRCL) |
| Exon 13 | 54804 A-T | Ile568Asn |
| Exon 13 | 54834 G-A | Arg578Gln |
| 3'UTR | 55169 C-A | |

Table 1: (continued)

| Novel polymorphisms in the human P2X7R | | |
|--|--------------|-------------------------|
| Region in P2X7 | Polymorphism | Protein Modification |
| 3'UTR | 55170 A-C | |
| 3'UTR | 55171 A-C | |
| 3'UTR | 55917 C-T | |
| 3'UTR | 54925 G-A | |

[0096] The polymorphism describes the position and the variation observed. The position and numbering of the polymorphism corresponds to the human P2X7R gene as defined in SEQ ID No 1. Primers used for SNP amplification and sequencing are shown in Table 1 a and listed in SEQ ID NO: 52 to SEQ ID NO: 111.

Table 1a. Primer sequences for SNP amplification and sequencing

| Primer Name | Orientation | Sequence | Begin | End |
|------------------|-------------|---------------------------|-------|-------|
| P2RX7_01.for | Sense | cgtaggacttggcgcttct | 2785 | 2803 |
| P2RX7_01.rev | Anti sense | gagcacgtctcagattcgaaa | 3224 | 3244 |
| P2RX7_02.for | Sense | ccatgaggcaggatgactattc | 24665 | 24687 |
| P2RX7_02.rev | Antisense | ctcctggatctcaccagtt | 25168 | 25187 |
| P2RX7_03.for | Sense | ctcgtccagctttgatattaagc | 25966 | 25988 |
| P2RX7_03.rev | Antisense | ggcccttagtgctagaaccaga | 26426 | 26447 |
| P2RX7_04.for | Sense | attcatccgctcagtgccc | 30794 | 30811 |
| P2RX7_04.rev | Antisense | gccatgtgaattttctaccgat | 31277 | 31298 |
| P2RX7_05.for | Sense | ttcgttgctggttaggatggg | 32314 | 32333 |
| P2RX7_05.rev | Antisense | caaggatgctcagggtagtagc | 32805 | 32826 |
| P2RX7_06.for | Sense | cactaggttgctgtatccatttct | 35277 | 35301 |
| P2RX7_06.rev | Antisense | gcaactgtgtgagagcttgg | 35731 | 35750 |
| P2RX7_07.for | Sense | tcaaccctgggtccagtggtg | 35950 | 35968 |
| P2RX7_07.rev | Antisense | caacaagtagctctcactcataagg | 36424 | 36448 |
| P2RX7_08.for | Sense | caataacacttgtgcgagttaggt | 37380 | 37403 |
| P2RX7_08.rev | Antisense | catctgtgtgccttggaacc | 37750 | 37770 |
| P2RX7_09.for | Sense | gtgagtggtaatcctgctactgc | 45321 | 45343 |
| P2RX7_09.rev | Antisense | aggccactcctgtactcg | 45743 | 45761 |
| P2RX7_10_11.for | Sense | ccaagtcacagcatgaggc | 47119 | 47137 |
| P2RX7_10_11.rev | Antisense | accagcgacgtatccac | 47632 | 47649 |
| P2RX7_12.for | Sense | aagcatgggggttcatttc | 50252 | 50268 |
| P2RX7_12.rev | Antisense | gcataaaagggaactcctgctagta | 50691 | 50714 |
| P2RX7_13a.for | Sense | gcttacagaacacatgcatgg | 54232 | 54252 |
| P2RX7_13a.rev | Antisense | gcacctgtaggcacagtgc | 54739 | 54757 |
| P2RX7_13b.for | Sense | atcaccacctcagagctgttc | 54620 | 54640 |
| P2RX7_13b.rev | Antisense | gttaacatggctactgcagcc | 55203 | 55223 |
| P2RX7_13d.for | Sense | gcttagaaaggaggcgactcc | 54484 | 54504 |
| P2XR7_Pro13.for | Sense | ttgtgacatttgcaaggctgcc | 2617 | 2638 |
| P2XR7_Pro7.rev | Antisense | tctgaagctctgctcctgag | 1955 | 1974 |
| P2XR7_Pro8.rev | Antisense | ctcaccttctggcttccagt | 1611 | 1630 |
| P2XR7_Pro9.for | Sense | cttaccactcccaggactaa | 1496 | 1515 |
| P2XR7_Pro10.for | Sense | gtctgcctgttctactgcat | 1149 | 1168 |
| P2XR7_Pro1.for | Sense | cagagaccttcagaaacttcg | 1841 | 1861 |
| P2XR7_Pro2.rev | Antisense | agatcaccagggaacacagtg | 2261 | 2280 |
| P2XR7_Pro3.for | Sense | ctcaactccactttcctcgg | 2133 | 2152 |
| P2XR7_Pro4.rev | Antisense | cctttcacttttttggtctcatg | 2655 | 2677 |
| P2XR7_Pro5.for | Sense | gggagaattctgaaaatgcc | 2691 | 2711 |
| P2XR7_Pro6.rev | Antisense | ggaccagagctctactcttc | 2951 | 2970 |
| P2XR7_Pro11.for | Sense | aggtcatagatcgacctgcc | 2296 | 2315 |
| P2XR7_Pro12.rev | Antisense | aagaagcgccaagtcctacg | 2785 | 2804 |
| P2XR7_Pro14.for | Sense | gcaatccagactgaagttgac | 2051 | 2071 |
| P2XR7_Pro15.rev | Antisense | actctgggtctgcagttggtg | 2428 | 2447 |
| P2XR7_Pro21.for | Sense | cctttaaatacagagaccttcaga | 1831 | 1854 |
| P2XR7_Pro22.for | Sense | gcccacctctgaacaccat | 2708 | 2727 |
| P2XR7_3UTR10.for | Sense | cccttggaactcttgctatcg | 55804 | 55824 |
| P2XR7_3UTR1.for | Sense | ggcagtacagtggttcaaga | 54858 | 54878 |
| P2XR7_3UTR2.rev | Antisense | gtgggacagtttctgtgcct | 55150 | 55170 |

| | | | | |
|-----------------|-----------|----------------------------|-------|-------|
| P2XR7_3UTR3.for | Sense | gagtccttaccatagcagg | 55183 | 55202 |
| P2XR7_3UTR4.rev | Antisense | gtcaaagaatttgtggccacc | 55643 | 55663 |
| P2XR7_3UTR5.for | Sense | catgaactgtcttttaatgtgtaaag | 55515 | 55540 |
| P2XR7_3UTR6.rev | Antisense | gagatacgggtttcaccatgttg | 55955 | 55976 |
| P2XR7_3UTR7.for | Sense | aattagctgggcatggtgcg | 55992 | 56011 |
| P2XR7_3UTR8.rev | Antisense | ttgagatggagctctcgtcttg | 56122 | 56140 |
| P2XR7_3UTR9.rev | Antisense | cactgtccacgtgactgctt | 56208 | 56227 |
| P2XR7_11.For | Sense | tcctacttcggtctgtaagagatt | 47281 | 47305 |
| P2XR7_11.Rev | Antisense | gggcctaattttcgtgcat | 47591 | 47609 |
| P2XR7_13G.For | Sense | aagaacctagaacctgagggcctt | 54333 | 54355 |
| P2XR7_13G.Rev | Antisense | ttgagatgggaggcagctt | 54541 | 54559 |
| P2XR7_13H.For | Sense | ttcggctcccaggacat | 54773 | 54789 |
| P2XR7_13H.Rev | Antisense | cacagagctttgcaggtgaa | 55248 | 55267 |

[0097] Another aspect of the present invention is in the form of a diagnostic kit for affective disorders comprising a specific oligonucleotide probe, or primer corresponding to P2XR7 polymorphisms. The diagnostic kit may comprise appropriate packaging and instructions for the use in the method of the invention. Said kit may further comprise appropriate buffer, and enzymes such as reverse transcriptase, and thermostable polymerases.

[0098] In a preferred embodiment of the invention, diagnosis can be performed on a mouse, rat or human. The invention is generally applied in vitro, e.g. using cells or other material obtained from an individual. However, it can also be applied on a living individual, or post mortem.

[0099] In accordance with the embodiments of the present invention, diagnosis of an affective disorder may be followed by prescription, or administration of an antidepressant drug. Administration and dosage of antidepressive drugs can vary between patients and are well known in the medical art, see, for example Benkert and Hippus, "Kompendium der Psychiatrischen Pharmakotherapie", Springer Verlag Publishing, 2000; Albers, "Handbook of Psychiatric Drugs: 2001-2002 Edition", Current Clinical Strategies Publishing, 2000. Preferred examples include between 5 mg and 80 mg per day, preferably 20 mg, fluoxetine; between 5 mg and 50 mg per day, preferably 20 mg, paroxetine; between 5 mg and 200 mg per day, preferably 50 mg, sertraline; between 5 mg and 300 mg per day, preferably 100 mg, fluvoxamine; between 5 mg and 100 mg per day, preferably 30 mg, mirtazapine; between 4 mg and 50 mg, preferably 8 mg, reboxetine; between 5 mg and 600 mg per day, preferably 200 mg, nefazodone; between 450 mg and 1800 mg per day, preferably 900 mg, lithium carbonate.

[0100] The P2XR7 protein is also useful for monitoring the efficacy and/or dosing of a drug or the likelihood of a patient to respond to a drug. Thus, in yet another embodiment the invention relates to a method for, monitoring the efficacy and/or dosing of a drug, e.g. an antidepressive drug, and/or the likelihood of a patient to respond to said drug which comprises determining the level of expression and/or activity of the P2XR7 protein in a patient before and after administration of the respective drug. As presented in the examples below, treatment with an antidepressive drug results in an upregulation in P2XR7 activity. In humans, P2XR7 activity can be monitored by Positron Emission Tomography (PET) or Single Photon Emission Computerised Tomography (SPECT) using a radiolabelled ligand tracer for P2XR7. Examples of P2XR7 ligands can be, but are not limited to, ATP, an antagonist binding P2XR7, an agonist binding P2XR7, or a small polynucleotide comprising at least 20 bases of the human P2XR7 gene. A modulation of P2XR7 activity, membrane distribution or expression levels would reflect the activity and potency of the antidepressive drug. Methods and techniques required for PET analysis are well known in the art, see, for example Paans and Vaalburg, Curr. Pharmac. Design 6 (2000), 1583-1591; van Waarde, Curr. Pharmac. Design. 6 (2000), 1593-1610; Paans et al, Methods 27 (2002), 195-207; Passchier et al., Methods 27 (2002), 278-286; Laruelle et al., Methods 27 (2002), 287-299.

[0101] In accordance with the present invention by the term "sample" is intended any biological sample obtained from an individual, cell line, tissue culture, or other source containing polynucleotides or polypeptides or portions thereof. As indicated, biological samples include body fluids (such as blood, sera, plasma, urine, synovial fluid and spinal fluid) and tissue sources found to express the polynucleotides of the present invention. Methods for obtaining tissue biopsies and body fluids from mammals are well known in the art. A biological sample which includes genomic DNA, mRNA or proteins is preferred as a source.

[0102] As described herein above, mutations of the P2XR7 encoding gene can occur on DNA level or on mRNA level and may result in an altered expression of P2XR7 or in the expression of P2XR7 ATP-gated ion channels which show either an altered function or no function when compared to the wild-type P2XR7 ATP-gated ion channel as described herein. Thus, various methods on DNA level, RNA level or protein level exist for determining whether the

ATP-gated ion channel P2X7R gene shows a mutation as described herein above. Consequently, mRNA, cDNA, DNA and genomic DNA are the preferred nucleic acid molecules to be used in the below mentioned methods. Also polypeptides or fragments thereof are preferred if a mutation in the P2X7R ATP-gated ion channel protein as described herein is to be determined.

[0103] Preferably, a point mutation leading to the replacement of an amino acid residue at the positions as indicated in Table 1 of the corresponding wild-type P2X7R amino acid sequence depicted in SEQ ID NO: 3 or 4 by another amino acid can be determined by PCR. Said PCR is followed by a restriction fragment length polymorphism (RFLP) analysis if due to the point mutation a recognition site for a restriction endonuclease is generated which is not present in the wild-type nucleotide sequence or a recognition site for a restriction enzyme is created which does not occur in the wild-type P2X7R. More preferably said mutation can be determined by PCR using primers and conditions that allow only an amplification of the wild-type nucleotide sequence encoding the corresponding wild-type amino acid at the respective position, but not of the nucleotide sequence of a nucleic acid molecule encoding a different amino acid residue at the corresponding position. It is even more preferred that PCR is performed to determine a mutation using primers and conditions that allow no amplification if the wild-type nucleotide sequence is present, but only if another amino acid residue is encoded at the respective position. Particularly preferred is a method using PCR and primers under conditions that allow amplification of a fragment comprising at least the nucleotide residues encoding the amino acid residue corresponding to positions of SEQ ID NO: 1.

Said PCR is followed by e.g., sequencing and/or single strand conformation analysis (SSCA). Said fragment is preferably of at least 25 nucleotides in length, more preferred of at least 50 nucleotides in length, even more preferred of at least 75 nucleotides in length, particularly preferred of at least 100 nucleotides in length, more particularly preferred of at least 200 nucleotides in length, also more particularly preferred at least 250 nucleotides in length, even more particularly preferred at least 300 nucleotides in length and most particularly preferred at least 600 nucleotides in length. Said primers are preferably of at least 12 nucleotides in length, more preferred of at least 15 nucleotides in length, even more preferred of at least 18 nucleotides in length and most preferred of at least 21 nucleotides in length as depicted in SEQ ID NOs: 52 to 111. The temperature for annealing said primers is preferably at least 50°C, more preferred at least 55°C and most preferred at least 58°C. The temperature for denaturation is preferably at least 95°C for preferably at least 10 sec, more preferably at least 20 sec, even more preferred at least 30 sec and most preferred at least 60 sec. However, depending on the length and the G-C content of the nucleic acid sequence to be amplified the temperature for denaturation may be shorter or longer. The temperature for extension of the annealed primers is preferably at least 10 sec, more preferably at least 20 sec, even more preferred at least 30 sec and most preferred at least 60 sec. A PCR reaction comprising the aforementioned conditions is exemplified in the Examples herein below. The subsequent sequencing and/or SSCA is carried out as known in the art. Preferably, the PCR fragments are separated on a 10% polyacrylamide gel at 4°C or also preferred at room temperature. PCR fragments showing a SSCA band shift are amplified with the primers under conditions as mentioned above and are subsequently sequenced. Alternatively, it is also possible to directly sequence genomic DNA in order to determine whether a mutation in the CLCN2 gene has occurred. A direct genomic sequencing approach is, for example, demonstrated for baker's yeast in Horecka, Yeast 16 (2000), 967-970.

Preferably, a deletion is determined by using hybridization techniques as known in the art. In particular, a primer is designed as mentioned herein above that is capable to only hybridize to wild-type genomic DNA as depicted in SEQ ID NO: 1 but not to a nucleotide sequence comprising a deletion of a fragment between nucleotides 54562 and 54582 of SEQ ID NO: 1. Also preferred is the method of fluorescent in situ hybridization (FISH) for determining on whole chromosomes, in particular on chromosome 12q23-q24 that said chromosome has the above mentioned deletion. Even more preferred is that a deletion of nucleotide residues as described herein may be determined by using PCR, wherein one primer of a pair of primers is located within the region of genomic DNA comprising said deletion. Preferably, said deletion is between nucleotide positions 54562 and 54582 as depicted in SEQ ID NO: 1. Thus, under the appropriate conditions no PCR fragment will result if the genomic DNA comprises said deletion. It is particularly preferred that PCR using primers which are located upstream or downstream of the deletion is performed to determine said deletion. Under appropriate conditions as mentioned herein above, both a fragment of genomic DNA of the wild-type nucleotide sequence as set forth in SEQ ID NO: 1 and a fragment of the nucleotide sequence comprising a deletion of preferably the nucleotides between positions 54562 and 54582 as depicted in SEQ ID NO: 1 will be amplified.

[0104] It is also possible to determine the above-described P2X7R mutations on the protein level. Some of the mutations described above lead to shortened versions of the P2X7R protein. Thus, it is conceivable to determine the occurrence of these mutations by determining the length or molecular weight of the P2X7R protein expressed in an individual, e.g. by SDS PAGE.

It is also possible to determine the mutations of the P2X7R ATP-gated channel as described herein by using the antibodies of the present invention. Said antibodies specific for said mutations of P2X7R proteins will be determined by assay techniques such as radioimmunoassays, competitive-binding assays, Western blot analysis and ELISA assay. Also preferred are classical immunohistological methods.

[0105] The finding, described in the present invention, that certain mutations in the P2X7R encoding gene and/or the corresponding protein are connected with affective disorders is indicative that the non- or dysfunction of the P2X7R protein is responsible for various forms of affective disorders. Thus, the finding of these mutations not only allows the diagnosis of affective disorders by determining whether the above-described mutations occur in an individual. It also allows to develop a treatment of affective disorders which has been diagnosed to be the result of a mutation in the P2X7R encoding gene. Such a treatment can, e.g., comprise the introduction of a nucleic acid molecule encoding a non-functional or functional wild-type P2X7R protein thereby restoring in said individual the P2X7R activity or the activation or repression of (a) P2X7R gene(s) in vivo. The term "activation or repression" in this context means that the expression of the gene is either enhanced (activation) or reduced (repression). An enhancement of expression can, e.g., be achieved by increasing the efficiency of transcription initiation, for example, by using suitable compounds which have an activating effect on transcription. Alternatively, an enhancement can be achieved by replacing the naturally occurring promoter by a more efficient promoter.

A repression may be achieved by suppressing expression of the gene, e.g., by specifically suppressing transcription from the respective promoter by suitable compounds or by rendering the promoter less efficient or non-functional.

[0106] In another embodiment the present invention also relates to a pharmaceutical composition. In accordance with the present invention the term "pharmaceutical composition" relates to a composition comprising a nucleic acid molecule comprising a nucleotide sequence which encodes an ATP-gated ion channel P2X7R and which is selected from the group consisting of:

- (a) a nucleotide sequence encoding a polypeptide comprising the amino acid sequence as depicted in SEQ ID NO: 3 or 4;
- (b) a nucleotide sequence comprising the nucleotide sequence as depicted in SEQ ID NO: 1 or SEQ ID NO: 2;
- (c) a nucleotide sequence which hybridizes to the nucleotide sequence of (a) or (b); and
- (d) a nucleotide sequence which is degenerated as a result of the genetic code to the nucleotide sequence of (c).

[0107] Such pharmaceutical compositions comprise a therapeutically effective amount of a nucleic acid molecule encoding a functional P2X7R protein and, optionally, a pharmaceutically acceptable carrier. The pharmaceutical composition may be administered with a physiologically acceptable carrier to a patient, as described herein. In a specific embodiment, the term "pharmaceutically acceptable" means approved by a regulatory agency or other generally recognized pharmacopoeia for use in animals, and more particularly in humans. The term "carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the therapeutic is administered.

[0108] Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a preferred carrier when the pharmaceutical composition is administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions can also be employed as liquid carriers, particularly for injectable solutions. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium ion, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. These compositions can take the form of solutions, suspensions, emulsion, tablets, pills, capsules, powders, sustained-release formulations and the like. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, etc. Examples of suitable pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E.W. Martin. Such compositions will contain a therapeutically effective amount of the aforementioned compounds, preferably in purified form, together with a suitable amount of carrier so as to provide the form for proper administration to the patient. The formulation should suit the mode of administration.

In another preferred embodiment, the composition is formulated in accordance with routine procedures as a pharmaceutical composition adapted for intravenous administration to human beings. Typically, compositions for intravenous administration are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also include a solubilizing agent and a local anesthetic such as lignocaine to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilised powder or water free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

The pharmaceutical composition of the invention can be formulated as neutral or salt forms. Pharmaceutically acceptable salts include those formed with anions such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric

acids, etc., and those formed with cations such as those derived from sodium, potassium, ammonium, calcium, ferric hydroxides, isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc.

In vitro assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of the practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from in vitro or animal model test systems. Preferably, the pharmaceutical composition is administered directly or in combination with an adjuvant.

The pharmaceutical composition is preferably designed for the application in gene therapy. The technique of gene therapy has already been described above in connection with the nucleic acid molecules of the invention and all what has been said there also applies in connection with the pharmaceutical composition. For example, the nucleic acid molecule in the pharmaceutical composition is preferably in a form which allows its introduction, expression and/or stable integration into cells of an individual to be treated.

[0109] For gene therapy, various viral vectors which can be utilized, for example, adenovirus, herpes virus, vaccinia, or, preferably, an RNA virus such as a retrovirus. Examples of retroviral vectors in which a single foreign gene can be inserted include, but are not limited to: Moloney murine leukemia virus (MoMuLV), Harvey murine sarcoma virus (Ha-MuSV), murine mammary tumor virus (MuMTV), and Rous Sarcoma Virus (RSV). A number of additional retroviral vectors can also incorporate multiple genes. All of these vectors can transfer or incorporate a gene for a selectable marker so that transduced cells can be identified and generated. By inserting a P2X7R sequence of interest encoding a functional P2X7R protein into the viral vector, along with another gene which encodes, for example, the ligand for a receptor on a specific target cell, for example, the vector is now target specific.

Retroviral vectors can be made target specific by inserting, for example, a polynucleotide encoding a sugar, a glycolipid, or a protein. Those of skill in the art will know of, or can readily ascertain without undue experimentation, specific polynucleotide sequences which can be inserted into the retroviral genome to allow target specific delivery of the retroviral vector containing the inserted polynucleotide sequence.

Since recombinant retroviruses are preferably defective, they require assistance in order to produce infectious vector particles. This assistance can be provided, for example, by using helper cell lines that contain plasmids encoding all of the structural genes of the retrovirus under the control of regulatory sequences within the LTR. These plasmids are missing a nucleotide sequence which enables the packaging mechanism to recognize an RNA transcript for encapsidation. Helper cell lines which have deletions of the packaging signal include, but are not limited to w2, PA317 and PA12, for example. These cell lines produce empty virions, since no genome is packaged. If a retroviral vector is introduced into such cells in which the packaging signal is intact, but the structural genes are replaced by other genes of interest, the vector can be packaged and vector virion produced. Alternatively, NIH 3T3 or other tissue culture cells can be directly transfected with plasmids encoding the retroviral structural genes gag, pol and env, by conventional calcium phosphate transfection. These cells are then transfected with the vector plasmid containing the genes of interest. The resulting cells release the retroviral vector into the culture medium. Another targeted delivery system for P2X7R polynucleotides is a colloidal dispersion system. Colloidal dispersion systems include macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. The preferred colloidal system of this invention is a liposome. Liposomes are artificial membrane vesicles which are useful as delivery vehicles in vitro and in vivo. It has been shown that large unilamellar vesicles (LUV), which range in size from 0.2-4.0 μ m can encapsulate a substantial percentage of an aqueous buffer containing large macromolecules. RNA, DNA and intact virions can be encapsulated within the aqueous interior and be delivered to cells in a biologically active form (Fraley, et al., Trends Biochem. Sci., 6:77, 1981). In addition to mammalian cells, liposomes have been used for delivery of polynucleotides in plant, yeast and bacterial cells. In order for a liposome to be an efficient gene transfer vehicle, the following characteristics should be present: (1) encapsulation of the genes of interest at high efficiency while not compromising their biological activity; (2) preferential and substantial binding to a target cell in comparison to non-target cells; (3) delivery of the aqueous contents of the vesicle to the target cell cytoplasm at high efficiency; and (4) accurate and effective expression of genetic information (Mannino, et al., Biotechniques, 6:682, 1988). The composition of the liposome is usually a combination of phospholipids, particularly high-phase-transition-temperature phospholipids, usually in combination with steroids, especially cholesterol. Other phospholipids or other lipids may also be used. The physical characteristics of liposomes depend on pH, ionic strength, and the presence of divalent cations. Examples of lipids useful in liposome production include phosphatidyl compounds, such as phosphatidylglycerol, phosphatidylcholine, phosphatidylserine, phosphatidylethanolamine, sphingolipids, cerbrosides, and gangliosides. Particularly useful are diacylphosphatidylglycerols, where the lipid moiety contains from 14-18 carbon atoms, particularly from 16-18 carbon atoms, and is saturated. Illustrative phospholipids include egg phosphatidylcholine, dipalmitoylphosphatidylcholine and distearoylphosphatidylcholine. The targeting of liposomes can be classified based on anatomical and mechanistic factors. Anatomical classification is based on the level of selectivity, for example, organ-specific, cell-specific, and organelle-specific. Mechanistic targeting can be distinguished based upon whether it is passive or active. Passive targeting utilizes the natural tendency of liposomes to distribute to

cells of the reticulo-endothelial system (RES) in organs which contain sinusoidal capillaries.

[0110] In another aspect the present invention relates to a method of treating an affective disorder comprising administering a therapeutically effective amount of the pharmaceutical composition comprising a nucleotide sequence encoding a functional ATP-gated ion channel as described herein above to a subject suffering from said disorder.

[0111] In the context of the present invention the term "subject" means an individual in need of a treatment of an affective disorder. Preferably, the subject is a vertebrate, even more preferred a mammal, particularly preferred a human.

The term "administered" means administration of a therapeutically effective dose of the aforementioned nucleic acid molecule encoding a functional P2X7R protein to an individual. By "therapeutically effective amount" is meant a dose that produces the effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques. As is known in the art and described above, adjustments for systemic versus localized delivery, age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

The methods are applicable to both human therapy and veterinary applications. The compounds described herein having the desired therapeutic activity may be administered in a physiologically acceptable carrier to a patient, as described herein. Depending upon the manner of introduction, the compounds may be formulated in a variety of ways as discussed below. The concentration of therapeutically active compound in the formulation may vary from about 0.1-100 wt %. The agents maybe administered alone or in combination with other treatments.

The administration of the pharmaceutical composition can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intra-arterial, intranodal, intramedullary, intrathecal, intratracheal, intranasally, intrabronchial, transdermally, intranodally, intrarectally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly. In some instances, for example, in the treatment of wounds and inflammation, the candidate agents may be directly applied as a solution dry spray.

The attending physician and clinical factors will determine the dosage regimen. As is well known in the medical arts, dosages for any one patient depends upon many factors, including the patient's size, body surface area, age, the particular compound to be administered, sex, time and route of administration, general health, and other drugs being administered concurrently. A typical dose can be, for example, in the range of 0.001 to 1000 µg; however, doses below or above this exemplary range are envisioned, especially considering the aforementioned factors.

[0112] The dosages are preferably given once a week, however, during progression of the treatment the dosages can be given in much longer time intervals and in need can be given in much shorter time intervals, e.g., daily. In a preferred case the immune response is monitored using herein described methods and further methods known to those skilled in the art and dosages are optimized, e.g., in time, amount and/or composition. Dosages will vary but a preferred dosage for intravenous administration of DNA is from approximately 10^6 to 10^{12} copies of the DNA molecule. If the regimen is a continuous infusion, it should also be in the range of 1 µg to 10 mg units per kilogram of body weight per minute, respectively. Progress can be monitored by periodic assessment. The pharmaceutical composition of the invention may be administered locally or systemically. Administration will preferably be parenterally, e.g., intravenously. Preparations for parenteral administration include sterile aqueous or non-aqueous solutions, suspensions, and emulsions. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Aqueous carriers include water, alcoholic/aqueous solutions, emulsions or suspensions, including saline and buffered media. Parenteral vehicles include sodium ion solution, Ringer's dextrose, dextrose and sodium ion, lactated Ringer's, or fixed oils. Intravenous vehicles include fluid and nutrient replenishers, electrolyte replenishers (such as those based on Ringer's dextrose), and the like. Preservatives and other additives may also be present such as, for example, antimicrobials, anti-oxidants, chelating agents, and inert gases and the like.

It is also envisaged that the pharmaceutical compositions are employed in co-therapy approaches, i.e. in co-administration with other medicaments or drugs, for example other drugs for preventing, treating or ameliorating affective disorders.

[0113] Another aspect of the present invention is a pharmaceutical composition comprising a compound, the administration of which to cells leads to a reduction or increase of the expression of a nucleic acid encoding an ATP-gated ion channel P2X7R in the cells or comprising a nucleic acid molecule the expression of which in cells or the administration of which to cells leads to a reduction or increase of the expression of a nucleic acid encoding an ATP-gated ion channel P2X7R in the cells. Said pharmaceutical composition may be useful for treating individuals having an increased or reduced amount of the P2X7R protein or expression level as described hereinabove. Preferably, said pharmaceutical composition leads to an increase of the expression of a nucleic acid encoding an ATP-gated ion channel P2X7R in the cells.

[0114] It is envisaged that the above-mentioned pharmaceutical composition, the administration of which to cells leads to a reduction of the expression of a nucleic acid encoding an ATP-gated ion channel P2X7R is an antisense

nucleic acid, a ribozyme, a co-suppressive nucleic acid, iRNA or siRNA.

An siRNA approach is, for example, disclosed in Elbashir ((2001), Nature 411, 494-498)). It is also envisaged in accordance with this invention that for example short hairpin RNAs (shRNAs) are employed in accordance with this invention as pharmaceutical composition. The shRNA approach for gene silencing is well known in the art and may

comprise the use of st (small temporal) RNAs; see, inter alia, Paddison (2002) Genes Dev. 16, 948-958. As mentioned above, approaches for gene silencing are known in the art and comprise "RNA"-approaches like RNAi or siRNA. Successful use of such approaches has been shown in Paddison (2002) loc. cit., Elbashir (2002) Methods 26, 199-213; Novina (2002) Mat. Med. June 3, 2002; Donze (2002) Nucl. Acids Res. 30, e46; Paul (2002) Nat. Biotech 20, 505-508; Lee (2002) Nat. Biotech. 20, 500-505; Miyagishi (2002) Nat. Biotech. 20, 497-500; Yu (2002) PNAS 99, 6047-6052 or Brummelkamp (2002), Science 296, 550-553. These approaches may be vector-based, e.g. the pSUPER vector, or RNA polIII vectors may be employed as illustrated, inter alia, in Yu (2002) loc. cit.; Miyagishi (2002) loc. cit. or Brummelkamp (2002) loc. cit.

A compound which leads to a reduction of the expression of the P2X7R gene may, e.g., be a compound which acts on the regulatory region of the gene and thereby reduces the level of transcription. Such compounds can be identified by methods as described herein below.

[0115] The invention also relates to the use of a nucleic acid molecule encoding a functional P2X7R protein as described herein above in connection with the pharmaceutical composition for the preparation of a pharmaceutical composition for treating an affective disorder.

[0116] Furthermore, the present invention relates to a method of treating an affective disorder comprising administering a therapeutically effective amount of the nucleic acid molecule according to the invention or a therapeutically effective amount of the corresponding encoded polypeptide to a subject suffering from said disorder.

[0117] In another preferred embodiment the present invention relates to a pharmaceutical composition comprising, inter alia, the polynucleotides according to the present invention, i.e. polynucleotides having mutations and/or deletions as described hereinabove. Such pharmaceutical compositions may, e.g., be useful for treating individuals having an increased or decreased amount of the P2X7R protein or having a P2X7R protein showing an increased or decreased activity which can be determined as described hereinabove. Preferably, such a pharmaceutical composition may be useful for treating individuals having a decreased amount of the P2X7R protein or having a P2X7R protein showing a decreased activity which can be determined as described hereinabove. It is envisaged that, e.g. a non-functional or preferably a hyperfunctional P2X7R protein comprised by said pharmaceutical composition is incorporated in a P2X7R complex which naturally exists in cells as described hereinabove. It is also envisaged that the above-described techniques for gene therapy can be used for treating an individual with the nucleic acid molecules of the present invention, mutatis mutandis.

[0118] With respect to the possible modes of administration and preferred embodiments the same applies as has been set forth above.

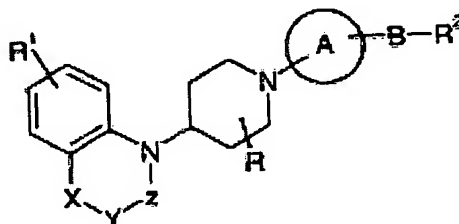
[0119] Additionally, the present invention also envisages the use of the nucleic acid molecules, the vectors, the polypeptides, the antibody and/or the aptamer according to the invention for the preparation of a pharmaceutical composition for the treatment of an affective disorder.

[0120] A further aspect of the present invention is the use of a modulator of P2X7R activity or expression for the preparation of a pharmaceutical composition for treating an affective disorder. In the context of the present invention the term "modulator" means (a) compound(s), a complex of compounds, (a) substance(s) or complex of substances which can modify, i.e. modulate the activity of P2X7R or the expression of P2X7R either directly or indirectly. The modulation can, for example, occur at the protein level. Particularly, the P2X7R protein may interfere with the modulator such that it is either more active or less active. The modulation can also occur on nucleic acid level. Namely, the gene is transcribed more frequently or less frequently giving rise to more or less protein. Modulation can also influence RNA or protein stability. Since it was surprisingly found that agonists of P2X7R improve the symptoms of mice selected for anxiety and depressive behaviour, the modulator of P2X7R activity used for the preparation of a pharmaceutical composition for treating an affective disorder is preferably an agonist. The term "agonist" means an agent or a compound that can interact with a receptor and initiate a physiological or a pharmacological response characteristic of that receptor. Examples of P2X7R agonist include but are not restricted to ATP, ATP-4, BzATP (2'-3'-O-(4-Benzoylbenzoyl)adenosine 5'-triphosphate (C₂₄H₂₄N₅O₁₅P₃)) and tenidap (5-chloro-2,3-dihydro-2-oxo-3-(2-thienylcarbonyl)-indole-1-carboxamide, i.e. C₁₅H₁₁ClN₂O₂S) or a derivative thereof. Particularly preferred, said agonist used to treat depression or anxiety is BzATP as demonstrated in Example 9 hereinbelow.

Although it was reported that activation of P2X7R could induce apoptosis and cell death in vitro (Di Virgilio et al., Cell Death Differ. 5 (1988), 191-199; Virginio et al., J. Physiol. 519 (1999), 335-346), the present application demonstrates in Example 9 hereinbelow that treatment of the brain of mice selected for anxiety and depressive behaviour with BzATP revealed no significant difference in the numbers of apoptotic cells between control mice and mice treated with BzATP. This result indicates that activation of P2X7R did not result in cerebral cell death in vivo which, thus, renders BzATP to be a candidate drug for treatment of affective disorders.

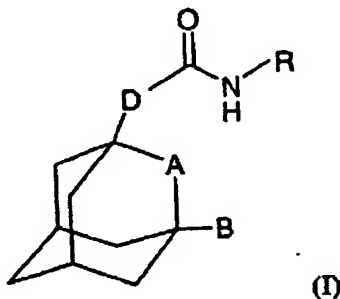
[0121] It is furthermore envisaged that said modulator is selected from the group consisting of piperidine and piperazine derivatives, adamantane derivatives, substituted phenyl compounds, oxidized ATP, 2-O-(4-benzoylbenzoyl)adenosine-5-triphosphate and 3-O-(4-benzoylbenzoyl)adenosine-5-triphosphate as, for example, described in WO 99/29660, WO 99/29661; WO 99/296896; WO 00/61569; WO 01/42194; WO 01/44170; WO 01/44213; WO 00/71529; WO 01/46200. The following compounds illustrate compounds which are also preferred to be used as modulators of P2X7R activity.

A compound of general formula:



where A is phenyl or a 5- or 6-membered heterocyclic ring containing one or two heteroatoms selected from O, N or S; and optionally substituted by C₁₋₆alkyl, halogen, nitro, amino, alkylamino, CF₃, SO₂Me, NHSO₂Me or cyano; B is S; and optionally substituted by C₁₋₆alkyl, halogen, nitro, amino, alkylamino, CF₃, SO₂Me, NHSO₂Me or cyano; C=O, NH or SO₂; X is C=O, CH(Me), O or (CH₂)_p where p is 0 or 1; Y is O, CH₂, NH or S; Z is C=O or SO₂, provided that when Z is C=O, then Y is O, CH₂ or S; R is hydrogen or C₁₋₆alkyl; R¹ is hydrogen, halogen; R² is phenyl optionally substituted by CO₂H, CO₂alkyl, CONH₂ or R² is OH, NHR³, NHCH(R⁴)(CHR⁵)_nR⁶, NH-R⁷-R⁸, SO₂NHalkyl, NHCOalkyl, NHSO₂alkyl, morpholine, NR⁹R¹⁰, piperazine substituted by phenyl, alkoxyphenyl, pyridyl or fluorophenyl; n is 0, 1 or 2; R³ is hydrogen, a bi- or tricyclic saturated ring system optionally containing a nitrogen atom, piperidinyl, alkylpyrrolidine, ethynylcyclohexyl, a 5-membered aromatic ring containing 2 or 3 heteroatoms, C₄₋₆ cycloalkyl optionally substituted by alkyl, cyano or hydroxy, or C₁₋₈ alkyl optionally containing an oxygen atom in the alkyl chain and being optionally substituted by one or more substituents selected from ethynyl, cyano, fluoro, dialkylamino, hydroxy, thioalkyl, CO₂R¹¹ or CONH₂; R⁴ is hydrogen or alkyl optionally substituted by hydroxy or alkoxy; R⁵ is hydrogen or hydroxy; R⁶ is CO₂R¹¹, NHCO₂R¹², CONH₂ or a 5 or 6-membered saturated ring containing an oxygen atom, a 5-membered heterocyclic ring containing one or two heteroatoms selected from O, N or S, or phenyl optionally substituted by one or more groups selected from alkyl, hydroxy, amino, alkoxy, or nitro; R⁷ is a cyclopentane ring; R⁸ is phenyl; R⁹ and R¹⁰ are independently hydrogen, benzyl, alkenyl, cycloalkyl, alkyl optionally substituted by hydroxy, alkoxy, cyano, dialkylamino, phenyl, pyridyl or CO₂R¹¹ or R⁹ and R¹⁰ together form a 5- to 7-membered saturated or partially saturated ring optionally containing a further heteroatom and optionally substituted by one or more groups selected from alkyl (optionally containing an oxygen atom in the chain and optionally substituted by hydroxy), COalkyl, CO₂R¹¹, COR¹³R¹⁴, CHO or piperidine, R¹¹ is hydrogen or alkyl; R¹² is alkyl; and R¹³ and R¹⁴ are independently hydrogen or alkyl, is or a pharmaceutically acceptable salt or solvate thereof.

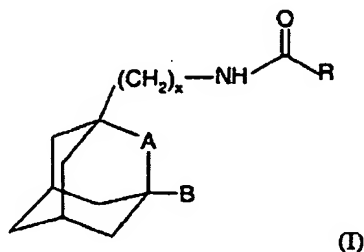
[0122] A compound of general formula:



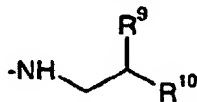
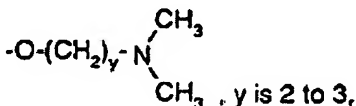
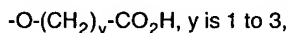
wherein A represents a group CH₂ or an oxygen atom; B represents a hydrogen or halogen atom; D represents a group CH₂, OCH₂, NHCH₂ or CH₂CH₂; R represents a phenyl, benzothiazolyl, indolyl, indazolyl, purinyl, pyridyl, pyrimidinyl or thiophenyl group, each of which may be optionally substituted by one or more substituents independently selected from a halogen atom or a cyano, carboxyl, hydroxyl, nitro, halo-C₁-C₆-alkyl, -N(R¹)-C(=O)-R², -C(O)-NR³R⁴, -NR⁵R⁶, C₃-C₈-cycloalkyl, 3- to 8-membered heterocyclyl, C₃-C₈-cycloalkyloxy, C₁-C₆-alkylcarbonyl, phenoxy, benzyl, C₁-C₆-

alkylthio, phenylthio, C₁-C₆-alkoxycarbonyl, C₁-C₆-alkylsulphinyl or C₁-C₆-alkylsulphonyl group, or a C₁-C₆-alkyl or C₁-C₆-alkoxy group optionally substituted by one or more substituents independently selected from a halogen atom or an amino, carboxyl, hydroxyl, C₁-C₆-alkoxy, (di)C₁-C₆-alkylamino, C₁-C₆-alkoxycarbonyl, imidazolyl, morpholinyl, piperidinyl or pyrrolidinyl group; R¹ represents a hydrogen atom or a C₁-C₆-alkyl or C₃-C₈-cycloalkyl group; R² represents a C₁-C₆-alkyl or C₃-C₈-cycloalkyl group; and R³, R⁴, R⁵ and R⁶ each independently represent a hydrogen atom or a C₁-C₆-alkyl or C₃-C₈-cycloalkyl group; with the provisos that when A is CH₂, B is H and D is CH₂, then R does not represent a phenyl, ortho-carboxyphenyl, methylphenyl or para-phenoxyphenyl group, and that when A is CH₂, D is CH₂ or CH₂CH₂ and R represents a substituted phenyl group, the substituent or substituents present do not comprise, in an ortho position, a C₁-C₆-alkoxy group substituted by an amino, (di)C₁-C₆-alkylamino, imidazolyl, morpholinyl, piperidinyl or pyrrolidinyl group; or a pharmaceutically acceptable salt or solvate thereof.

[0123] A compound of general formula:

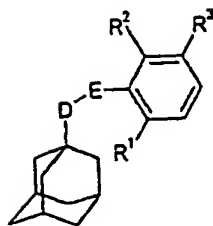


wherein x represents 1 or 2; A represents a group CH₂ or an oxygen atom; B represents a hydrogen or halogen atom; R represents a phenyl, pyridyl, indolyl, indazolyl, pyrimidinyl or thiophenyl group, each of which may be optionally substituted by one or more substituents independently selected from a halogen atom or an amino, cyano, carboxyl, hydroxyl, nitro, C₁-C₆-alkyl, halo-C₁-C₆-alkyl, -N(R¹)-C(=O)-R², -C(O)NR³R⁴, -NR⁵R⁶, C₃-C₈-cycloalkyl, 3- to 8-membered heterocyclyl, C₃-C₈-cycloalkyloxy, C₁-C₆-alkylcarbonyl, C₁-C₆-alkoxycarbonyl, C₁-C₆-alkylsulphinyl or C₁-C₆-alkylsulphonyl group, or a C₁-C₆-alkoxy, C₁-C₆-alkylamino, phenoxy, benzyl, C₁-C₆-alkylthio or phenylthio group optionally substituted by one or more substituents independently selected from a 15 halogen atom or an amino, cyano, carboxyl, hydroxyl, nitro, 1-pyrrolidinyl, 1-piperidinyl, C₁-C₆-alkyl, C₁-C₆-alkoxy, (di)C₁-C₆-alkylamino, halo-C₁-C₆-alkyl, C₁-C₆-alkoxycarbonyl or one of the following groups:



R¹ represents a hydrogen atom or a C₁-C₆-alkyl or C₃-C₈-cycloalkyl group; R² represents a C₁-C₆-alkyl or C₃-C₈-cycloalkyl group; R³ and R⁴ each independently represent a hydrogen atom or a C₁-C₆-alkyl or C₃-C₈-cycloalkyl group; R⁵ represents a hydrogen atom or a C₁-C₆-alkyl or C₃-C₈-cycloalkyl group; R⁶ represents a C₃-C₈-cycloalkyl group and, additionally, a C₁-C₆-alkyl group when R⁵ is not a hydrogen atom; R⁷ represents a hydrogen atom or a C₁-C₆-alkyl or C₃-C₈-cycloalkyl group; R⁸ represents a C₁-C₆-alkyl or C₃-C₈-cycloalkyl group; R⁹ represents a hydrogen atom or a hydroxyl group; and R¹⁰ represents a hydrogen atom or a phenyl or imidazolyl group; with the provisos that R does not represent an unsubstituted pyridyl group when A represents a group CH₂ and B represents a hydrogen atom, and that when R represents a substituted phenyl, indolyl or indazolyl group, the substituent or substituents present do not comprise an amido, carboxyl, (di)C₁-C₆-alkylamido or C₁-C₆-alkoxycarbonyl group in an ortho position; or a pharmaceutically acceptable salt or solvate thereof.

[0124] A compound of general formula:

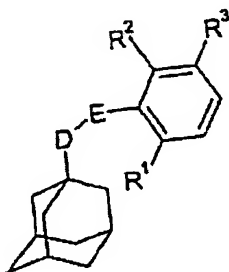


wherein D represents CH_2 or CH_2CH_2 ; E represents $\text{C}(\text{O})\text{NH}$ or $\text{NHC}(\text{O})$; R^1 and R^2 each independently represent a hydrogen or halogen atom, or an amino, nitro, $\text{C}_1\text{-C}_6$ -alkyl or trifluoromethyl group; R^3 represents a group of formula:

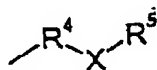


X represents an oxygen or sulphur atom or a group NH , SO or SO_2 ; Y represents an oxygen or sulphur atom or a group NR^{11} , SO or SO_2 ; Z represents a group $-\text{OH}$, $-\text{SH}$, $-\text{CO}_2\text{H}$, $\text{C}_1\text{-C}_6$ -alkoxy, $\text{C}_1\text{-C}_6$ -alkylthio, $\text{C}_1\text{-C}_6$ -alkylsulphinyl, $\text{C}_1\text{-C}_6$ -alkylsulphonyl, $-\text{NR}^6\text{R}^7$, $-\text{C}(\text{O})\text{NR}^8\text{R}^9$, imidazolyl, 1-methylimidazolyl, $-\text{N}(\text{R}^{10})\text{C}(\text{O})\text{-C}_1\text{-C}_6$ -alkyl, $\text{C}_1\text{-C}_6$ -alkylcarbonyloxy, $\text{C}_1\text{-C}_6$ -alkoxycarbonyloxy, $-\text{OC}(\text{O})\text{NR}^{12}\text{R}^{13}$, $-\text{OCH}_2\text{OC}(\text{O})\text{R}^{14}$, $\text{OCHOC}(\text{O})\text{OR}^{15}$ or $-\text{OC}(\text{O})\text{OCH}_2\text{OR}^{16}$, R^4 represents a $\text{C}_2\text{-C}_6$ -alkyl group; R^5 represents a $\text{C}_1\text{-C}_6$ -alkyl group; R^6 , R^7 , R^8 , R^9 , R^{10} , R^{12} , and R^{13} each independently represent a hydrogen atom, or a $\text{C}_1\text{-C}_6$ -alkyl group optionally substituted by at least one hydroxyl group; R^{11} represents a hydrogen atom, or a $\text{C}_1\text{-C}_6$ -alkyl group optionally substituted by at least one substituent independently selected from hydroxyl and $\text{C}_1\text{-C}_6$ -alkoxy; and R^{14} , R^{15} and R^{16} each independently represent a $\text{C}_1\text{-C}_6$ -alkyl group; with the provisos that (i) when E represents $\text{NEC}(\text{O})$, X represents O, S or NH and Y represents O, then Z represents $-\text{NR}^6\text{R}^7$ where R^6 represents a hydrogen atom and R^7 represents either a hydrogen atom or a $\text{C}_1\text{-C}_6$ -alkyl group substituted by at least one hydroxyl group, and (ii) when E represents $\text{NHC}(\text{O})$, X represents O, S or NH, Y represents NH, and R^5 represents CH_2CH_2 , then Z is not $-\text{OH}$ or imidazolyl; or a pharmaceutically acceptable salt or solvate thereof.

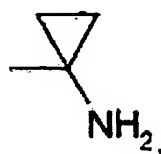
[0125] A compound of general formula:



wherein D represents CH_2 or CH_2CH_2 ; E represents $\text{C}(\text{O})\text{NH}$ or $\text{NHC}(\text{O})$; R^1 and R^2 each independently represent hydrogen, halogen, amino, nitro, $\text{C}_1\text{-C}_6$ -alkyl or trifluoromethyl, but R^1 and R^2 may not both simultaneously represent hydrogen; R^3 represents a group of formula

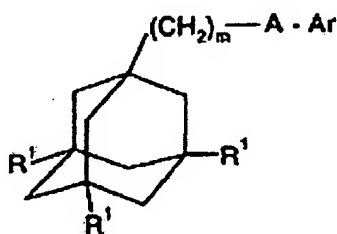


R^4 represents a $\text{C}_1\text{-C}_6$ -alkyl group; X represents an oxygen or sulphur atom or a group NR^{13} , SO or SO_2 ; R^5 represents hydrogen, or R^5 represents $\text{C}_1\text{-C}_6$ -alkyl or $\text{C}_2\text{-C}_6$ -alkenyl, each of which may be optionally substituted by at least one substituent selected from halogen, hydroxyl, (di) $\text{C}_1\text{-C}_6$ -alkylamino, $-\text{Y-R}^6$,

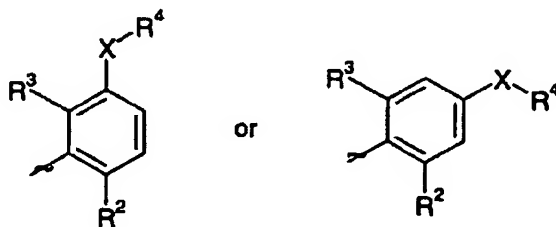


and a 5- or 6-membered heteroaromatic ring comprising from 1 to 4 heteroatoms independently selected from nitrogen, oxygen and sulphur which heteroaromatic ring may itself be optionally substituted by at least one substituent selected from halogen, hydroxyl and C₁-C₆-alkyl; Y represents an oxygen or sulphur atom or a group NH, SO or SO₂; R⁶ represents a group -R⁷Z where R⁷ represents a C₂-C₆-alkyl group and Z represents an -OH, -CO₂H, -NR⁸R⁹, -C(O)NR¹⁰R¹¹ or -N(R¹²)C(O)-C₁-C₆-alkyl group, and, in the case where Y represents an oxygen or sulphur atom or a group NH, R⁶ additionally represents hydrogen, C₁-C₆-alkyl, C₁-C₆-alkylcarbonyl, C₁-C₆-alkoxycarbonyl, -C(O)NR¹⁴R¹⁵, -CH₂OC(O)R¹⁶, -CH₂OC(O)OR¹⁷ or -C(O)OCH₂OR¹⁸; R⁸, R⁹, R¹⁰, R¹¹ and R¹² each independently represent a hydrogen atom or a C₁-C₆-alkyl group; R¹³ represents hydrogen, C₃-C₈-cycloalkyl, C₃-C₈-cycloalkylmethyl, or R¹³ represents a C₁-C₆-alkyl group optionally substituted by at least one substituent selected from hydroxyl to and C₁-C₆-alkoxy; and R¹⁴, R¹⁵, R¹⁶, R¹⁷, and R¹⁸ each independently represent a C₁-C₆-alkyl group; with the proviso that when E is C(O)NH, X is O, NH or N(C₁-C₆-alkyl), then R⁵ is other than a hydrogen atom or an unsubstituted C₁-C₆-alkyl group; or a pharmaceutically acceptable salt or solvate thereof.

[0126] A compound of general formula:



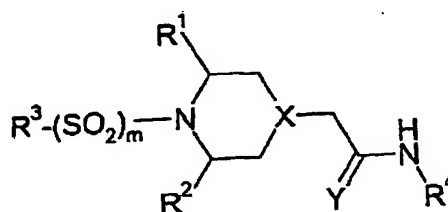
wherein m represents 1, 2 or 3; each R¹ independently represents a hydrogen or halogen atom; A represents C(O)NH or NHC(O); Ar represents a group



X represents a bond, an oxygen atom or a group CO, (CH₂)₁₋₆, CH=, (CH₂)₁₋₆O, O(CH₂)₁₋₆, O(CH₂)₂₋₆O, O(CH₂)₂₋₃O (CH₂)₁₋₃, CR¹(OH), (CH₂)₁₋₃O(CH₂)₁₋₃, (CH₂)₁₋₃O(CH₂)₂₋₃O, NR⁵, (CH₂)₁₋₆NR⁵, NR⁵(CH₂)₁₋₆, (CH₂)₁₋₃NR⁵(CH₂)₁₋₃O (CH₂)₂₋₆NR⁵, O(CH₂)₂₋₃NR⁵(CH₂)₁₋₃, (CH₂)₁₋₃NR⁵(CH₂)₂₋₃O, NR⁵(CH₂)₂₋₆O, NR⁵(CH₂)₂₋₃O(CH₂)₁₋₃, CONR⁵, NR⁵CO, S(O)_n, S(O)_nCH₂, CH₂S(O)_n, SO₂NR⁵ or NR⁵SO₂; n is 0, 1 or 2; R¹ represents a hydrogen atom or a C₁-C₆-alkyl group; one of R² and R³ represents a halogen, cyano, nitro, amino, hydroxyl, or a group selected from (i) C₁-C₆-alkyl optionally substituted by at least one C₃-C₆-cycloalkyl, (ii) C₃-C₈-cycloalkyl, (iii) C₁-C₆-alkyloxy optionally substituted by at least one C₃-C₆-cycloalkyl, and (iv) C₃-C₈-cycloalkyloxy, each of these groups being optionally substituted by one or more fluorine atoms, and the other of R² and R³ represents a hydrogen or halogen atom; either R⁴ represents a 3- to 9-membered saturated or unsaturated aliphatic heterocyclic ring system containing one or two nitrogen atoms and optionally an oxygen atom, the heterocyclic ring system being optionally substituted by one or more substituents independently selected from fluorine atoms, hydroxyl, carboxyl, cyano, C₁-C₆-alkyl, C₁-C₆-hydroxyalkyl, -NR⁶R⁷, -(CH₂)_rNR⁶R⁷ and CONR⁶R⁷, r is 1, 2, 3, 4, 5 or 6; R⁵ represents a hydrogen atom or a C₁-C₆-alkyl or C₃-C₈-cycloalkyl

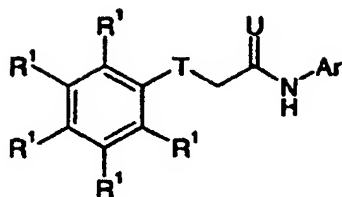
group; R⁶ and R⁷ each independently represent a hydrogen atom or a C₁-C₆-alkyl, C₂-C₆-hydroxyalkyl or C₃-C₈-cycloalkyl group, or R⁶ and R⁷ together with the nitrogen atom to which they are attached form a 3- to 8-membered saturated heterocyclic ring; with the provisos that, (a) when A represents C(O)NH and R⁴ represents an unsubstituted saturated heterocyclic ring system containing one nitrogen atom, then X is other than a bond, and (b) when A represents C(O)NH and X represents a group (CH₂)₁₋₆ or O(CH₂)₁₋₆, then R⁴ does not represent a bond, and (c) when A represents NHC(O) and R⁴ represents an unsubstituted 3- to 8-membered saturated aliphatic heterocyclic ring system containing one nitrogen atom, then X is other than a bond, and (d) when A represents NHC(O) and X represents O(CH₂)₁₋₆, NH(CH₂)₁₋₆ or SCH₂, then R⁴ does not represent an unsubstituted 1-piperidinyl or unsubstituted 1-pyrrolidinyl group, and (e) when A represents NHC(O) and X represents O(CH₂)₂₋₃NH(CH₂)₂, then R⁴ does not represent an imidazolyl group; or a pharmaceutically acceptable salt or solvate thereof.

[0127] A compound of general formula:

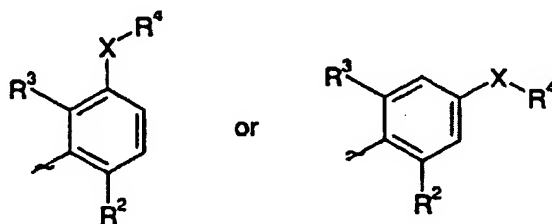


X represents a nitrogen atom or a group C(R⁵); Y represents an oxygen or sulphur atom or a group NR⁶; either R¹ and R² each independently represent a hydrogen atom or a C₁-C₄-alkyl group but do not both simultaneously represent a hydrogen atom, or R¹ and R² together represent a group -CH₂ZCH₂-; Z represents a bond, an oxygen or sulphur atom or a group CH₂ or NR⁷; m is 0 or 1; R³ represents a 5- to 10-membered unsaturated ring system which may comprise from 1 to 4 ring heteroatoms independently selected from nitrogen, oxygen and sulphur, the ring system being optionally substituted by one or more substituents independently selected from halogen, nitro, cyano, NR⁸R⁹, C₁-C₄-alkyl-C(O)NH-, NHR¹²C(O)-, C₁-C₄-alkyl-SO₂-, C₁-C₄-alkyl-SO₂NH-, C₁-C₄-alkyl-NHSO₂-, C₁-C₄-alkoxy, and C₁-C₄-alkyl optionally substituted by one or more fluorine atoms; R⁴ represents a phenyl or pyridinyl group, each of which is substituted in an ortho position with a substituent selected from halogen, C₁-C₄-alkoxy, C₁-C₄-alkylthio, and C₁-C₄-alkyl optionally substituted by one or more fluorine atoms, the phenyl or pyridinyl group being optionally further substituted by one or more substituents independently selected from halogen, cyano, hydroxyl, C₁-C₄-alkylthio, C₁-C₄-alkyl-NH-, NHR¹³-C₁-C₄-alkyl-, C₁-C₄-alkyl-SO₂-, C₁-C₄-alkyl-SO₂NH-, C₁-C₄-alkyl-NHSO₂-, C₁-C₄-alkyl-C(O)NH-, C₁-C₄-alkyl-NHC(O)-, -D-G, C₁-C₄-alkoxy optionally substituted by -NR¹⁴R¹⁵ or by R¹⁶, and C₁-C₄-alkyl optionally substituted by one or more fluorine atoms or by one or more hydroxyl groups, or R⁴ represents a 9- or 10-membered unsaturated bicyclic ring system which may comprise from 1 to 4 ring heteroatoms independently selected from nitrogen, oxygen and sulphur, the bicyclic ring system being optionally substituted by one or more substituents independently selected from halogen, oxo, C₁-C₄-alkyl, C₁-C₄-alkoxy, C₁-C₄-alkylthio and -NR¹⁰R¹¹; D represents an oxygen atom or a group (CH₂)_{sub.n} or CH₂NH; n is 1, 2 or 3; G represents a piperazinyl, morpholinyl or 2,5-diazabicyclo[2.2.1]heptyl group, or G represents a piperidinyl group optionally substituted by amino; R⁵ represents a hydrogen atom, or a hydroxyl or C₁-C₄-alkoxy group; R⁶ represents a hydrogen atom, or a cyano, nitro, hydroxyl, C₁-C₄-alkyl or C₁-C₄-alkoxy group; R⁷, R⁸ and R⁹ each independently represent a hydrogen atom or a C₁-C₄-alkyl group; R¹⁰ and R¹¹ each independently represent a hydrogen atom or a C₁-C₄-alkyl group, or R¹⁰ and R¹¹ together with the nitrogen atom to which they are attached form a 5- or 6-membered saturated heterocyclic ring comprising one or two ring nitrogen atoms; R¹² represents a hydrogen atom, or a C₁-C₄-alkyl group optionally substituted by amino; R¹³ represents a hydrogen atom, or a C₁-C₄-alkyl group optionally substituted by hydroxyl; R¹⁴ and R¹⁵ each independently represent a hydrogen atom or a C₁-C₄-alkyl group optionally substituted by hydroxyl, or R¹⁴ and R¹⁵ together with the nitrogen atom to which they are attached form a 5- or 6-membered saturated heterocyclic ring comprising one or two ring nitrogen atoms; and R¹⁶ represents a 1-(C₁-C₄-alkyl)-piperidinyl group; with the proviso that when m is 0, X is N and Y is O, then R⁴ does not represent 2-benzothiazolyl; or a pharmaceutically acceptable salt or solvate thereof.

[0128] A compound of general formula:

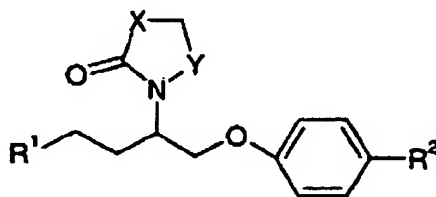


wherein: each R¹ independently represents a hydrogen or halogen atom, or a trifluoromethyl, cyano, nitro, C₁-C₆-alkyl or C₁-C₆-alkoxy group; T represents an oxygen atom or a group NH; U represents an oxygen or sulphur atom or a group NH; Ar represents a group:



X represents a bond, an oxygen atom or a group CO, CH₂, CH₂O, O(CH₂)_m, CH₂OCH₂, NR⁵, CH₂NR⁵, NR⁵CH₂, CH₂NR⁵CH₂, CONR⁵, S(O)_n or SO₂NR⁵, m is 1, 2 or 3; 15 n is 0, 1 or 2; one of R² and R³ represents a halogen, cyano, nitro, amino, hydroxyl, or a group selected from C₁-C₆-alkyl optionally substituted by at least one C₃-C₈-cycloalkyl, C₃-C₈-cycloalkyl, C₁-C₆-alkyloxy optionally substituted by at least one C₃-C₈-cycloalkyl, C₃-C₈-cycloalkyloxy, S(O)_pC₁-C₆-alkyl or S(O)_qC₃-C₈-cycloalkyl, each of these groups being optionally substituted by one or more fluorine atoms, and the other of R² and R³ represents a hydrogen or halogen atom or a methyl group; p is 0, 1 or 2; q is 0, 1 or 2; R⁴ represents di(C₁-₂alkyl)N(CH₂)_t, where t is 0, 1 or 2 or imidazolyl, or R⁴ represents a 3- to 9-membered saturated heterocyclic ring system containing one or two nitrogen atoms, the heterocyclic ring system being optionally substituted by one or more substituents independently selected from fluorine atoms, hydroxyl, C₁-C₆-alkyl, acetyl, hydroxyC₁-C₆-alkyl, -NR⁶R⁷, -(CH₂)_rNR⁶R⁷, -CONR⁶R⁷ and pyrimidinyl, or R⁴ represents a 3- to 8-membered saturated carbocyclic ring system substituted by one or more substituents independently selected from -NR⁶R⁷, -(CH₂)_rNR⁶R⁷, -CONR⁶R⁷ the ring system being optionally further substituted by one or more substituents independently selected from fluorine atoms, hydroxyl and C₁-C₆-alkyl; r is 1, 2, 3, 4, 5 or 6; R⁵ represents a hydrogen atom or a C₁-C₆-alkyl or C₃-C₈-cycloalkyl group; and R⁶ and R⁷ each independently represent a hydrogen atom or a C₁-C₆-alkyl or C₃-C₈-cycloalkyl group, or R⁶ and R⁷ together with the nitrogen atom to which they are attached form a 3- to 8-membered saturated heterocyclic ring, provided that when R³ represents a cyano group, then X is other than a bond; or a pharmaceutically acceptable salt or solvate thereof.

[0129] A compound of general formula:



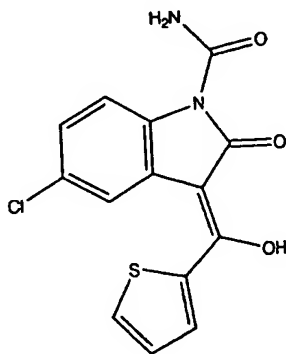
wherein X represents an oxygen or sulphur atom or a group NH, CH₂, CH₂CH₂ or OCH₂; Y represents a group CH₂ or C=O; R¹ represents a pyridyl or pyrimidinyl group; R² represents a phenyl, pyridyl or pyrimidinyl group, each of which may be optionally substituted by one or more substituents independently selected from a halogen atom or an amino, cyano, hydroxyl, nitro, C₁-C₆-alkyl, halo-C₁-C₆-alkyl, C₁-C₆-alkoxy, C₁-C₆-alkylthio, (di)C₁-C₆-alkylamino, C₁-C₆-alkylcarbonyl, C₁-C₆-alkoxycarbonyl, C₁-C₆-alkylsulphonyl, C₁-C₆-alkylsulphonyl, -NR³SO₂R⁴ or -SO₂NR⁵R⁶ group, or a group -Z-(CH₂)_p-Z-(CH₂)_q-H wherein each Z independently represents a nitrogen or oxygen atom, p is an integer from 2 to 5 and q is 0 or an integer from 1 to 5; R³ and R⁴ each independently represent a hydrogen atom or

a C₁-C₆-alkyl group; and R⁵ and R⁶ each independently represent a hydrogen atom or a C₁-C₆-alkyl group, or together with the nitrogen atom to which they are attached form a pyrrolidinyl or piperidinyl group; or a pharmaceutically acceptable salt or solvate thereof.

[0130] An additional embodiment of the invention provides a method for treating affective disorders by administering an agent modulating the activity of P2X7R, such as an antagonist of the P2X7R. The term "antagonist" means an agent or drug or a compound that opposes the physiological effects of another. Examples of P2X7R antagonists include, but are not restricted to, adamantane derivatives, isoquinolines and their derivatives, substituted phenyl compounds, piperidine derivatives, piperazine derivatives. P2X7R antagonists are described in the art and include the compounds found in Chen et al., Bioconjugate Chem. 13 (2002), 1100-1111; WO 99/29660; WO 99/29661; WO 99/296896; WO 00/61569; WO 01/42194; WO 01/44170; WO 01/44213; WO 00/71529; WO 01/46200. P2X7R activity can also be modulated by RNA-based interference mechanisms and methods such as, but not limited to, small interference RNA (siRNA) molecules, and long double-stranded RNA (dsRNA).

[0131] Since it was unexpectedly found that agonists of P2X7R improve the symptoms of mice selected for anxiety and depressive behaviour, the present invention relates in a further embodiment to a method for treating affective disorders such as anxiety and depressive behaviour by administering an agent modulating the activity of P2X7R such as an agonist of the P2X7R. What is even more striking is the finding of the present application shown in Example 10 that antagonists of P2X7R have no antidepressive effects although this is being taught by the prior art, for example, WO 03/042190, WO 03/042191, WO 03/049353 or US 2004/0029841. WO 03/042190, WO 03/042191, WO 03/059353 or US 2004/0029841 describe compositions of P2X7R antagonists and methods of treating P2X7 mediated diseases by administering these compounds. However, while the prior art may make a link between P2X7R and, e.g., treating depression, it is generally implied that antagonists of P2X7R have to be used in the treatment of, e.g., depression. Thus, the finding of the present invention that antagonists have no antidepressive effects, but rather agonists of P2X7R have an antidepressive effect could not have been expected and is, thus, even more surprising. The present application, therefore, provides, inter alia, the basis for the development of effective medicaments having therapeutic benefits against, e.g., depression. In particular, said medicaments comprising an agonist of P2X7R are effective in treating affective disorders, in particular for treating those disorders mentioned herein, and in particular for treating depression. Examples of P2X7R agonists include but are not restricted to ATP, ATP-4, and BzATP (2'-3'-O-(4-Benzoylbenzoyl)adenosine 5'-triphosphate (C₂₄H₂₄N₅O₁₅P₃)). Preferably, the P2X7R agonist to be used for treating affective disorders is BzATP. More preferably, BzATP is used to treat depression or anxiety as demonstrated in Example 9 hereinbelow.

[0132] The present application provides another unexpected finding in that the chemical compound called tenidap or a derivative thereof also functions as a modulator of P2X7R which can thus be used for treating affective disorders. So far, various medical applications are described for tenidap or a derivative thereof. However, the use of tenidap or a derivative thereof for treating affective disorders is neither known nor suggested in the prior art. Accordingly, the present application relates to the use of tenidap or a derivative thereof or 3-substituted-2-oxindole-1-carboxamides for the preparation of a pharmaceutical composition for treating an affective disorder. Of course, also a method of treatment of an affective disorder comprising administering a therapeutically effective amount of tenidap or a derivative thereof or 3-substituted-2-oxindole-1-carboxamides to a subject suffering from said disorder is envisaged. The composition of tenidap (5-chloro-2,3-dihydro-2-oxo-3-(2-thienylcarbonyl)-indole-1-carboxamide, i.e. C₁₅H₁₁ClN₂O₂S)) having the following structural formula



and other 3-substituted-2-oxindole-1-carboxamides and their use as antiinflammatory and analgesic agents, and as inhibitors of both the cyclooxygenase (Cox) and lipoxygenase (5-LPO) enzymes was first disclosed in US 4,556,672. Of course, various modifications of, e.g., side groups or atoms which are well known in the art can be made to the

composition of tenidap.

Derivatives of tenidap or 3-substituted-2-oxindole derivatives are described, for example, in US 4,556,672; US 4,658,037; US 4,721,712; US 5,290,802; US 5,118,703; US 5,270,331; US 5,298,522; US 5,086,186; US 5,449,788 and US 5,795,902. Various processes for the synthesis of tenidap and other 3-substituted-2-oxindole-1-carboxamides are well known in the art, see for example US 4,652,658; US 4,665,194; US 4,952,703; EP-B1 155 828, WO 90/04393, WO 94/07488, WO 94/17061, WO 95/20574; WO 97/36895; van Deurzen et al., *J. Mol. Catal. B-Enzym.*, 2 (1996), 33-42; Porcs-Makkay and Simig, *Org. Process. Res. Dev.*, 4 (2000), 10-16; Kumar et al., *Org. Process. Res. Dev.*, 5 (2001), 61-64. The anhydrous crystalline form of the sodium salt of tenidap is described in US 5,036,099 and WO 88/05656. Injectable composition and pharmaceutical composition for rectal administration of tenidap are mentioned in EP-B1 508 311 and EP-B1 508 310, respectively. It is also described in the prior art that tenidap or a derivative thereof can be administered in combination with tetracycline (US 5,308,839) or methotrexate (WO 96/35419) for the treatment of rheumatoid arthritis. Inhibition of the photodecomposition of tenidap and other 3-substituted-2-oxindole-1-carboxamides is disclosed in WO 96/33701.

Further applications of tenidap or a derivative thereof and other 3-substituted-2-oxindole-1-carboxamides have been described for the inhibition of interleukin-1 biosynthesis in mammals and for the treatment interleukin-1 mediated disorders (US 4,861,794); for the inhibition of elastase release from neutrophils (US 5,006,547); for the suppression of T-cell function in mammals and to treat T-cell mediated autoimmune disorders of the systemic or organ specific type (US 4,853,409; Dolhain et al., *Scand. J. Immunol.* 42(1995), 686-693). Tenidap is also used for the treatment of Alzheimer's disease (WO 96/31209; US 5,545,656).

Tenidap or a derivative thereof or its pharmaceutically base salts have also been shown to inhibit activation of collagenase, treat collagenase mediated disorders and diseases, and inhibit the activity of myeloperoxidase in mammals (US 5,008,283). Tenidap can reduce total serum cholesterol, LDL cholesterol and triglycerides (US 5,122,534), and can be used for the treatment of ischemia induced myocardial injury and cytokine mediated myocardial injury (EP-B1 679 396). However, none of the aforementioned documents discloses a use of tenidap or derivatives thereof or 3-substituted-2-oxindole-1-carboxamides thereof for treating, for example, affective disorders such as depression.

[0133] Sanz et al., *Eur. J. Pharmacol.* 355 (1998), 235-244 suggest that tenidap can enhance the activity of the P2X7 receptor. It is suggested that tenidap may act by increasing ATP levels or improving the effect of ATP on P2X7. ATP is the natural ligand of P2X7R. Accordingly, tenidap or a derivative thereof is a modulator of P2X7R as is described herein since a modulator is either directly or indirectly modulating the activity or expression of P2X7R. By making use of the teaching of the present invention that modulators of P2X7R are useful for treating affective disorders, it is envisaged that tenidap or a derivative thereof is used as a modulator of P2X7R activity for the preparation of a pharmaceutical composition for the treatment of an affective disorder, examples of which are described herein. The preparation of pharmaceutical compositions, the modes of administration etc. are described supra and infra and apply to the use of tenidap or a derivative thereof for the preparation of a pharmaceutical composition, mutatis mutandis. Moreover, also the embodiments relating to the uses of and methods for treating affective disorders described herein apply to the use of tenidap or a derivative thereof for treating affective disorders or the corresponding method of treatment, mutatis mutandis.

[0134] The present application moreover envisages that modulators of P2X7R activity can be used in any combinations thereof for treating an affective disorder. For example, BzATP and tenidap or a derivative thereof or 3-substituted-2-oxindole-1-carboxamides may be used together, e.g., simultaneously or by successive administration for treating an affective disorder.

[0135] In a preferred embodiment the pharmaceutical composition described herein optionally comprises further molecules which have cell protective properties capable of altering the characteristics of the components of the invention thereby, for example, modulating, preferably blocking possible undesired, adverse or negative side effects of these components. One such possible undesired, adverse or negative side effect is the formation of pores in the cell membrane of treated cells which ultimately leads to apoptosis. Accordingly, said further molecules belong to the class of beta-adrenergic receptor modulators including agonists or antagonists having membrane-stabilizing properties. Beta-adrenergic receptor modulators including agonists and antagonists are compounds which decrease or increase the positive chronotropic, positive inotropic, bronchodilator and vasodilator responses caused by beta-adrenergic receptor agonists or antagonists. The magnitude of this decreased or increased response is proportional to the existing sympathetic tone and the concentration of beta-adrenergic receptor blocking agent which reaches the receptor sites. A beta-adrenergic receptor modulator in the context of the present invention is thus an antagonist or agonist. The activity of a beta-adrenergic receptor antagonist or agonist can be determined as is well known in the art. The activity of beta-adrenergic receptors can be determined by measuring the accumulation of cyclic adenosine mono-phosphate (cAMP) in Chinese hamster ovary (CHO) cells. CHO cells can be uniquely transfected with the cDNA coding for the human beta 1-, beta2-, or beta3-adrenergic receptor under the control of the CMV promoter or any other suitable promoter element. Transfection of the cells is performed using standard cell transfection methods, see for example, Joyner, "Gene Targeting: A Practical Approach", Oxford University Press, New York, 1993. Cells overexpressing one of the

beta-adrenergic gene are then grown to confluence in Ham's F12 media (Gibco BRL) containing 10% fetal bovine serum, 500 mg/ml Geneticin, 100 U/ml penicillin, 100 mg/ml streptomycin and 250 ng/ml fungizone according to the procedure described in American Type Culture Collection Catalogue of Cell Lines and Hybridomas, Seventh Edition, 1992, p. 36, ATCC CCL 61 CHO-K1. Beta-adrenergic modulator compounds can be prepared as 10 mM stock solutions in DMSO (0.1% DMSO, final concentration), diluted in Ham's F12 media and added to the cells at 10^{-10} to 10^{-5} M along with 10^{-3} M isobutylmethylxanthine to inhibit phosphodiesterase activity. The media and cells are then incubated for 5 minutes at 37°C. At the end of this period, the media is aspirated and the cells lysed in 0.01 N HCl. The cellular content of cAMP can then be determined by radioimmunoassay (RIA) using a kit from New England Nuclear (Burlington, Mass.). There is a direct correlation between the cellular content of cAMP and the activation/inhibition of the beta-adrenergic receptor. Other methods for determining the activity of a beta-adrenergic receptors are well described in the art, see for example, Vansal and Feller, J. Recept. Signal. Transduct. Res. 19 (1999) 853-863; Durocher et al., Anal. Biochem. 284 (2000) 316-326.

[0136] Examples of compounds which fit the definition of a beta-adrenergic receptor modulating agent include but are not limited to known beta-adrenergic receptor antagonist such as timolol, sotalol, esmolol, catechol, propranolol, betaxolol, penbutolol, metoprolol, acebutolol, atenolol, metoprolol, pindolol, and bisoprolol, and their salts, hydrates, solvates and any crystal forms in which they may occur. Further examples of beta-adrenergic receptor blocking agents are described in US 5,776,930. Preferred examples of beta-adrenergic receptor antagonists are DL-propranolol, D-propranolol and labetalol. DL-propranolol and labetalol are are beta-adrenergic receptor antagonists with membrane-stabilizing properties, while D-propranolol is an optical isomer with poor beta-adrenergic blocking activity. The optional addition of beta-adrenergic receptor antagonists or agonists to the pharmaceutical composition of the present invention for treating an affective disorder may be useful in the context of administering P2X7R agonists. This is because the prior art suggests that the activation of P2X7R by agonists may result in cell death by triggering the formation of pores within the cell membrane. However, as is demonstrated in Example 9 of the present application the pore-forming activity effect described for P2X7R agonists by the prior art was only observed for very few cells. Recently, Alzola et al., Cell Signal. 13 (2001), 465-473 have shown that concentrations of 10 to 300 μ M DL-propranolol, D-propranolol or labetalol can inhibit the pore-forming activity of P2X7R without affecting the opening of the cation channel activity of P2X7R. From FR 2768626 it is also known that beta-adrenergic modulators, e.g. agonists are useful as apoptosis inhibiting agents. Accordingly, in a preferred embodiment of the present invention, beta-adrenergic receptor modulators including antagonists or agonists are administered in combination with P2X7R agonists for the treatment of affective disorders. Said beta-adrenergic receptor antagonists or agonists are preferably administered in a concentration of 10 to 300 μ M.

[0137] Dosage, pharmaceutical preparation and delivery of P2X7R modulating agent for use in accordance with the present invention may be formulated in conventional manner according to methods found in the art, using one or more physiological carriers or excipient, see, for example Ansel et al., "Pharmaceutical Dosage Forms and Drug Delivery Systems", 7th edition, Lippincott Williams & Wilkins Publishers, 1999. Thus, the P2X7R modulating agent and its physiologically acceptable salts and solvates may be formulated for administration by inhalation, insufflation (either through the mouth, or nose), oral, buccal, parenteral, or rectal administration.

[0138] For oral administration, the pharmaceutical composition of the P2X7 modulating agent may take the form of, for example, tablets or capsules prepared by conventional means with pharmaceutical acceptable excipients such as binding agents (e.g., pregelatinised maize starch, polyvinylpyrrolidone, hydroxypropyl methylcellulose), fillers (e.g., lactose, microcrystalline cellulose, calcium hydrogen phosphate), lubricants (e.g., magnesium stearate, talc, silica), disintegrants (e.g., potato starch, sodium starch glycolate), or wetting agents (e.g., sodium lauryl sulphate). Liquid preparations for oral administration may take the form of, for example, solutions, syrups, or suspensions, or may be presented as a dry product for constitution with water or other suitable vehicle before use. Such liquid preparation may be prepared by conventional means with pharmaceutically acceptable additives such as suspending agents (e.g., sorbitol, syrup, cellulose derivatives, hydrogenated edible fats), emulsifying agents (e.g., lecithin, acacia), non-aqueous vehicles (e.g., almond oil, oily esters, ethyl alcohol, fractionated vegetable oils), preservatives (e.g., methyl or propyl-p-hydroxycarbonates, soric acids). The preparations may also contain buffer salts, flavouring, coloring and sweetening agents as deemed appropriate. Preparations for oral administration may be suitably formulated to give controlled release of the agent modulating P2X7R activity.

[0139] For administration by inhalation, the agent modulating P2X7R activity for use according to the present invention is conveniently delivered in the form of an aerosol spray presentation from a pressurised pack or a nebulizer, with the use of a suitable propellant (e.g., dichlorodifluoromethane, trichlorofluoromethane, dichlorotetrafluoroethane, carbon dioxide or other suitable gas). In the case of a pressurised aerosol, the dosage unit may be determined by providing a valve to deliver a metered amount. Capsules and cartridges of, for example, gelatine, for use in an inhaler or insufflator may be formulated containing a powder mix of the P2X7R activity modulating agent and a suitable powder base such as lactose or starch.

[0140] An agent modulating P2X7R activity may be formulated for parenteral administration by injection, for example, by bolus injection or continuous infusion. Site of injections include intra-venous, intra-peritoneal or sub-cutaneous.

Formulations for injection may be presented in units dosage form (e.g., in phial, in multi-dose container), and with an added preservative. The agent modulating P2X7R activity may take such forms as suspensions, solutions or emulsions in oily or aqueous vehicles, and may contain formulatory agents such as suspending, stabilizing, or dispersing agents. Alternatively, the agent may be in powder form for constitution with a suitable vehicle (e.g., sterile pyrogen-free water) before use.

[0141] An agent modulating P2X7R activity may, if desired, be presented in a pack, or dispenser device which may contain one or more unit dosage forms containing the said agent. The pack may for example comprise metal or plastic foil, such as blister pack. The pack or dispenser device may be accompanied with instruction for administration.

[0142] In a more preferred embodiment the aforementioned methods or uses are envisaged to treat affective disorders selected from the group consisting of major depression, generalized anxiety disorder and bipolar disorder.

[0143] In a particularly preferred embodiment said major depression is selected from the group consisting of major depression, dysthymia, atypical depression, premenstrual dysphoric disorder and seasonal affective disorder.

[0144] In another particularly preferred embodiment said generalized anxiety disorder is selected from the group consisting of panic disorder, phobias, agoraphobia, social phobia, specific phobia, obsessive-compulsive disorder, post-traumatic stress disorder, separation anxiety disorder, mania, hypomania and cyclothymic disorder.

[0145] A still also particularly preferred embodiment is that said bipolar disorder is bipolar disorder type I or bipolar disorder type II.

[0146] Additionally, the present invention relates to a kit comprising the nucleic acid molecule, the vector, the host, the polypeptide, the antibody or the aptamer, the primer or pair of primers of the invention or the molecule as identified or characterized in a method herein below of the present invention.

Advantageously, the kit of the present invention further comprises, optionally (a) reaction buffer(s), storage solutions and/or remaining reagents or materials required for the conduct of scientific or diagnostic assays or the like. Furthermore, parts of the kit of the invention can be packaged individually in vials or bottles or in combination in containers or multicontainer units.

The kit of the present invention may be advantageously used, inter alia, for carrying out the method of producing a polypeptide of the invention, the method(s) of identification and/or characterization of molecules specifically interacting with P2X7R ATP-gated ion channels as described herein below and/or it could be employed in a variety of applications referred herein, e.g., as diagnostic kits, as research tools or therapeutic tools. Additionally, the kit of the invention may contain means for detection suitable for scientific, medical and/or diagnostic purposes. The manufacture of the kits follows preferably standard procedures which are known to the person skilled in the art.

[0147] Furthermore, the present invention relates to a method for identifying compounds or mixtures of compounds which are capable of specifically interacting with a polypeptide of the present invention, comprising the steps of (a) contacting a polypeptide of the present invention with a candidate compound or mixture of compounds to be tested; and (b) determining whether said is capable of specifically interacting with said polypeptide. The polypeptide may be provided directly or by expression of a corresponding nucleic acid molecule or vector of the invention, e.g., in vitro or in a suitable host cell.

[0148] Additionally, the present invention relates to a method for the characterization of compounds which are capable of altering characteristics of the polypeptides of the present invention, comprising the steps of (a) contacting a polypeptide of the invention with said compound; and (b) determining whether the compound alters a characteristic of said polypeptide.

[0149] The term "altering characteristic of the polypeptide of the present invention" means that the functional characteristics to the polypeptides of the present invention in comparison to functional characteristics which they had before being contacted with the compounds identified by the above-described method: as described hereinabove are altered; i.e. changed.

[0150] Said identification and/or characterization of which are capable of interacting with or altering characteristics of the polypeptide of this invention, may be, inter alia, achieved by transfecting an appropriate host with a nucleic acid molecule of invention. Said hosts comprise, but are not limited to, HEK 293 cells or are injected into frog oocytes, preferably a *Xenopus* oocyte for functional expression (Goldin, *Methods Enzymol.* 207 (1992), 266). Expressed P2X7R ATP-gated channels can be examined using standard two-electrode voltage clamp techniques (Stuhmer, *Methods Enzymol.* 207 (1992), 319; Kohler, *Science* 273 (1996), 1709). After expression of a P2X7R ATP-gated ion channel as defined herein, membrane currents may be deduced in the absence and/or presence of the molecule to be identified and/or characterized. Methods for the deduction of membrane currents are well known in the art and comprise, e.g., patch clamp methods as described in Hamill, *Pflüger's Arch.* 391 (1981), 85-100 or two-electrode voltage clamp in oocytes, as described in Methfessel, *Pflüger's Archive* 407 (1986), 577-588. In accordance with the present invention the term "interacting with the polypeptides of the present invention" means that the polypeptides of the present invention interact directly and/or indirectly with compounds identified by the method described above. Furthermore, the present invention relates to a method of screening for molecules which are capable of interacting with the polypeptide of this invention, comprising the steps of (a) contacting a polypeptide of the invention with a molecule; and (b) measuring

and/or detecting a response; and (c) comparing said response to a standard response as measured in the absence of said candidate molecule.

[0151] The present invention also relates to a method for identifying a compound which is capable of enhancing or reducing the expression of the P2X7R gene comprising the steps of contacting a cell which expresses the P2X7R gene from its natural promoter or a reporter gene driven by the P2X7R promoter and determining whether the expression of the gene is increased or reduced when compared to conditions in which the compound is not present.

Potential candidate molecules or candidate mixtures of molecules may be, inter alia, substances, compounds or compositions which are of chemical or biological origin, which are naturally occurring and/or which are synthetically, combinatorially and/or chemically produced or compounds or compositions described hereinabove. Thus, candidate molecules may be proteins, protein-fragments, peptides, amino acids and/or derivatives thereof or other compounds, such as ions, which bind to and/or interact with wild-type P2X7R ATP-gated ion channels. Such binding and/or interacting candidate compounds may be found employing, inter alia, yeast two-hybrid systems or modified yeast two-hybrid systems as described, for example in Fields, Nature 340 (1989), 245-246; Gyuris, Cell 75 (1993), 791-801; or Zervos, Cell 72 (1993), 223-232.

[0152] Furthermore, potential candidate molecules may be contacted with a cell, such as an oocyte or a HEK 293 cell, which expresses a polypeptide of the invention or with a membrane patch comprising a polypeptide of the invention and a corresponding response (inter alia, a dose-response response, a current-response, or single current channel response) may be measured in order to elucidate any effect said candidate molecule causes.

[0153] Within the scope of the present invention are also methods for identifying, characterizing and for screening of molecules which are capable of interacting with the P2X7R ATP-gated ion channels according to the invention which comprise so-called high-throughput screening methods and similar approaches which are known in the art (Spencer, Biotechnol. Bioeng. 61 (1998), 61-67; Oldenburg, Annu. Rev. Med. Chem. 33 (1998), 301-311) carried out using 96-well, 384-well, 1536-well (and other) commercially available plates. Further methods to be employed in accordance with the present invention comprise, but are not limited to, homogenous fluorescence readouts in high-throughput screenings (as described, inter alia, in Pope, Drug Discovery Today 4 (1999), 350-362). The method of the present invention for identification, characterization and/or screening of molecules capable of interacting with P2X7R ATP-gated ion channels can, inter alia, employ hosts as defined herein which express the polypeptide of the present invention. Cell-based assays, instrumentation for said assays and/or measurements are well-known in the art and described, inter alia, in Gonzalez, Drug Discovery Today 4 (1999), 431-439 or Ramm, Drug Discovery Today 4 (1999), 401-410. It is also envisaged that the high throughput screens described herein are conducted by using, for example cRNA, i.e. synthetic RNA from a cDNA construct) that can be introduced in host cells, such as *Xenopus* oocytes using routine methods in the art. As an example, direct nucleic acid injection can be employed, such as the Eppendorf microinjection system (Micromanipulator 5171 and Transjector 5242). The injected/transformed cells can be analyzed for ion currents about 4 hours later using patch-clamp techniques which are commonly practiced in the art.

[0154] Additionally, the present invention relates to a method for the production of a pharmaceutical composition comprising the steps of a method of the invention for identifying, characterizing and/or screening of molecules which are capable of interacting with and/or altering the characteristics of a P2X7R ATP-gated ion channel of the invention and further comprising a step, wherein a derivative of said identified, characterized and/or screened molecule is generated. Such a derivative may be generated by, inter alia, peptidomimetics.

[0155] The invention furthermore relates to a method for the production of a pharmaceutical composition comprising the steps of a method of the invention for identifying, characterizing, screening and/or derivatizing of molecules which are capable of interacting with and/or altering the characteristics of a P2X7R ATP-gated ion channel and formulating the molecules identified, characterized, screened and/or derivatized in pharmaceutically acceptable form.

In a more preferred embodiment the present invention relates to a method wherein said molecule(s) comprise(s) (a) neuroprotective, (a) nootropic and/or (a) antiepileptic molecule(s).

[0156] Yet another embodiment of the invention is the use of a P2X7R polypeptide, in particular those according to the present invention, to identify biological, chemical, or pharmacological agents that can have an antidepressive effect. The term 'agent' refers to a chemical compound or composition capable of inducing a desired therapeutic or prophylactic effect when properly administered to a subject or cell. For example, the present invention allows the generation of cells expressing P2X7R for the identification and characterization of agents which modulate ionic influx and efflux. For example, HEK293 cells, or other cell lines (e.g., HCN-1A, HCN-2, HIT-T15, RIN-m5F, betaTC3, PC12, HT22, SH-SY5Y, Neuro2A or CA77), can be stably transfected with cDNA encoding the human P2X7R and plated in 12, 96 and 384 well plates. Said cells are cultured in appropriate medium. Examples of such medium are well known in the art, see, for example Freshney, "Culture of Animal Cells: A Manual of Basic Technique, 4th edition, Wiley-Liss Publishing, 2000.

[0157] Said cells can then be pre-incubated with said agents for 15 min prior to stimulation with 3 mM ATP for 10 minutes. Reactions are then terminated by rapid aspiration of the extracellular medium in each well. The cells in each well are subsequently extracted overnight with 1 ml 10% HN03. Potassium (K⁺) content in the extracts can be determined by atomic absorbance spectrophotometry. Agent function is then measured by the percent inhibition or stimu-

lation of the K⁺ release triggered by 3 mM ATP and compared to K⁺ release in the absence of the agents. P2X7R activity can also be monitored according to the movement of calcium (Ca²⁺; see Denyer et al., Drug Discov. Today 7 (1998), 323-332; González et al., Drug Discov. Today 9 (1999), 431-439; Helmchen and Waters, Eur. J. Pharmacol. 447 (2002), 119-129). Agents can also be verified in the absence of ATP.

[0158] P2X7R activity can also be monitored according to secretion of neurotransmitters such as glutamate and GABA. Neurotransmitter levels in treated cells can be quantified by suitable methods, e.g., Enzyme Linked Immunoabsorbent Assay (ELISA), Radio Immuno Assay (RIA), High Performance Liquid Chromatography (HPLC). Using these methods, a large number of compounds can be screened for increase in neurotransmitter (for example, glutamate) secretion. The release of glutamate can be measured for example by Fluorometric glutamate release assays (e.g.,

Amplex Red Glutamic Acid/Glutamate Oxidase Assay Kit, Molecular Probes) or High-Throughput ElectroPhysiology. [0159] In a further aspect the present invention uses the P2X7R polypeptides disclosed herein or polypeptides of the present invention in a method for identifying compounds or agents having agonist activity to said P2X7R polypeptides or to the polypeptides of the present invention. Agents and compounds are defined and described hereinabove and hereinbelow. In particular, cells that express the P2X7 gene are contacted with candidate agents, molecules or compounds as described hereinabove and either calcium influx or ethidium bromide entry is measured by methods known in the art, described hereinabove and in particular described in Example 8 hereinbelow. The cells used in the method for identifying agonists to P2X7R are preferably cells of a hippocampal cell line. Hippocampal cell lines are prepared by methods known in the art, for example, described in EP 0 773 287 or EP 0 773 292. Non limiting examples of hippocampal cell lines are rat H19-7 hippocampal cells (ATCC-2526) described in Eves et al. Proc. Natl. Acad. Sci. USA 89 (1992), 4373-4377, mouse HN9.10 hippocampal cells described in Lee et al. J. Neurosci. 10 (1992), 1779-1787 or rat Hi5B hippocampal cells described in Renfranz et al., Cell 66 (1991), 713-729. Preferably, the hippocampal cells used in accordance with the aforementioned method are cells of the HT-series (see Davis and Maher (1994), Brain Res. 652, 169-173), Morimoto and Koshland (1990), Neuron 5, 875-880). It is also preferred that the hippocampal cells express the endogenous P2X7R gene. However, it is also envisaged that such cells may be genetically modified by introducing an exogenous P2X7R gene using methods commonly known in the art. More preferably, HT-22 cells are used for identifying agonists to the P2X7R polypeptides described herein or to the polypeptides of the present invention and HT-39 cells are used as a negative control as described in Example 8 hereinbelow.

[0160] In another embodiment, cells are transfected with nucleic acid constructs encoding a reporter gene regulated by the P2X7R promoter (see above), an increase or decrease in the expression of the reporter gene in response to biological or pharmaceutical agents can be analyzed using methods that detect levels or status of protein or mRNA present in the corresponding cell or detect biological activities of the reporter gene. Suitable reporter molecules or labels, which may be used, include radionucleotides, enzymes, fluorescent, chemiluminescent or chromogenic agents as well as substrates, co-factors, inhibitors, magnetic particles, and the like. Designing such drug screening assays are well known in the art; see Harvey ed., 'Advances in drug discovery techniques', John Wiley and Sons, 1998; Vogel and Vogel eds., 'Drug discovery and evaluation: Pharmaceutical assays', Springer-Verlag Berlin, 1997). For example, drug screening in animal models, in vitro tests using animal cells, or in vivo tests involving toxicology tests in animals. An in vitro model can be used for screening libraries of compounds in any of a variety of drug screening techniques.

[0161] Candidate agents encompass numerous chemical classes, though typically they are organic molecules, preferably small organic compounds having a molecular weight of more than 50 and less than about 2,500 Daltons. Candidate agents comprise functional groups necessary for structural interaction with proteins, particularly hydrogen bonding, and typically include at least an amine, carbonyl, hydroxyl or carboxyl group, preferably at least two of the functional chemical groups. The candidate agents often comprise carbocyclic or heterocyclic structures and/or aromatic or polyaromatic structures substituted with one or more of the above functional groups.

[0162] Candidate agents are also found among biomolecules including peptides, amino acids, saccharides, fatty acids, steroids, purines, pyrimidines, nucleic acids and derivatives, structural analogs or combinations thereof. Candidate agents are obtained from a wide variety of sources including libraries of synthetic or natural compounds. For example, numerous means are available for random and directed synthesis of a wide variety of organic compounds and biomolecules, including expression of randomized oligonucleotides and oligopeptides. Alternatively, libraries of natural compounds in the form of bacterial, fungal, plant and animal extracts are available or readily produced. Additionally, natural or synthetically produced libraries and compounds are readily modified through conventional chemical, physical and biochemical means, and may be used to produce combinatorial libraries. Known pharmacological agents may be subjected to directed or random chemical modifications, such as acylation, alkylation, esterification, amidification, etc. to produce structural analogs.

[0163] Another technique for drug screening, which may be used, provides for high throughput screening of compounds having suitable binding affinity to the protein of interest as described in published PCT application WO 84/03564. In this method, as applied to the proteins of the invention large numbers of different small test compounds, e.g. aptamers, peptides, low-molecular weight compounds etc., are provided or synthesized on a solid substrate, such as plastic pins or some other surface. The test compounds are reacted with the proteins or fragments thereof, and washed.

Bound proteins are then detected by methods well known in the art. Purified proteins can also be coated directly onto plates for use in the aforementioned drug screening techniques. Alternatively, non-neutralizing antibodies can be used to capture the peptide and immobilize it on a solid support. In another embodiment, one may use competitive drug screening assays in which neutralizing antibodies capable of binding the protein specifically compete with a test compound for binding the protein. In this manner, the antibodies can be used to detect the presence of any peptide, which shares one or more antigenic determinants with the protein.

[0164] The present invention further particularly provides a method, wherein the pharmaceutical composition to be produced further comprises neuroprotective substances, nootropic substances, brilliant blue, piperidine or derivatives thereof, adamantane derivatives, substituted phenyl compounds, oxidized ATP, 2-O-(4-benzoylbenzoyl)adenosine-5-triphosphate or 3-O-(4-benzoylbenzoyl)adenosine-5-triphosphate. It is also envisaged that the pharmaceutical compositions to be produced further comprise antidepressants such as fluoxetine, paroxetine, sertraline, fluoxetine, mirtazapine, reoxetine, nefazodone or lithium carbonate.

[0165] In a preferred embodiment of the present invention, the compounds of the aforementioned methods comprise antagonist(s), partial antagonist(s), partial agonist(s) and/or agonist(s) for an altered ATP-gated ion channel P2X7R.

[0166] In accordance with the present invention, the term "antagonist" denotes molecules/substances, which are capable of inhibiting and/or reducing an agonistic effect. The term "antagonist" comprises competitive, non-competitive, functional and chemical antagonists as described, inter alia, in Mutschler, "Arzneimittelwirkungen" (1986), Wissenschaftliche Verlagsgesellschaft mbH, Stuttgart, Germany. The term "partial antagonist" in accordance with the present invention means a molecule/substance that is capable of incompletely blocking the action of agonists through, inter alia, a non-competitive mechanism.

In the context of the present invention, an antagonist is preferably a drug that does not provoke a response itself, but blocks agonist-mediated responses. It is a chemical entity that opposes the receptor-associated responses normally induced by another bioactive agent. For the P2X7R, the antagonists have an IC₅₀ between 10 nanomolar and 300 micromolar.

[0167] As "agonist", in accordance with this invention, molecules/substances are denoted which have an affinity as well as an intrinsic activity. Mostly, said intrinsic activity (α) is defined as being proportional to the quotient of the effect, triggered by said agonist (EA) and the effect which can be maximally obtained in a given biological system (E_{max}): therefore, the intrinsic activity can be defined as

$$\alpha \sim \frac{E_A}{E_{\max}}$$

[0168] The highest relative intrinsic activity results from EA/E_{max}=1. Agonists with an intrinsic activity of 1 are full agonists, whereas substances/molecules with an intrinsic activity of >0 and <1 are partial agonists. Partial agonists show a dualistic effect, i.e. they comprise agonistic as well as antagonistic effects.

Preferably, in the context of the present invention, an agonist (or full agonist) is an endogenous substance or a drug that can interact with a receptor and initiate a maximal or complete physiological or a pharmacological response characteristic of that receptor. ATP, the natural ligand for the P2X7R, is an agonist with an EC₅₀ of 300 micromolar while the synthetic P2X7R agonist Bz-ATP has an EC₅₀ of 8 micromolar. Thus, agonists of P2X7R have an EC₅₀ equal or below 300 micromolar. The EC₅₀ is defined as the concentration of agonist that provokes a response half way between the baseline response and maximum response on a dose response curve where the X-axis plots concentration of an agonist and the Y-axis plots ion current. An inverse agonist (also called negative antagonist) is a drug which acts at the same receptor as that of an agonist, yet produces an opposite effect. A partial agonist is an endogenous substance or a drug that also provokes physiological or a pharmacological response but, the maximum response is less than the maximum response to a full agonist, regardless of the amount of drug applied. In the case of P2X7R, partial agonists have EC₅₀s higher than 300 micromolar.

[0169] The person skilled in the art can, therefore, easily employ the compounds and the methods of this invention in order to elucidate the agonistic and/or antagonistic effects and/or characteristics of a compound/molecule/substance to be identified and/or characterized in accordance with any of the above described methods. Preferably, an identified antagonist of the ATP-gated ion channel P2X7R comprising the mutation(s) and/or deletion(s) described hereinabove may be useful to reestablish the properties normally shown by wild-type P2X7R ATP-gated ion channels. An identified agonist of the ATP-gated ion channel P2X7R comprising the mutation(s) and/or deletion(s) described hereinabove may be useful to reestablish the lost functionality of the P2X7R ATP-gated ion channel.

[0170] The Figures show:

Figure 1a. Genomic map of the region on the human chromosome 12 associated to bipolar affective disorder. Genes found between markers NBG11 and NBG2 are depicted.

Figure 1b. Graphic illustrating the multipoint analysis using ASPEX on independent sib-pairs.

Figure 1c. Graphic illustrating the multipoint analysis using ASPEX on all sib-pairs

Figure 1d. Graphic illustrating the ASPEX sib_phase by considering only independent sib-pairs

Figure 1e. Graphic illustrating the ASPEX sib_phase by considering all sib-pairs

Figure 1f. Effect of the P2XR7v13A polymorphism on basal cortisol levels before and after administration of dexamethasone (DST test). Individuals were subjected to the test within the first ten days of admission. Individuals with the AG and GG genotypes have significantly lower cortisol levels pre- and post-dexamethasone administration.

Figure 1g. Effect of the P2XR7v13A polymorphism on cortisol response during the Dex/CRH test. Individuals were subjected to the test within the first ten days of admission (i.e. At admission) and at the last ten days before discharge (i.e. at discharge). Individuals with the GG genotype have lower cortisol levels in response to the Dex/CRH test at admission and at discharge. These results are indicative of an abnormal HPA axis.

Figure 1h. Effect of the P2XR7v13A polymorphism on ACTH response during the Dex/CRH test. Individuals were subjected to the test within the first ten days of admission (i.e. at admission) and at the last ten days before discharge (i.e. at discharge). Individuals with the GG genotype have lower ACTH levels in response to the Dex/CRH test, at admission and at discharge. These results are indicative of an abnormal HPA axis.

Figure 1i. Duration of antidepressant treatment until remission. Depression is diagnosed according to the Hamilton Depression Rating Scale (HAM-D; Hamilton, Br. J. Soc. Clin. Psychol. 6 (1967) 278-296). A HAM-D score of 10 or below is regarded as remission of the depressive symptoms.

Figure 1j. Effect of the P2XR7v13C polymorphism on basal cortisol levels before and after administration of dexamethasone (DST test). Individuals were subjected to the test within the first ten days of admission. Individuals with the CC genotypes have elevated cortisol levels post-dexamethasone administration.

Figure 1k. Effect of the P2XR7v13C polymorphism on cortisol response during the Dex/CRH test. Individuals were subjected to the test within the first ten days of admission (i.e. at admission) and at the last ten days before discharge (i.e. at discharge). Individuals with the AC or CC genotype have elevated cortisol levels in response to the Dex/CRH test at admission, indicating an abnormal HPA axis.

Figure 1l. Effect of the P2XR7v13C polymorphism on ACTH response during the Dex/CRH test. Individuals were subjected to the test within the first ten days of admission (i.e. at admission) and at the last ten days before discharge (i.e. at discharge). Individuals with the CC genotype have lower ACTH levels in response to the Dex/CRH test, at admission and at discharge. These results are indicative of an abnormal HPA axis.

Figure 2. RT-PCR analysis of the complete coding sequence of P2X7R in different tissues

Figure 3. P2X7R expression in the olfactory bulb, hypothalamus and ependymal cells in the brain of a stress-free mouse. Magnification 100X.

Figure 4. P2X7R expression in the hippocampus/dentate gyrus and subcommissural organ in the brain of a stress-free mouse. Magnification 100X.

Figure 5. Floating behaviour in the forced swim test. Passive stress coping behaviour decreased after long-term treatment with the antidepressant paroxetine (Par28: treated with paroxetine for 28 days, per os). Basal n=8; vehicle n=8; Par28 n=8.

Figure 6. Comparative analysis of P2X7R expression in the olfactory bulb of stress-free, vehicle-treated and antidepressant-treated mice. Magnification 100X.

Figure 7. Comparative analysis of P2X7R expression in the hypothalamus of stress-free, treated-treated and antidepressant-treated mice. Magnification 100X.

Figure 8. Comparative analysis of P2X7R expression in ependymal cells of stress-free, vehicle-treated and antidepressant-treated mice. Magnification 100X.

Figure 9. Comparative analysis of P2X7R expression in the hippocampus of stress-free, vehicle-treated and antidepressant-treated mice. Magnification 25X.

Figure 10. P2X7R expression in the hippocampus of a vehicle treated mouse. Magnification 25X.

Figure 11. P2X7R expression in the hippocampus of a mouse treated with the antidepressant paroxetine. Magnification 25X.

Figure 12. Detailed expression of P2X7R in the dentate gyrus of a mouse treated with the antidepressant paroxetine. Magnification 400x.

Figure 13. Comparative analysis of P2X7R expression and apoptotic cells in the hippocampus of a mouse treated with the antidepressant paroxetine. Magnification 100X.

Figure 14. Floating behaviour in the forced swim test. Passive stress coping behaviour increased after acute intrahippocampal (bilateral, dentate gyrus) of siRNA targeting P2X7R. Vehicle n=7; control RNA n=10; P2X7R siRNA n=9.

Figure 15. Comparative analysis of P2X7R expression in the hippocampus of mice treated with vehicle, control RNA and of siRNA targeting P2X7R. Magnification 100X upper row, 25X lower row.

Figure 16a, b, c, d, e. Three splicing variants caused by polymorphisms in the introns of P2X7R.

Figure 17. Expression of P2X7R in immortalized hippocampal cell lines.

Figure 18. Increase calcium influx in hippocampal cells treated with a P2X7R agonist compound (BzATP).

Figure 19a, b. Entry of ethidium bromide dye into hippocampal cells (a) treated with P2X7R agonist compound (BzATP) or (b) pre-treated with a P2X7R antagonist compound.

Figure 19c. Agonist action of BzATP and tenidap on P2X7R activity. The calcium channel activity of human P2X7R was measured under basal conditions for four seconds to 10 seconds. A. Negative control consisting of cells loaded with 10 μ M Fluo-4-AM without further treatment. B. Cells treated with 20 μ M BzATP after four seconds of basal measurement. C. Cells treated with 50 μ M tenidap after four seconds of basal measurement.

Figure 20. Effect of intrahippocampal injection of a P2X7R agonist compound (BzATP) on behaviour in the forced swim test.

Figure 21. Open field test measuring locomotor activity of mice treated with a P2X7R agonist compound (BzATP).

Figure 22. Comparative analysis of apoptotic cells in the hippocampus of a mouse treated with control vehicle solution or a P2X7R agonist compound (BzATP).

Figure 23. Effect of intrahippocampal injection of the P2X7R antagonist KN-62 and oATP on behaviour during the forced swim test

Figure 24. Open field test measuring locomotor activity of mice treated with the P2X7R antagonist KN-62 and oATP.

[0171] A better understanding of the present invention and of its many advantages will be had from the following examples, offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

EXAMPLE 1

Linkage analysis of Bipolar Affective Disorder in a homogeneous human population

[0172] 41 families of different sizes containing a total of 485 sampled individuals from the region of Saguenay/Lac St-Jean were used in the linkage analysis. Individuals were distributed according to their diagnoses as follows: 105 individuals afflicted with Bipolar Disorder type I (BPI) or schizoaffective disorder bipolar type; 42 individuals diagnosed with Bipolar Disorder type II (BP II); 54 individuals with recurrent major depression; and 57 individuals with single episode major depression. The remaining 227 individual were unaffected and normal. For the purpose of the calculation, the following classification was used: individuals diagnosed with either BPI, schizoaffective disorder, bipolar type, BP II and recurrent major depression were considered as affected (n=201); individuals with a single major depression episode were scored as unknown phenotype (n=57); and all others diagnoses as unaffected (n=227).

[0173] Blood samples from each individual were collected in 10-ml K3 EDTA Vacutainer tube (Becton-Dickinson) and genomic DNA was isolated by Puregene DNA Isolation kit (Gentra Systems). Blood was poured into 50 ml conical tube and diluted with four volume of Red Blood Cell Lysis Solution. After an incubation of 10 minutes at room temperature, the tube was centrifuged for 10 minutes at 2,000 g and supernatant was removed leaving behind cell pellet and 200-400 µl of the residual liquid. Cells were resuspended by vortexing the tube and 9 ml of Cell Lysis Solution were added with up and down pipetting. 40 µl of RNase A Solution (20 mg/ml) were added and the sample was mixed by inverting the tube several times. Sample was incubated at 37°C for 15 minutes and cooled to room temperature. 3 ml of Protein Precipitation Solution were added to cell lysate. Tube was vigorously vortexed for 30 seconds and centrifuged at 2,000 g for 10 minutes. Supernatant was poured into a new tube containing 9 ml of 100% isopropanol. Sample was mixed by inverting gently several times. Tube was centrifuged at 2,000 g for 5 minutes. The DNA white pellet was washed with 10 ml 70% ethanol and the tube was centrifuged at 2,000 g for 3 minutes. Ethanol was poured off and pellet allowed to partially air dry. DNA was solubilized in 500 µl of DNA Hydration Solution. Final concentration was adjusted to 300-400 µg/ml.

[0174] A fluorescent-based method was used for the genotyping of microsatellite markers. Briefly, the region encompassing each repeated sequence was amplified by PCR using an unlabeled primer and a fluorescent-labeled primer (Applied biosystems inc, CA, USA). The marker-associated dyes and the corresponding PCR product length are listed in table 2. The PCR reaction was performed using 10ng of DNA sample, 0,2 unit of Taq platinum DNA polymerase (Invitrogene, CA, USA), 20 mM Tris-Cl (pH 8.4), 50 mM KCl, 1.5mM MgCl₂, 100µM of dNTP, and 1,5 µM of each primer in a final volume of 7 µl. The samples were incubated at 95°C for 3 minutes to activate the Taq platinum DNA polymerase, then 10 cycles of PCR amplification were performed as follows: 95°C for 15 seconds; 58°C for 15 seconds; 72°C for 30 seconds; after that 15 cycles were performed as follow: 89°C for 15 seconds; 58°C for 15 seconds; 72°C for 30 seconds. Finally, the samples were incubated at 72°C for 30 min. Following the PCR amplification samples were pooled according to their dye-labeled primer and their PCR product length (pool of four samples). Pooled sample were separated on an ABI 3100 DNA analyzer (Applied Biosystems inc, CA, USA). The resulting data were analysed using Genemapper2 (Applied Biosystems inc, CA, USA), and compiled in a 4D database (ACIUS) designed in a Macintosh environment as previously described (Morissette et al., Am. J. Med. Genet. (Neuropsychiatr. Genet.) 88 (1999), 567-587)

[0175] Markers used in the following linkage analysis are shown in table 2. Recombination fraction (q) between successive markers was computed according to the analyzed families.

Table 2.

| Genomic markers used for the linkage analysis | | | | | |
|---|----------------|--------------------|--------------|--------------------------|--------------------|
| Locus | Associated dye | Allele length (bp) | Distance (g) | Cumulative distance (cM) | Heterozygosity (%) |
| D12S1619 | VIC | 170-210 | 0.0135 | 0.00 | 74.5 |
| NBG11 | VIC | 204-218 | 0.006 | 1.37 | 65.5 |
| D12S1666 | FAM | 241-281 | 0.001 | 1.97 | 66.9 |
| NBG5 | VIC | 253-261 | 0.001 | 2.07 | 38.3 |
| D12S1721 | VIC | 263-299 | 0.005 | 2.17 | 72.1 |
| NBG8 | VIC | 166-188 | 0.011 | 2.67 | 73.3 |
| NBG6 | NED | 182-218 | 0.0115 | 3.79 | 73.9 |

Table 2. (continued)

| Genomic markers used for the linkage analysis | | | | | |
|--|----------------|--------------------|--------------|--------------------------|--------------------|
| Locus | Associated dye | Allele length (bp) | Distance (g) | Cumulative distance (cM) | Heterozygosity (%) |
| NBG9 | VIC | 156-180 | 0.0035 | 4.95 | 68.9 |
| NBG10 | FAM | 174-186 | 0.001 | 5.30 | 49.7 |
| NBG12 | NED | 165-207 | 0.009 | 5.40 | 64.2 |
| NBG4 | NED | 171-199 | 0.001 | 6.31 | 66.4 |
| NBG3 | VIC | 182-206 | 0.006 | 6.41 | 64.8 |
| NBG2 | VIC | 171-199 | | 7.01 | 54.2 |
| - Haldane's map function was used for cumulative distance in cMorgans. | | | | | |

[0176] For bipoint parametric analysis, MOD score analysis were used where parametric LOD score were maximized over genetic models.

[0177] The following results were obtained under MOD score analysis for recessive models.

Table 3.

| MOD score analysis for recessive models | | | |
|---|--------------|--------------------------|--------------------------|
| Locus | Distance (g) | Cumulative distance (cM) | LOD score (q_{\max}) |
| D12S1619 | 0.0135 | 0.00 | 3.46 (0.10) |
| NBG11 | 0.006 | 1.37 | 4.06 (0.04) |
| D12S1666 | 0.001 | 1.97 | 1.22 (0.14) |
| NBG5 | 0.001 | 2.07 | 0.66 (0.16) |
| D12S1721 | 0.005 | 2.17 | 2.82 (0.10) |
| NBG8 | 0.011 | 2.67 | 1.51 (0.00) |
| NBG6 | 0.0115 | 3.79 | 4.77 (0.06) |
| NBG9 | 0.0035 | 4.95 | 0.75 (0.22) |
| NBG10 | 0.001 | 5.30 | 0.74 (0.00) |
| NBG12 | 0.009 | 5.40 | 1.41 (0.16) |
| NBG4 | 0.001 | 6.31 | 3.56 (0.08) |
| NBG3 | 0.006 | 6.41 | 3.96 (0.08) |
| NBG2 | | 7.01 | 2.59 (0.10) |

[0178] Model-free LOD score studies using ANALYZE, sib_phase from the ASPEX V1.85 package (David Hinds and Neil Risch 1999; [ftp://lahmed.stanford.edu/pub/aspeex](http://lahmed.stanford.edu/pub/aspeex), see also <http://watson.hgen.pitt.edu/docs/usage.html>) and SIMWALK2 (Sobel and Lange, Am J Hum Genet 58 (1996), 1323-1337) were performed to analyze the allele sharing among affected sib-pairs. The ANALYZE program weights sibships according to their size. The ASPEX sib_phase program uses allele frequencies to reconstruct missing information, and is tailored for data sets where parents are missing, but additional typed children may be used to reconstruct and phase the parents. SimWalk2 is a statistical genetics computer application for haplotype, parametric linkage, non-parametric linkage (NPL), identity by descent (IBD) and mistyping analyses on any size of pedigree. SimWalk2 uses Markov chain Monte Carlo (MCMC) and simulated annealing algorithms to perform these multipoint analyses.

[0179] ASPEX sib_phase was used with two computational strategies: First, by using strictly independent sib pairs; secondly, by using all affected sib-pair combinations. ASPEX was performed for bi-point and multipoint calculations.

[0180] The bi-point results observed with ANALYZE and ASPEX are shown in Table 4.

Table 4.

| Bi-point results observed with ANALYZE and ASPEX | | | | | |
|--|--------------|--------------------------|---------------------------------|--------------------------------------|-----------------------------------|
| Locus | Distance (q) | Cumulative distance (cM) | Sib-pair from ANALYZE LOD score | sib_phase LOD score indep. sib-pairs | sib_phase LOD score all sib-pairs |
| D12S1619 | 0.0135 | 0.00 | 2.31 | 2.55 | 3.14 |
| NBG11 | 0.006 | 1.37 | 2.83 | 2.72 | 3.27 |
| D12S1666 | 0.001 | 1.97 | 1.01 | 2.52 | 3.14 |
| NBG5 | 0.001 | 2.07 | 0.50 | 2.52 | 3.13 |
| D12S1721 | 0.005 | 2.17 | 1.57 | 2.51 | 3.12 |
| NBG8 | 0.011 | 2.67 | 0.51 | 2.24 | 2.75 |
| NBG6 | 0.0115 | 3.79 | 2.55 | 2.11 | 2.64 |
| NBG9 | 0.0035 | 4.95 | 0.49 | 1.65 | 1.97 |
| NBG10 | 0.001 | 5.30 | 0.77 | 1.45 | 2.10 |
| NBG12 | 0.009 | 5.40 | 0.47 | 1.44 | 2.17 |
| NBG4 | 0.001 | 6.31 | 1.21 | 1.29 | 3.07 |
| NBG3 | 0.006 | 6.41 | 1.84 | 1.29 | 3.07 |
| NBG2 | | 7.01 | 1.24 | 1.22 | 3.00 |
| SIMWALK2 computed four different statistics based on descent trees. These statistics measure the degree of clustering among the marker alleles descending from the founders. | | | | | |

[0181] Statistic A is the number of different founder-alleles contributing alleles to the affected it is most powerful at detecting linkage to a recessive trait. Statistic B is the maximum number of alleles among the affected descended from any one founder-allele and most powerful at detecting linkage to a dominant trait. Statistic C is the 'entropy' of the marker alleles among the affected. Statistic D is the extent of allele sharing among all affected pairs as measured by their IBD kinship coefficient. Statistics C and D are more general statistics indicating whether a few founder-alleles are overly represented among the affected.

[0182] Table 5 shows the results observed with SIMWALK2. The authors signal that p-values should be generally conservative. They are expressed as -Log(p-values). For correspondence purpose, -Log(0.05)=1.30, -Log(0.01)=2, -Log(0.001)=3 etc.

Table 5.

| SIMWALK2 analysis | | | | | | |
|-------------------|--------------|----------------------|--------------------------|--------------------------|--------------------------|--------------------------|
| Locus | Distance (q) | Cumul. Distance (cM) | STAT(A) -Log(p-value) | STAT(B) -Log(p-value) | STAT(C) -Log(p-value) | STAT(D) -Log(p-value) |
| D12S1619 | 0.0135 | 0.00 | 1.4550 | 0.4103 | 1.1306 | 1.1310 |
| NBG11 | 0.006 | 1.37 | 2.0157 | 1.4375 | 1.5955 | 1.9845 |
| D12S1666 | 0.001 | 1.97 | 2.0236 | 0.9765 | 1.4727 | 1.4614 |
| NBG5 | 0.001 | 2.07 | 1.7596 | 0.8558 | 1.3866 | 1.3602 |
| D12S1721 | 0.005 | 2.17 | 1.6628 | 1.1692 | 1.4235 | 1.6384 |
| NBG8 | 0.011 | 2.67 | 1.5374 | 0.6940 | 1.0623 | 1.1552 |
| NBG6 | 0.0115 | 3.79 | 1.5896 | 0.4452 | 1.0935 | 1.1786 |
| NBG9 | 0.0035 | 4.95 | 1.2677 | 0.3815 | 0.8412 | 0.9133 |
| NBG10 | 0.001 | 5.30 | 1.1117 | 0.3642 | 0.6987 | 0.7554 |

Table 5. (continued)

| SIMWALK2 analysis | | | | | | |
|-------------------|--------------|----------------------|--------------------------|--------------------------|--------------------------|--------------------------|
| Locus | Distance (q) | Cumul. Distance (cM) | STAT(A) -Log(p-value) | STAT(B) -Log(p-value) | STAT(C) -Log(p-value) | STAT(D) -Log(p-value) |
| NBG12 | 0.009 | 5.40 | 1.0809 | 0.3485 | 0.6694 | 0.7179 |
| NBG4 | 0.001 | 6.31 | 1.1024 | 0.4148 | 0.6368 | 0.8544 |
| NBG3 | 0.006 | 6.41 | 1.1040 | 0.4146 | 0.6373 | 0.8559 |
| NBG2 | | 7.01 | 1.0963 | 0.5380 | 0.6587 | 0.9356 |

[0183] Multipoint result observed with ASPEX when only independent sib-pairs were used (Figure 1b). The maximum LOD score value was observed at NBG11.

[0184] Multipoint result observed with ASPEX when all sib-pairs were considered (Figure 1c). The maximum LOD score value was observed at NBG11 but a second peak appeared at NBG4 and NBG3.

[0185] Multipoint and bi-point LOD score values computed by ASPEX were similar. The second peak, observed when all sib-pairs are used, may be explained by the presence of a recombinant affected individual, with many affected sibs, sharing the chromosomal region telomeric to NBG12. This kind of individuals has a large impact on LOD score values when all sib-pairs are used instead of one sib-pair. This situation was observed in two sibships.

[0186] Strata analysis was subsequently performed. Although HOMOG did not detect evidence for heterogeneity, a homogeneity test was constructed based on allele sharing found in selected chromosomal regions. Only 20 of the 41 families were used for this analysis since the others were not genotyped in all these regions. For each marker within the selected regions, the proportion of alleles shared IBD by affected sib-pairs was estimated with ASPEX (sib_phase). For each region retained, the proportion of shared alleles was used as variable for a Principal Component Analysis and the first principal component as an index of linkage. Correlation analysis was done on these indexes to detect heterogeneity (correlation < 0) or epistasis (correlation > 0). Fisher algorithm was used to classify into two groups of families as linked or unlinked to a particular locus. A negative correlation was observed between the chromosome 12 region and the chromosome 15 area ($r=-0.51$; $p=0.023$). Cluster analysis suggested that 11 families out of 20 were linked to chromosome 12. This sub-sample was called the strata.

[0187] This strata included 11 families (266 sampled individuals) that include 52 BPI or schizoaffective disorder, bipolar type, 20 BP11 and 28 recurrent major depression

[0188] The following MOD score values illustrated in Table 6 were obtained under recessive models.

Table 6.

| MOD scores under recessive models | | | |
|-----------------------------------|--------------|--------------------------|-------------------------|
| Locus | Distance (q) | Cumulative distance (cM) | LOD score (q_{max}) |
| D12S1619 | 0.0135 | 0.00 | 4.03 (0.08) |
| NBG11 | 0.006 | 1.37 | 4.98 (0.00) |
| D12S1666 | 0.001 | 1.97 | 1.49 (0.12) |
| NBG5 | 0.001 | 2.07 | 0.79 (0.14) |
| D12S1721 | 0.005 | 2.17 | 4.23 (0.06) |
| NBG8 | 0.011 | 2.67 | 2.79 (0.00) |
| NBG6 | 0.0115 | 3.79 | 5.06 (0.06) |
| NBG9 | 0.0035 | 4.95 | 1.57 (0.14) |
| NBG10 | 0.001 | 5.30 | 1.73 (0.00) |
| NBG12 | 0.009 | 5.40 | 1.65 (0.12) |
| NBG4 | 0.001 | 6.31 | 4.60 (0.08) |
| NBG3 | 0.006 | 6.41 | 4.84 (0.06) |
| NBG2 | | 7.01 | 2.80 (0.06) |

[0189] Model-free LOD score results obtained with ANALYZE and ASPEX applied to the strata are shown in Table 7.

Table 7.

| Model-free LOD score obtained with ANALYZE and ASPEX | | | | | |
|--|--------------|--------------------------|-------------------|---|-----------------------------------|
| Locus | Distance (q) | Cumulative distance (cM) | ANALYZE LOD score | sib_phase LOD score independent sib-pairs | sib_phase LOD score all sib-pairs |
| D12S1619 | 0.0135 | 0.00 | 4.54 | 5.29 | 7.65 |
| NBG 11 | 0.006 | 1.37 | 4.29 | 5.34 | 7.70 |
| D12S1666 | 0.001 | 1.97 | 2.77 | 5.36 | 7.74 |
| NBG5 | 0.001 | 2.07 | 0.67 | 5.36 | 7.74 |
| D12S1721 | 0.005 | 2.17 | 4.48 | 5.35 | 7.74 |
| NBG8 | 0.011 | 2.67 | 2.97 | 4.87 | 7.00 |
| NBG6 | 0.0115 | 3.79 | 4.05 | 4.59 | 6.76 |
| NBG9 | 0.0035 | 4.95 | 2.03 | 3.72 | 5.41 |
| NBG10 | 0.001 | 5.30 | 2.00 | 3.42 | 5.89 |
| NBG12 | 0.009 | 5.40 | 0.89 | 3.44 | 6.11 |
| NBG4 | 0.001 | 6.31 | 2.84 | 3.71 | 9.00 |
| NBG3 | 0.006 | 6.41 | 3.89 | 3.71 | 9.01 |
| NBG2 | | 7.01 | 1.91 | 3.52 | 8.73 |

[0190] Model-free results observed with SIMWALK2 are illustrated in Table 8.

Table 8.

| Model-free LOD score obtained with SIMWALK2 | | | | | | |
|---|--------------|--------------------------|--------------------------|--------------------------|--------------------------|--------------------------|
| Locus | Distance (q) | Cumulative Distance (cM) | STAT(A) -Log(p-value) | STAT(B) -Log(p-value) | STAT(C) -Log(p-value) | STAT(D) -Log(p-value) |
| D12S1619 | 0.0135 | 0,00 | 2,5963 | 0,9565 | 3,2156 | 2,3584 |
| NBG11 | 0.006 | 1,37 | 3,0698 | 1,7400 | 3,7747 | 3,0103 |
| D12S1666 | 0.001 | 1,97 | 2,9340 | 1,6546 | 3,5812 | 2,7223 |
| NBG5 | 0.001 | 2,07 | 2,9781 | 1,2722 | 3,6505 | 2,7846 |
| D12S1721 | 0.005 | 2,17 | 2,9680 | 1,2630 | 3,6844 | 2,7752 |
| NBG8 | 0.011 | 2,67 | 3,0954 | 1,0804 | 3,4399 | 2,5654 |
| NBG6 | 0.0115 | 3,79 | 3,1632 | 1,0672 | 3,2670 | 2,5956 |
| NBG9 | 0.0035 | 4,95 | 2,2106 | 1,0137 | 2,7765 | 2,4456 |
| NBG10 | 0.001 | 5,30 | 2,5513 | 1,0251 | 2,7625 | 2,1914 |
| NBG12 | 0.009 | 5,40 | 2,4893 | 0,9868 | 2,6841 | 2,0920 |
| NBG4 | 0.001 | 6,31 | 2,9028 | 1,1312 | 3,4063 | 2,8156 |
| NBG3 | 0.006 | 6,41 | 2,9070 | 1,1326 | 3,4637 | 2,8300 |
| NBG2 | | 7,01 | 2,8430 | 1,1108 | 3,3135 | 2,7978 |

[0191] Multipoint results on the strata with ASPEX sib_phase by considering only independent sib-pairs (Figure 1b) or all sib-pairs (Figure 1c) are shown in Figures 1d and 1e. As previously reported a second peak appeared when all

sib-pairs were observed.

A confidence interval was calculated. GENEFINDER (Liang et al., Am. J. Hum. Genet. 66 (2000), 1631-1641) was used to estimate the location of the susceptibility gene (say t). The method is based on the IBD (Identity by Descent) sharing of affected sib-pairs for multiple markers. For the purpose of our analysis, pedigrees were divided into sibship.

5 56 nuclear families and 183 sib-pairs were used. Liang KY, Huang CY, Beaty TH (2000) A unified sampling approach for multipoint analysis of qualitative and quantitative traits in sib pairs. Am J Hum Genet 66:1631-1641
 [0192] The GENEFINDER results points to localization of a susceptibility gene for affective disorders at 3.19 ± 0.446 cM telomeric to the marker D12S1721 (D12S1721 is approximately located at 136.82 cM on the sex-averaged Marshfield chromosome 12 map).

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| | |
|-------|---------------------|
| 95% | C.I.: [2.32, 4.06]; |
| 99% | C. I.: [2.03, 4.35] |
| 99.9% | C. I.: [1.71, 4.67] |

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[0193] From the strata, 24 nuclei, and 107 sib-pairs were obtained, and the location of the susceptibility gene was estimated at 3.07 ± 0.57 (see map above). The following confidence interval (C.I.) was obtained:

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| | |
|-------|---------------------|
| 95% | C.I.: [1.95, 4.19]; |
| 99% | C. I.: [1.59, 4.55] |
| 99.9% | C. I.: [1.18, 4.96] |

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[0194] An association study using the NBG microsatellite markers was done with CLUMP (Sham & Curtis, Ann. Hum. Genet. 59 (1995), 97-105). Samples were distributed as follow: 83 male/case; 124 female/case; 95 male/control; and 101 female/control. One thousand simulations were used to estimate p-values. The observed results are summarized in Table 9.

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Table 9.

| Association study using the NBG microsatellite | | | | | | |
|--|--------|---------|--------------------------|--------------------------|--------------------------|--------------------------|
| Locus | Sample | | T1statistic (p-value) | T2statistic (p-value) | T3statistic (p-value) | T4statistic (p-value) |
| | Case | Control | | | | |
| NBG11 | 204 | 129 | 0.226 | 0.562 | 0.410 | 0.421 |
| NBG5 | 206 | 194 | 0.972 | 0.980 | 0.948 | 0.971 |
| NBG8 | 206 | 194 | 0.983 | 1.000 | 0.994 | 0.978 |
| NBG6 | 206 | 194 | 0.147 | 0.074 | 0.759 | 0.485 |
| NBG9 | 206 | 190 | 0.512 | 0.940 | 0.786 | 0.583 |
| NBG10 | 206 | 190 | 0.594 | 0.480 | 0.403 | 0.709 |
| NBG12 | 206 | 190 | 0.002 | 0.019 | 0.003 | 0.117 |

T1 statistic is the usual chi-squared statistic on the raw contingency table

T2 statistic is the usual chi-squared statistic apply on he contingency table obtained after collapsing columns with small expected values together

T3 statistic is the largest chi-squared statistic got by comparing one column of the original table against the total of the others columns

T4 statistic is the largest chi-squared statistic got by comparing any combination of alleles against the rest.

[0195] Only the NBG12 marker gave significant association at the 1% level. For the others markers, there was no single alleles that seems to be associated with bipolar disorder. It seems that no founder-alleles was overly represented among the affected. There is no significant result for association of genotypes with the NBG markers.

[0196] Further microsatellite marker based association studies using CLUMP was performed on samples containing additional control and case individuals. One thousand simulations were used to estimate p-values.

Table 9a.

| Empirical p-values observed with CLUMP for statistics T1 and T3 for allelic and genotypic analyses of microsatellite markers | | | | | | |
|--|-----------|----------|-----------------|-------------------|-----------------|-----------------|
| Name | Effective | | Alleles | | Genotypes | |
| | case | controls | T1 (p-value) | T3 (p-value) | T1 (p-value) | T3 (p-value) |
| NBG11 | 204 | 98 | 0.250 | 0.421 | 0.680 | 0.553 |
| D12S1666 | 208 | 175 | 0.366 | 0.543 | 0.393 | 0.476 |
| NBG5 | 213 | 179 | 0.969 | 0.934 | 0.997 | 1.000 |
| D12S1721 | 210 | 176 | 0.693 | 0.463 | 0.805 | 0.838 |
| NBG8 | 213 | 179 | 0.754 | 0.921 | 0.973 | 0.929 |
| NBG6 | 213 | 179 | 0.008 | 0.356 | 0.172 | 0.449 |
| NBG9 | 213 | 175 | 0.759 | 0.768 | 0.690 | 0.606 |
| NBG10 | 213 | 175 | 0.521 | 0.178 | 0.122 | 0.173 |
| D12S1349 | 212 | 180 | 0.887 | 0.864 | 0.782 | 0.816 |
| NBG12 | 213 | 175 | 0.002 | <10 ⁻³ | 0.018 | 0.552 |
| NBG4 | 207 | 178 | 0.418 | 0.506 | 0.813 | 0.545 |
| NBG3 | 209 | 175 | 0.171 | 0.829 | 0.601 | 0.897 |
| D12S378 | 211 | 180 | 0.171 | 0.405 | 0.540 | 0.560 |
| NBG2 | 210 | 170 | 0.896 | 0.749 | 0.210 | 0.613 |
| D12S1614 | 210 | 179 | 0.803 | 0.692 | 0.710 | 0.831 |
| D12S342 | 211 | 180 | 0.394 | 0.740 | 0.445 | 0.622 |
| D12S340 | 209 | 179 | 0.890 | 0.869 | 0.895 | 0.838 |
| D12S1639 | 209 | 180 | 0.087 | 0.170 | 0.652 | 0.295 |
| D12S1634 | 211 | 181 | 0.361 | 0.248 | 0.505 | 0.590 |
| D12S2075 | 203 | 181 | 0.023 | 0.157 | 0.085 | 0.451 |

[0197] HWE hypothesis was satisfied at the 5% level for each microsatellite marker after application of the conservative Bonferroni corrections for multiple testing (Bland & Altman, Brit. J. Med. 310 (1995) 170). Table 9a lists empirical p-values observed with CLUMP for allele and genotype association analyses. Empirical p-values less than 0.005 were observed at marker NBG12 for T1 and T3 statistics under allelic association analysis. T1 statistic suggested allelic association between bipolar affective disorders and NBG6 (empirical p-value=0.008). Moreover, a barely significant empirical p-value of 0.023 was observed at the most distal marker D12S2075.

[0198] In conclusion, the parametric and model-free multipoint results suggest to investigate genes located between D12S1619 and D12S1666. Moreover, according to GENEFINDER results, genes situated centromeric to NBG9 should be considered for association and linkage disequilibrium analysis. Moreover, positive association was seen with the NBG6 marker, which is located in intron 9 of the P2X7R gene.

EXAMPLE 2

Physical mapping and Mutation analysis of chromosome 12 associating the P2X7R to Bipolar Affective Disorders

[0199] The most conservative prediction for the disease-associated region is included between markers NBG11 and NBG2 (see Figure 1a). This region was delimited according to linkage and association analysis described in Example 1, using genethon markers and NBG markers. The approximate length of this region is 5,2 Mb. Two major gaps (between FLJ10701 and FLJ32372, and between FLJ1466 and MONDOA) were included in this region. At least 73 genes were listed in this area, where 48 are known genes and 25 are unknown but associated to mRNA and/or EST clusters based

on the last genome assembly available at UCSC (November 2002). Predicted genes were not listed. However, the estimation of CI 99% (confidence interval) using GENEFINDER has limited the most interesting region between markers D12S1666 and NBG9. This genomic region covers 1,6 Mb and includes at least 28 genes, and has no major gap. Thus, the term fBAD (familial Bipolar Affective Disorders) region was used to describe the genomic segment between D12S1666 and NBG9. Genes found within this region include CaMKK2, CABP, P2X7, P2X4, PIN, PLA2, G1B, CIT, PXN, Rab35, and APC5. However, given the present art, it would not have been obvious to an ordinary person skilled in the art to select P2X7R as the gene associated with affective diseases. Other genes from the ones listed above would be obvious.

[0200] For example, the CaMKK2 gene (also known as Ca²⁺/Calmodulin-dependent protein kinase kinase beta, or CaMKKb) is a serine/threonine protein kinase involved in Ca²⁺ dependent signalling pathways. CaMKK2 can activate in vitro the downstream kinases CaMKIV and CaMKI, which modulate gene transcription through phosphorylation of transcription factors (e.g., CREB, SRF, MEF2; Corcoran and Means, J. Biol. Chem. 276 (2001), 2975-2978; Soderling, Trends Biochem. Sci. 24 (1999), 232-236). Its role in the Ca²⁺ cascade is not critical. Some studies suggest that CaMKs could be activated without the CaMKs phosphorylation (Matsushita and Nairn, J. Biol. Chem. 274 (1998), 10086-10093). However, CaMKK phosphorylation step would contribute to amplification of the Ca²⁺ signal since CaMKK is more sensitive to activation by Ca²⁺/Calmodulin, therefore CaMKK would be an important mediator when the levels of intracellular Ca²⁺ are low (Anderson et al., J. Biol. Chem. 273 (1998), 31880-31889).

[0201] CaMKK2 is an obvious target for depression since prior art suggest that cAMP-dependent signaling pathways (mediated by PKA activation) is affected in brain from patients with Bipolar Affective Disorders (Field et al., J. Neurochem. 73 (1997), 1704-1710; Rahman et al., J. Neurochem. 68 (1997), 297-304; Takahashi et al., J. Neurosci. 19 (1999), 610-618). According to a study using lymphoblastic cell lines, Bipolar disorder could be related to a elevated intracellular calcium levels (Yoon et al., Mol. Psychiatry 6 (2001), 678-683). Moreover, some groups found relations between antidepressant drugs and CaMK activation (Budziszewska et al., Br. J. Pharmacol. 130 (2000), 1385-1393; Consogno et al., Neuropsychopharmacology 24 (2001), 21-30; Mori et al., Neuropharmacology 40 (2001), 448-456; Zanotti et al., Neuropharmacology 37 (1998), 1081-1089). Furthermore, inhibition of CaMKK by PKA-mediated phosphorylation suggest a close relationship between both pathways (Matsushita et al., J. Biol. Chem. 273 (1999), 21473-21481). These observations would suggest to a person skilled in the art that CaMKK2 is the gene responsible for bipolar affective disease.

[0202] Another obvious candidate for affective disorders would have been the CABP1 gene which generates four neuronal Ca²⁺-binding protein by alternative usage of the 9 coding exons, which are L-CABP, S-CABP, calbrain, and caldendrin (Haeseleer et al., J. Biol. Chem. 275 (2000), 1247-1260). Their expression is almost totally restricted to brain tissues. A functional study on calbrain reveals its negative effect on Ca²⁺/Calmodulin-dependent CaMKII activity by competitively interacts with the CaM-binding domain of CaMKII (Yamaguchi et al., J. Biol. Chem. 274 (1999), 3610-3616). One would expect similar roles in Ca²⁺ signaling for other CABP1 alternative products. Participation of CABP1 gene in Ca²⁺-dependent signaling pathways would make it obvious to one skilled in the art to select this gene as a candidate for bipolar affective disorder. However, all CABP1 exons were analyzed for the presence of mutations, and surprisingly only two mutations were detected in noncoding regions.

[0203] The PIN gene (Protein inhibitor of NOS (Nitric oxide synthase)) is another obvious candidate responsible for bipolar affective disorder. Nitric oxide (NO) in the brain, may be involved in apoptosis, synaptogenesis, and neuronal development. Because NO cannot be stored in vesicles like other neurotransmitters, its release is regulated by the activity of NOS (Nitric oxide synthase). PIN is a direct inhibitor of NOS by binding and destabilizing the active homodimer complex of NOS (Jaffrey et al., Science 274 (1996), 774-777). PIN is highly conserved throughout the evolution and is expressed in many cell types. A recent clinical study evaluating plasma nitrate levels in depressive states suggests that NO production is increased in depression (Suzuki et al., J. Affect. Disord. 63 (2001), 221-224) and may result from a deficiency in NOS inhibition. Moreover in a mouse model, NO synthase antagonists have been linked to antidepressant properties (Harkin et al., 1999; Karolewicz et al., Eur. J. Pharmacol. 372 (1999), 215-220). Thus, PIN would be an obvious However, due to the pleiotropic action of NO, a deficiency in PIN function would generate many unrelated disorders throughout the body. Thus, without the information presented in the disclosure herein, a person of ordinary skills in the art would have predicted PIN and not P2X7R as the gene associated with affective disorders.

[0204] The human phospholipase A2 group IB (PLA2G1B) catalyses the release of fatty acids from glycerol-3-phosphocholines. Phospholipase A2 genes (PLA2) are expressed in many tissues. Some studies have demonstrated associations between excessive PLA2 activity in brain and affective disorders (Chang et al., Neurochem. Res. 23 (1998), 887-892; Hibbeln et al., Biol. Psychiatry 25 (1989), 945-961). Moreover, other genetic studies have found associations between PLA2G1B gene and bipolar affective disorder (Dawson et al., Psychiatr. Genet. 5 (1995), 177-180). Thus, PLA2G1B represent a likely candidate for affective disorders. However in the present example, only a single silent mutation was found within exon 3 of the PLA2G1B gene.

[0205] The human citron kinase gene, Rho-associated protein (CIT) is a 183 kDa protein which associates to the GTPase Rho. CIT shares strong similarity with ROCK and ROK proteins which are other Rho-associated kinases

(Madaule et al., Nature 394 (1998), 491-494). Rho GTPases are involved in many processes such as cytoskeletal organization, membrane trafficking, cell growth, and transcriptional activation (Van Aelst and D'Souza-Schorey, Genes Dev. 11 (1997), 2295-2322). Studies on brain variants of Citron-K (without the kinase domain) reveal the association with postsynaptic density proteins (PSD-95), suggesting a role in either synapse organization or function (Zhang et al., J. Neurosci. 19 (1999), 96-108; Furuyashiki et al., J. Neurosci. 19 (1999), 109-118).

[0206] The human paxillin (PXN) gene encodes for a 68 kDa protein found in focal adhesions. It is within focal adhesions where adhesion molecules dynamically interact with the cytoskeleton (Salgia et al., J. Biol. Chem. 270 (1995), 5039-5047). The signaling pathways that regulate these dynamic interactions begin to be elucidated. Many observations suggest that paxillin is involved in transducing signals from growth factor receptors to focal adhesions.

The paxillin is expressed in many tissues including brain.

[0207] However as set forth below, the gene causative for affective diseases is identified as being the P2X7 receptor (P2X7R).

[0208] Mutations were searched in coding sequences and exon-intron boundaries of the above mentioned genes since such mutations are more likely to give a functionally significant Single Nucleotide Polymorphisms (SNP). The starting sample was composed of 16 unrelated affected individuals from the Saguenay/Lac St-Jean region, which gives an 80% power to detect polymorphisms with a frequency of 0.05. To identify polymorphisms, targeted sequences were first amplified by PCR. Then, PCR products are purified on Whatman GF/C membranes (VWR, Montreal, Canada), and quantified using the PicoGreen dsDNA quantitation assay (Molecular probes, Oregon, USA). 4 ng of purified PCR products are sequenced using the DYEnamic ET terminator cycle sequencing kit (Amersham Biosciences, Baie D'Urfé, Canada). The sequencing products are resolved on an ABI PRISM 3730XL DNA analyzer, and an ABI PRISM 3700 DNA analyzer. The PCR products are sequenced in both directions. The SNPs identified in studied genes are listed in Table 10.

Table 10.

| Mutation analysis between markers D12S1666 and NBG9 | | | | |
|---|-----------|-------------|---------|---------------|
| Genes | Positions | Variations | Alleles | Modifications |
| Rab35 | Exon06 | RABE06A | 486G-A | Silent Asn162 |
| Rab35 | Intron04 | RABI04A | 51C-T | unknown |
| Rab35 | Intron03 | RABI03A | 33G-A | unknown |
| Rab35 | Intron02 | RABI02B | 85G-A | unknown |
| Rab35 | Intron02 | RABI02A | 76C-G | unknown |
| PXN | Exon1 | PXNE11A | 1527C-T | Silent Thr509 |
| PXN | Exon06 | PXNE06A | 750C-T | Silent Ser250 |
| PXN | Exon02 | PXNE02A | 217G-A | Gly73Ser |
| PLA2G1B | Exon03 | PLA2G1BE03A | 294C-T | Silent Ser98 |
| PIN | 5'UTR01 | PINUTR01A | -49T-G | unknown |
| PIN | 5'UTR01 | PINUTR01B | -80T-C | unknown |
| PIN | Intron02 | PINI02A | 26C-T | unknown |
| PIN | Intron02 | PINI02B | 50C-T | unknown |
| CaBP | Intron04 | CaBPI04A | 35C-T | unknown |
| CaBP | exon01 | CaBPE01A | -23A-G | unknown |
| OASL | Exon02 | OASLE02A | 213G-T | Silent Gly72 |
| OASL | Exon02 | OASLE02B | 408C-T | Silent Leu136 |
| OASL | Exon05 | OASLE05A | 1042G-A | Va1348Met |
| OASL | Exon06 | OASLE06A | 1509G-A | Silent Ser503 |
| P2X7R | 5'UTR | P2XR7UTR5L | 362T-C | unknown |
| P2X7R | 5'UTR | P2XR7UTR5M | 532T-G | unknown |
| P2X7R | 5'UTR | P2XR7UTR5K | 1100A-G | unknown |
| P2X7R | 5'UTR | P2XR7UTR5J | 1122A-G | unknown |
| P2X7R | 5'UTR | P2XR7UTR5I | 1171C-G | unknown |
| P2X7R | 5'UTR | P2XR7UTR5F | 1351T-C | unknown |
| P2X7R | 5'UTR | P2XR7UTR5N | 1702G-A | unknown |

Table 10. (continued)

| Mutation analysis between markers D12S1666 and NBG9 | | | | |
|---|-----------|------------|--------------|---------------|
| Genes | Positions | Variations | Alleles | Modifications |
| P2X7R | 5'UTR | P2XR7UTR5G | 1731T-G | unknown |
| P2X7R | 5'UTR | P2XR7UTR5H | 1860C-T | unknown |
| P2X7R | 5'UTR | P2XR7UTR5A | 2162C-A | unknown |
| P2X7R | 5'UTR | P2XR7UTR5B | 2238C-T | unknown |
| P2X7R | 5'UTR | P2XR7UTR5D | 2373A-G | unknown |
| P2X7R | 5'UTR | P2XR7UTR5E | 2569G-A | unknown |
| P2X7R | 5'UTR | P2XR7UTR5C | 2702G-A | unknown |
| P2X7R | Intron01 | P2XR7I01C | 3166G-C | unknown |
| P2X7R | Intron01 | P2XR7I01A | 24778C-T | unknown |
| P2X7R | Intron01 | P2XR7I01B | 24830C-T | unknown |
| P2X7R | Exon02 | P2XR7v02A | 24942T-C | Val76Ala |
| P2X7R | Exon03 | P2XR7E03A | 26188C-T | Arg117Trp |
| P2X7R | Intron03 | P2XR7I03A | 26308A-G | unknown |
| P2X7R | Intron03 | P2XR7I03B | 26422G-A | unknown |
| P2X7R | Intron04 | P2XR7I04A | 32394G-A | unknown |
| P2X7R | Intron04 | P2XR7v05B | 32434T-C | unknown |
| P2X7R | Exon05 | P2XR7E05D | 32493G-A | Gly150Arg |
| P2X7R | Exon05 | P2XR7v05A | 32507C-T | Tyr155His |
| P2X7R | Exon05 | P2XR7E05C | 32783C-T | Silent Cys168 |
| P2X7R | Intron05 | P2XR7I05C | 32783A-C | unknown |
| P2X7R | Intron05 | P2XR7I05D | 35309T-C | unknown |
| P2X7R | Intron05 | P2XR7I05B | 35374C-T | unknown |
| P2X7R | Intron05 | P2XR7I05A | 35378A-C | unknown |
| P2X7R | Exon06 | P2XR7E06A | 35438G-A | Glu186Lys |
| P2X7R | Exon06 | P2XR7E06B | 35454T-C | Leu191Pro |
| P2X7R | Intron06 | P2XR7I06C | 35549T-C | unknown |
| P2X7R | Intron06 | P2XR7I06G | 35641G-C | unknown |
| P2X7R | Intron06 | P2XR7I06D | 35725A-C | unknown |
| P2X7R | Intron06 | P2XR7I06F | 36001T-G | unknown |
| P2X7R | Intron06 | P2XR7I06E | 36064A-T | unknown |
| P2X7R | Intron06 | P2XR7I06A | 36091De1GTTT | unknown |
| P2X7R | Intron06 | P2XR7I06B | 36108C-G | unknown |
| P2X7R | Intron07 | P2XR7I07A | 36374C-T | unknown |
| P2X7R | Intron07 | P2XR7I07B | 36378G-A | unknown |
| P2X7R | Intron07 | P2XR7I07C | 36387T-A | unknown |
| P2X7R | Intron07 | P2XR7I07D | 36398G-C | unknown |
| P2X7R | Intron07 | P2XR7I07E | 37439C-T | unknown |
| P2X7R | Intron07 | P2XR7I07F | 37513T-C | unknown |
| P2X7R | Exon08 | P2XR7E08C | 37604C-T | Arg270Cys |
| P2X7R | Exon08 | P2XR7v08A | 37605G-A | Arg270His |
| P2X7R | Exon08 | P2XR7v08B | 37623G-A | Arg276His |
| P2X7R | Exon08 | P2XR7E08D | 37633C-T | Silent Asp279 |
| P2X7R | Intron09 | P2XR7v11A | 47214C-T | unknown |
| P2X7R | Exon11 | P2XR7v11B | 47383G-A | Ala348Thr |
| P2X7R | Exon11 | P2XR7v11C | 47411C-G | Thr357Ser |
| P2X7R | Intron11 | P2XR7I11D | 47563T-C | unknown |
| P2X7R | Intron12 | P2XR7I12A | 54307C-T | unknown |
| P2X7R | Intron12 | P2XR7I12B | 54308G-A | unknown |

Table 10. (continued)

| Mutation analysis between markers D12S1666 and NBG9 | | | | |
|---|-----------|--------------|-----------------------------------|----------------------------------|
| Genes | Positions | Variations | Alleles | Modifications |
| P2X7R | Exon13 | P2XR7v13F | 54399C-T | Ala433Val |
| P2X7R | Exon13 | P2XR7v13A | 54480A-G | Gln460Arg |
| P2X7R | Exon13 | P2XR7v13B | 54523C-T | Silent Pro474 |
| P2X7R | Exon13 | P2XR7v13G | 54562DelCCCTGAGAG CCACAGGTGCCT | Del of 7aa 488 to 494 PESHRCL |
| P2X7R | Exon13 | P2XR7v13C | 54588A-C | Glu496A1a |
| P2X7R | Exon13 | P2XR7v13H | 54664C-G | Silent His521 |
| P2X7R | Exon13 | P2XR7E13D | 54703G-T | Silent Leu534 |
| P2X7R | Exon13 | P2XR7E13J | 54804A-T | Ile568Asn |
| P2X7R | Exon13 | P2XR7v13I | 54834G-A | Arg578Gln |
| P2X7R | Exon13 | P2XR7v13E | 54847G-A | Silent Pro582 |
| P2X7R | 3'UTR | P2XR7UTR3A | 55169C-A | unknown |
| P2X7R | 3'UTR | P2XR7UTR3B | 55170A-C | unknown |
| P2X7R | 3'UTR | P2XR7UTR3C | 55171A-C | unknown |
| P2X7R | 3'UTR | P2XR7UTR3D | 55917C-T | unknown |
| P2X7R | 3'UTR | P2XR7UTR3E | 54925G-A | unknown |
| P2X4R | 5'UTR | P2XR4UTR5I | -1956G-A | unknown |
| P2X4R | 5'UTR | P2XR4UTR5H | -1649G-A | unknown |
| P2X4R | 5'UTR | P2XR4UTR5G | -800G-A | unknown |
| P2X4R | 5'UTR | P2XR4UTR5A | -648C-A | unknown |
| P2X4R | 5'UTR | P2XR4UTR5B | -537A-G | unknown |
| P2X4R | 5'UTR | P2XR4UTR5C | -437A-G | unknown |
| P2X4R | 5'UTR | P2XR4UTR5J | -206VNRG | unknown |
| P2X4R | 5'UTR | P2XR4UTR5D | -211C-G | unknown |
| P2X4R | 5'UTR | P2XR4UTR5F | -150VNRGGGCCCC | unknown |
| P2X4R | 5'UTR | P2XR4UTR5E | -98G-T | unknown |
| P2X4R | Intron01 | P2XR4I01A | 31G-T | Silent mutation Ala87 |
| P2X4R | Exon02 | P2XR4E02A | 262G-A | unknown |
| P2X4R | Intron02 | P2XR4I02A | 4600C-T | unknown |
| P2X4R | Intron03 | P2XR4I03A | 15G-A | unknown |
| P2X4R | Intron03 | P2XR4I03B | 72G-A | unknown |
| P2X4R | Exon04 | P2XR4E04A | 355G-A | Ile119Val |
| P2X4R | Exon04 | P2XR4E04A | 375G-A | Silent Val125 |
| P2X4R | Intron04 | P2XR4I04B | 17T-C | unknown |
| P2X4R | Intron04 | P2XR4I04A | 32G-A | unknown |
| P2X4R | Exon05 | P2XR4E05A | 465T-C | Silent Ser155 |
| P2X4R | Exon07 | P2XR4E07A | 724A-G | Ser242Gly |
| P2X4R | Intron08 | P2XR4I08A | DelT | unknown |
| P2X4R | Exon09 | P2XR4E09A | 944A-G | Tyr315Cys |
| P2X4R | Intron10 | P2XR4I10A | 11G-T | unknown |
| P2X4R | Intron10 | P2XR4I10B | G-C | unknown |
| P2X4R | Intron10 | P2XR4I10C | A-G | unknown |
| P2X4R | Intron11 | P2XR4I11B | C-G | unknown |
| P2X4R | Intron11 | P2XR4I11C | T-A | unknown |
| P2X4R | Intron11 | P2XR4I11A | 374C-T | unknown |
| CaMKK2 | 3'UTR | CaMKK2UTR3bA | 733C-T | unknown |
| CaMKK2 | 3'UTR | CaMKK2UTR3aB | 390G-A | unknown |
| CaMKK2 | 3'UTR | CaMKK2UTR3aA | 239G-A | unknown |

Table 10. (continued)

| Mutation analysis between markers D12S1666 and NBG9 | | | | |
|---|-----------|--------------|------------------------|---------------|
| Genes | Positions | Variations | Alleles | Modifications |
| CaMKK2 | Intron 15 | CaMKK2I15B | 325T-C | unknown |
| CaMKK2 | Intron15 | CaMKK2I15A | 169G-A | unknown |
| CaMKK2 | Intron14 | CaMKK2I14A | 224A-G | unknown |
| CaMKK2 | Intron10 | CaMKK2I10A | 156DelGTGATCCGCCT G | unknown |
| CaMKK2 | intron09 | CaMKK2I09B | 528A-G | unknown |
| CaMKK2 | intron09 | CaMKK2I09A | 521A-G | unknown |
| CaMKK2 | Exon09 | SNP6f18v5 | 1095C-A | Silent Ile365 |
| CaMKK2 | Exon09 | SNP6f18v4 | 1087C-T | Arg363Cys |
| CaMKK2 | Exon05 | CaMKKE05A | 687C-T | Silent Pro229 |
| CaMKK2 | Intron03 | CaMKK2I03A | 10C-T | unknown |
| CaMKK2 | Intron02 | CaMKK2I02A | 39C-T | unknown |
| CaMKK2 | Intron01 | CaMKK2I01B | 2911G-C | unknown |
| CaMKK2 | Intron01 | CaMKK2I01 A | 89C-A | unknown |
| CaMKK2 | Exon01 | SNP6f18v2 | 253A-T | Thr85Ser |
| CaMKK2 | Exon01 | SNP6f18v1 | 29G-A | Ser10Asn |
| CaMKK2 | 5'UTR01 | CaMKK2UTR01B | 253T-C | unknown |
| CaMKK2 | 5'UTR01 | CaMKK2UTR01A | 63C-A | unknown |
| APC5 | Intron01 | APC5I01A | 10G-T | unknown |
| APC5 | Intron01 | APC5I01B | 50A-T | unknown |
| APC5 | Intron05 | APC5I05A | 73T-C | unknown |
| APC5 | Intron06 | APC5I06A | 73T-G | unknown |
| APC5 | Exon1 | APC5E11A | 1416C-T | Silent His472 |

[0209] Each SNP in genes Rab35, PXN, PLA2G1B, PIN, CaBP, OASL, P2X4R, CaMKK2 and APC5 was designated according to the gene where it was found, and its location in that gene (intronic or exonic regions). Each SNP in the P2X7R gene was designated according to their position on SEQ ID NO: 1. The allele describes the position and the variation observed. In coding regions, the position is relative to the start codon, whereas the intronic SNPs are positioned relative to the beginning of the corresponding intron (when known). Primers used for identifying the SNPs in the P2X7R and the location of each SNPs included in tables 2 and 12 are defined in table 1a and SEQ ID NOs 52 to 111.

[0210] Association studies using missense SNPs were performed. Missense SNPs or SNPs that could be close to the splice sites were used, because it is more likely that diseases would be associated to an improper function in proteins. Case group was composed by bipolar I individuals, schizoaffective bipolar type (182 subjects) and bipolar II diagnosed persons (31 subjects). Many controls from the Saguenay/Lac-St-Jean region, were sampled from Steinert, Glaucoma and Paget DNA banks. The control individuals were not diagnosed for affective disorders. According to the lifetime risks of bipolar disorders (1%), there is no need to screen controls for psychiatric disorders.

[0211] Direct sequencing of PCR products is by far the most accurate method of analysis and is the method of choice in view of our sequencing platform capacity. PCR products were analyzed by direct sequencing as described above. After sequencing analysis, individuals are automatically typed for the corresponding SNP using a home-developed program, GENO.pl. The results of SNP genotyping are compiled in a 4D database.

[0212] The association hypothesis was tested with CLUMP (Sham & Curtis 1995, Ann. Hum. Genet. 59:97-105). One thousand simulations were used to estimate p-values. Results are illustrated in table 11. The T1 statistic, which is the usual chi-squared statistic on the raw contingency table, was used to test for allelic association. Moreover, the largest chi-squared statistic got by comparing one column of the original table against the total of the other columns, called T3 statistic, was added to the previous one to test for potential genotype association since T1 statistic results may be biased when the contingency table contains cells with low values.

Table 11. Association hypothesis using CLUMP

| gene | SNPs | Effective | | Allele Analysis p-value (T1) | Genotype Analysis | |
|--------|-----------|-----------|----------|------------------------------------|-------------------|-----------------|
| | | Cases | Controls | | p-value (T2) | p-value (T3) |
| P2X7R | P2XR7v11B | 208 | 211 | 0.795 | 0.036 | 0.028 |
| | P2XR7v13A | 212 | 214 | 0.344 | 0.250 | 0.186 |
| | P2XR7v13E | 212 | 211 | 0.780 | 0.017 | 0.017 |
| CAMKK2 | SNP6f18v5 | 206 | 135 | 1.00 | 1.00 | 1.00 |
| | SNP6f18v4 | 206 | 135 | 0.816 | 0.962 | 0.841 |
| | SNP6f18v2 | 205 | 135 | 0.057 | 0.110 | 0.095 |
| | SNP6f18v1 | 206 | 135 | 0.512 | 0.532 | 0.385 |

[0213] The association studies using SNPs in P2X7, P2X4, and CaMKK2 reveal associations significant at level of about 5% or less. Three genotype associations in P2X7 were observed. However, SNPs P2XR7v11B and P2XR7v13E are closely linked together based on a contingency table. There is also an allele association at level of 5,7% for

SNP6f18v2 in CaMKK2. The information associated to each relevant SNP can be found in Tables 10 and 12.

[0214] Further association studies using CLUMP were performed on samples that contain more case and control individuals. One thousand simulations were used to estimate p-values.

Table 11a.

| Empirical p-values and odds ratio (OR) with 95% confidence interval observed with CLUMP for alleles and genotypes analysis of SNPs | | | | | | | | | |
|--|-------------------------|------------------------|-----------|----------|-----------------|------|-----------------|---------------|---------------|
| Gene | Marker (marker rank) | Allele Frequencies | Effective | | Alleles Alleles | | | Genotypes | |
| | | | case | controls | T1 p-value | OR | OR 95% CI | T1 p-value | T3 p-value |
| P2XR7 | P2XR7UTR5F (1) | C (0.18); T (0.82) | 212 | 208 | 0.280 | 1.21 | 0.86- 1.71 | 0.067 | 0.069 |
| | P2XR7UTR5G (2) | G (0.09); T (0.91) | 211 | 204 | 0.481 | 1.19 | 0.76- 1.87 | 0.261 | 0.231 |
| | P2XR7UTR5H (3) | C (0.95); T (0.05) | 210 | 202 | 0.549 | 1.19 | 0.67- 2.13 | 0.768 | 0.582 |
| | P2XR7UTR5A (4) | A (0.05); C (0.95) | 210 | 207 | 0.526 | 1.26 | 0.68- 2.34 | 0.754 | 0.517 |
| | P2XR7UTR5B (5) | C (0.78); T (0.22) | 211 | 207 | 0.629 | 1.09 | 0.79- 1.50 | 0.104 | 0.128 |
| | P2XR7UTR5D (6) | A (0.96); G (0.04) | 211 | 205 | 0.268 | 1.43 | 0.77-2.65 | 0.598 | 0.240 |
| | P2XR7UTR5E (7) | A (0.04); G (0.96) | 211 | 210 | 0.658 | 1.23 | 0.65-2.33 | 0.139 | 0.234 |
| | P2XR7UTR5C (8) | A (0.22); G (0.78) | 208 | 210 | 0.889 | 1.04 | 0.75-1.44 | 0.168 | 0.293 |
| | P2XR7I01B (9) | C (0.98); T (0.02) | 210 | 207 | 0.352 | 1.71 | 0.67-4.39 | 0.348 | 0.348 |
| | P2XR7v02A (10) | C (0.05); T (0.95) | 211 | 208 | 0.189 | 1.49 | 0.84-2.64 | 0.397 | 0.167 |
| | P2XR7I04A (11) | A (0.01); G (0.99) | 211 | 211 | 0.344 | 0.25 | 0.03-2.23 | 0.356 | 0.356 |

Table 11a. (continued)

| Empirical p-values and odds ratio (OR) with 95% confidence interval observed with CLUMP for alleles and genotypes analysis of SNPs | | | | | | | | | |
|---|-------------------------|-----------------------|-----------|----------|-----------------|------|-----------------|---------------|---------------|
| Gene | Marker (marker rank) | Allele Frequencies | Effective | | Alleles Alleles | | | Genotypes | |
| | | | case | controls | T1 p-value | OR | OR 95% CI | T1 p-value | T3 p-value |
| | P2XR7v05B (12) | C (0.75); T (0.25) | 212 | 211 | 0.854 | 1.03 | 0.76-1.41 | 0.234 | 0.335 |
| | P2XR7E05D (13) | A (0.01); G (0.99) | 211 | 211 | 0.726 | 1.51 | 0.42-5.38 | 0.735 | 0.735 |
| | P2XR7v05A (14) | C (0.48); T (0.52) | 211 | 209 | 0.638 | 1.07 | 0.82-1.40 | 0.895 | 0.895 |
| | P2XR7E05C (15) | C (0.97); T (0.03) | 210 | 211 | 0.195 | 0.45 | 0.16-1.31 | 0.349 | 0.276 |
| | P2XR7I07E (16) | C (0.64); T (0.36) | 208 | 214 | 0.394 | 0.87 | 0.66-1.16 | 0.057 | 0.064 |
| | P2XR7v08A (17) | A (0.24); G (0.76) | 210 | 212 | 0.221 | 1.22 | 0.90-1.67 | 0.433 | 0.496 |
| | P2XR7v08B (18) | A (0.05); G (0.95) | 210 | 213 | 0.386 | 0.71 | 0.36-1.41 | 0.520 | 0.662 |
| | P2XR7V11A (19) | C (0.88); T (0.12) | 213 | 149 | 0.394 | 0.80 | 0.50-1.29 | 0.387 | 0.463 |
| | P2XR7v11 B (20) | A (0.36); G (0.64) | 208 | 211 | 0.795 | 1.04 | 0.79-1.38 | 0.036 | 0.028 |
| | P2XR7v11C (21) | C (0.89); G (0.11) | 211 | 212 | 0.409 | 0.82 | 0.52-1.28 | 0.303 | 0.661 |
| | P2XR7v13F (22) | C (0.99); T (0.01) | 196 | 207 | 0.030 | 3.24 | 1.04-10.12 | 0.039 | 0.039 |
| | P2XR7v13A (23) | A (0.84); G (0.16) | 212 | 214 | 0.344 | 1.21 | 0.85-1.72 | 0.250 | 0.186 |

Table 11a. (continued)

| Empirical p-values and odds ratio (OR) with 95% confidence interval observed with CLUMP for alleles and genotypes analysis of SNPs | | | | | | | | | |
|--|-------------------------|-----------------------|-----------|----------|-----------------|------|-----------------|---------------|---------------|
| Gene | Marker (marker rank) | Allele Frequencies | Effective | | Alleles Alleles | | | Genotypes | |
| | | | case | controls | T1 p-value | OR | OR 95% CI | T1 p-value | T3 p-value |
| | P2XR7v13B (24) | C (0.89); T (0.11) | 207 | 212 | 0.494 | 0.83 | 0.53-1.31 | 0.315 | 0.699 |
| | P2XR7v13C (25) | A (0.77); C(0.23) | 211 | 213 | 0.731 | 0.95 | 0.68-1.31 | 0.557 | 0.616 |
| | P2XR7V13H (26) | C (0.98); G (0.02) | 211 | 213 | 0.238 | 1.75 | 0.68-4.49 | 0.236 | 0.236 |
| | P2XR7E13D (27) | G (0.89); T (0.11) | 211 | 213 | 0.435 | 0.82 | 0.53-1.28 | 0.268 | 0.680 |
| | P2XR7E13J (28) | A (0.03); T (0.97) | 204 | 199 | 0.179 | 0.48 | 0.16-1.42 | 0.329 | 0.329 |
| | P2XR7v13E (29) | A (0.36); G (0.64) | 212 | 213 | 0.841 | 1.04 | 0.79-1.37 | 0.026 | 0.025 |
| | P2XR7UTR3E (30) | A (0.04); G (0.96) | 205 | 197 | 1.000 | 0.96 | 0.45-2.04 | 1.000 | 1.000 |
| | P2XR7UTR3A (31) | A (0.47); C (0.53) | 208 | 209 | 0.932 | 0.99 | 0.75-1.30 | 0.264 | 0.239 |
| | P2XR7UTR3B (32) | A (0.92); C (0.08) | 208 | 210 | 0.174 | 0.65 | 0.38-1.14 | 0.151 | 0.303 |
| | P2XR7UTR3C (33) | A (0.95); C (0.05) | 208 | 210 | 0.395 | 0.71 | 0.36-1.40 | 0.508 | 0.667 |
| | | | | | | | | | |
| P2XR4 | UTR5A | A (0.18); C (0.82) | 212 | 210 | 0.285 | 0.82 | 0.57-1.18 | 0.514 | 0.484 |

Table 11a. (continued)

| Empirical p-values and odds ratio (OR) with 95% confidence interval observed with CLUMP for alleles and genotypes analysis of SNPs | | | | | | | | | |
|---|-------------------------|-----------------------|-----------|----------|-----------------|------|-----------------|---------------|---------------|
| Gene | Marker (marker rank) | Allele Frequencies | Effective | | Alleles Alleles | | | Genotypes | |
| | | | case | controls | T1 p-value | OR | OR 95% CI | T1 p-value | T3 p-value |
| | UTR5B | A (0.69); G (0.31) | 212 | 210 | 0.670 | 0.93 | 0.70-1.25 | 0.833 | 0.833 |
| | 106A | C (0.84); T (0.16) | 207 | 192 | 0.212 | 0.78 | 0.53-1.16 | 0.398 | 0.217 |
| | E07A | A (0.84); G (0.16) | 212 | 208 | 0.294 | 0.81 | 0.55-1.19 | 0.536 | 0.479 |
| | UTR3A | C (0.74); G (0.26) | 211 | 203 | 0.015 | 1.50 | 1.11-2.02 | 0.021 | 0.014 |
| | UTR3B | A (0.97); T (0.03) | 211 | 209 | 0.653 | 0.81 | 0.33-1.97 | 0.649 | 0.649 |
| | UTR3C | C (0.03); G (0.97) | 211 | 209 | 0.653 | 0.81 | 0.33-1.97 | 0.672 | 0.672 |
| | | | | | | | | | |
| CAMK K2 | E09B | A (0.03); C (0.97) | 208 | 214 | 0.830 | 0.85 | 0.36-2.00 | 0.829 | 0.829 |
| | E09A | C (0.83); T (0.17) | 208 | 214 | 0.202 | 0.78 | 0.54-1.14 | 0.446 | 0.473 |
| | E01B | A (0.35); T (0.65) | 207 | 214 | 0.048 | 1.33 | 1.01-1.76 | 0.126 | 0.218 |
| | E01A | C (0.93); T (0.07) | 208 | 214 | 0.189 | 1.44 | 0.86-2.39 | 0.439 | 0.237 |

[0215] Thirty-three SNPs in P2X7R, seven SNPs in P2X4R, and four SNPs in CAMKK2, with minor allele frequency higher or equal to 1% were genotyped (Table 11a). The genotype distributions of these SNPs did not deviate significantly from HWE. At the 5% level, statistically significant increases of minor allele frequency were observed in the bipolar affective disorder group at p2XR7v13F (p-value=0.030, OR=3.24, 95% CI=1.04-10.12), P2XR4UTR3A (p-value=0.015, OR=1.50, 95% CI=1.11-2.02) and CAMKK2E01B (p-value=0.048, OR=1.33, 95% CI=1.01-1.76). The distribution of genotypes at SNPs P2XR7v13F and P2XR4UTR3A also differed significantly at this level for T1 and T3 statistics, with an increase of heterozygotes in the case sample. One SNP from exon 11 of P2X7R, P2XR7v11B, and another from exon 13, P2XR7v13E, displayed difference in genotype distributions with minimum p-value of 0.028 and 0.025 observed both with T3 statistic. Again, increase in heterozygote frequency of 12% and 13% were respectively observed in the bipolar sample at these polymorphisms.

[0216] Significant haplotypic association tests led to p-values less than 0.5% for different SNP groups overlapping the P2X7R gene (Table 11b). Considering the SNPs collection ranging from SNP32507 to SNP54847 (table 11c) as an example for haplotype distribution, we observed the largest difference of frequencies between cases and controls with the haplotype no 1 (table 11d). The haplotype no 2 is another example of haplotype that is more frequently observed in cases group. On the other hand, the frequency for haplotype no 3 is slightly increased in control sample (difference of frequencies = 0.091). Table 11e presents the peptidic products derived from the nucleotidic haplotypes shown in table 11d.

Table 11b.

| Haplotypes showing allelic association significant at the 0.5% level for T1 or T3 statistics. | | | | | | | |
|---|-------|-----------------------|---------------------|---------|-----------------|-----------------|-------------------------|
| Haplotype (marker ranks ¹) | #SNPs | Distance ² | Haplotype effective | | T1 statistic | T3 statistic | #haplotype ³ |
| | | (bp) | case | control | (p- value) | (p- value) | |
| P2XR7101 B- P2XR7v13A (9-23) | 15 | 29618 | 361 | 257 | 0.0003 | 0.0252 | 20 |
| P2XR7v02A- P2XR7v13B (10-24) | 15 | 29550 | 361 | 260 | 0.00008 | 0.0294 | 20 |
| P2XR7104A- P2XR7v13C (11-25) | 15 | 22164 | 360 | 264 | 0.0003 | 0.0323 | 19 |
| P2XR7v05B- P2XR7v13H (12-26) | 15 | 22200 | 361 | 265 | 0.0004 | 0.0065 | 18 |
| P2XR7E05D- P2XR7E13D (13-27) | 15 | 22180 | 365 | 268 | 0.0035 | 0.0287 | 16 |
| P2XR7v05A- P2XR7E13J (14-28) | 15 | 22267 | 352 | 246 | 0.0007 | 0.0163 | 15 |
| P2XR7E05C- P2XR7v13E (15-29) | 15 | 22269 | 353 | 250 | 0.0012 | 0.0200 | 10 |
| P2XR7107E- P2XR7UTR3E (16-30) | 15 | 17452 | 355 | 247 | 0.0020 | 0.0192 | 11 |

The marker ranks of SNPs in the haplotype indicated in table 11b refer to those genotyped in table 11a

²Distance between the two most distal SNPs of the haplotype

³Number of haplotypes with frequencies > 1 % in case or control groups.

Table 11c.

| Position and Allele for haplotype-forming SNPs. Haplotypes are described in table 11d. | | |
|--|--------------|----------|
| SEQ ID NO | Polymorphism | Position |
| 1 | C-T | 32507 |
| 1 | C-T | 32548 |

Table 11c. (continued)

| Position and Allele for haplotype-forming SNPs. Haplotypes are described in table 11d. | | |
|--|--------------|----------|
| SEQ ID NO | Polymorphism | Position |
| 1 | C-T | 37439 |
| 1 | G-A | 37605 |
| 1 | G-A | 37623 |
| 1 | C-T | 47214 |
| 1 | G-A | 47383 |
| 1 | C-G | 47411 |
| 1 | C-T | 54399 |
| 1 | A-G | 54480 |
| 1 | C-T | 54523 |
| 1 | A-C | 54588 |
| 1 | C-T | 54664 |
| 1 | G-T | 54703 |
| 1 | T-A | 54804 |
| 1 | G-A | 54847 |

Table 11d.

| haplotypes with significant difference of frequencies between affected and control individuals. | | | | | | | | | | |
|---|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| Haplotype | 32507 | 32548 | 37439 | 37605 | 37623 | 47214 | 47383 | 47411 | 54399 | 54480 |
| No 1 | C | C | C | A | G | C | G | C | C | A |
| No 2 | C | C | C | G | G | C | G | C | C | A |
| No 3 | C | C | T | G | G | C | A | C | C | A |

| Haplotype | 54523 | 54588 | 54664 | 54703 | 54804 | 54847 | F _{affected} | F _{controls} |
|-----------|-------|-------|-------|-------|-------|-------|-----------------------|-----------------------|
| No 1 | C | A | C | G | T | G | 0.20 | 0.13 |
| No 2 | C | C | C | G | T | G | 0.05 | 0.01 |
| No 3 | C | A | C | G | T | A | 0.11 | 0.20 |

Table 11e.

| Corresponding amino acids for cSNPs described in table 11c. They are positioned according to SEQ ID NO3. | | | | | | | |
|--|-----|-----|-----|-----|-----|-----|-----|
| Position in SEQ ID NO3 | 155 | 168 | 270 | 276 | 348 | 357 | 433 |
| Haplotype 1 | Y | C | H | R | A | T | A |
| Haplotype 2 | Y | C | R | R | A | T | A |
| Haplotype 3 | Y | C | R | R | T | T | A |

| Position in SEQ ID NO3 | 460 | 474 | 496 | 521 | 534 | 568 | 582 |
|------------------------|-----|-----|-----|-----|-----|-----|-----|
| Haplotype 1 | Q | P | E | H | L | I | P |
| Haplotype 2 | Q | P | A | H | L | I | P |
| Haplotype 3 | Q | P | E | H | L | I | P |

EXAMPLE 3**Polymorphisms found in the P2X7R in individuals suffering from depression**

[0217] Association studies using SNPs in the P2X7R gene was performed in a case/control sample (535 individuals) from a German population. The case group was composed of 36 individuals diagnosed with bipolar type I or type II, and 279 individuals diagnosed with unipolar disorders (i.e. depression) representing 133 affected males and 182 affected females. Among controls, we count The remaining 220 control individuals were normal (i.e. diagnosed as non depressive), and comprising 81 males, 182 females and 14 of unknown gender. The same sexual distribution was noted in both groups.

[0218] SNPs were identified in this sample by using a subgroup of 24 affected individuals. SNPs in the P2X7R gene detected in the German population were similar if not identical to the SNPs seen in the Saguenay/Lac-St-Jean population (see table 12). Other rare missense SNPs were also noted in the German population, such as Arg117Trp (P2XR7E03A), Glu186Lys (P2XR7E06A), Leu191Pro (P2XR7E06B), Ile568Asn (P2XR7E13J). These amino acids are quite conserved between ortholog P2X7 genes. It is possible that the Ile568Asn (P2XR7E13J) mutation may be involved in the surface expression of P2X7.

Table 12.

| Comparison between polymorphisms in the Saguenay/Lac-St-Jean population and the German population in the human P2XR7R gene | | | | | | |
|--|---------------------------|--------|-----------|--------------|--------------------|---------------------|
| Associated exons or Introns | Variation (SNP or others) | Allele | Position* | Modification | Frequency (Canada) | Frequency (Germany) |
| 5'UTR | P2XR7UTR5L | T-C | 362 | unknown | 0,13 | 0,08 |
| 5'UTR | P2XR7UTR5M | T-G | 532 | unknown | 0,16 | 0,1 |
| 5'UTR | P2XR7UTR5K | A-G | 1100 | unknown | 0,13 | 0,13 |
| 5'UTR | P2XR7UTR5J | A-G | 1122 | unknown | 0,13 | 0,13 |
| 5'UTR | P2XR7UTR5I | C-G | 1171 | unknown | 0,06 | 0,02 |
| 5'UTR | P2XR7UTR5F | T-C | 1351 | unknown | 0,3 | 0,12 |
| 5'UTR | P2XR7UTR5N | G-A | 1702 | unknown | - | 0,02 |
| 5'UTR | P2XR7UTR5G | T-G | 1731 | unknown | 0,17 | 0,15 |
| 5'UTR | P2XR7UTR5H | C-T | 1860 | unknown | 0,07 | 0,15 |
| 5'UTR | P2XR7UTR5A | C-A | 2162 | unknown | 0,07 | 0,12 |
| 5'UTR | P2XR7UTR5B | C-T | 2238 | unknown | 0,3 | 0,27 |
| 5'UTR | P2XR7UTR5D | A-G | 2373 | unknown | 0,07 | 0,12 |
| 5'UTR | P2XR7UTR5E | G-A | 2569 | unknown | 0,1 | 0,02 |
| 5'UTR | P2XR7UTR5C | G-A | 2702 | unknown | 0,31 | 0,27 |
| Intron01 | P2XR7I01C | G-C | 3166 | unknown | 0,03 | - |
| Intron01 | P2XR7I01A | C-T | 24778 | unknown | 0,03 | - |
| Intron01 | P2XR7I01B | C-T | 24830 | unknown | 0,03 | RARE |
| Exon02 | P2XR7v02A | T-C | 24942 | Val76Ala | 0,06 | 0,08 |
| Exon03 | P2XR7E03A | C-T | 26188 | Arg117Trp | - | RARE |
| Intron03 | P2XR7I03A | A-G | 26308 | unknown | 0,7 | 0,44 |
| Intron03 | P2XR7I03B | G-A | 26422 | unknown | 0,18 | 0,12 |
| Intron04 | P2XR7I04A | G-A | 32394 | unknown | 0,03 | 0,01 |

Table 12. (continued)

| Comparison between polymorphisms in the Saguenay/Lac-St-Jean population and the German population in the human P2X7R gene | | | | | | |
|---|---------------------------|---------|-------------|---------------|--------------------|---------------------|
| Associated exons or Introns | Variation (SNP or others) | Allele | Position* | Modification | Frequency (Canada) | Frequency (Germany) |
| Intron04 | P2XR7v05B | T-C | 32434 | unknown | 0,33 | 0,29 |
| Exon05 | P2XR7E05D | G-A | 32493 | Gly150Arg | RARE | 0,02 |
| Exon05 | P2XR7E05E | G-A | 32506 | Silent Val154 | - | RARE |
| Exon05 | P2XR7v05A | C-T | 32507 | Tyr155His | 0,33 | 0,44 |
| Exon05 | P2XR7E05C | C-T | 32548 | Silent Cys168 | RARE | 0,02 |
| Intron05 | P2XR7I05C | A-C | 32783 | unknown | 0,25 | - |
| Intron05 | P2XR7I05D | T-C | 35309 | unknown | ND | 0,35 |
| Intron05 | P2XR7I05B | C-T | 35374 | unknown | 0,7 | 0,67 |
| Intron05 | P2XR7I05A | A-C | 35378 | unknown | 0,7 | 0,65 |
| Exon06 | P2XR7E06A | G-A | 35438 | Glu186Lys | - | 0,02 |
| Exon06 | P2XR7E06B | T-C | 35454 | Leu191Pro | - | 0,02 |
| Intron06 | P2XR7I06C | T-C | 35549 | unknown | 0,04 | 0,08 |
| Intron06 | P2XR7I06G | G-C | 35641 | unknown | - | 0,02 |
| Intron06 | P2XR7I06D | A-C | 35725 | unknown | 0,21 | 0,27 |
| Intron06 | P2XR7I06F | T-G | 36001 | unknown | 0,17 | 0,3 |
| Intron06 | P2XR7I06E | A-T | 36064 | unknown | 0,11 | 0,1 |
| Intron06 | P2XR7I06A | DelGTTT | 36091-36094 | unknown | 0,14 | 0,3 |
| Intron06 | P2XR7I06B | C-G | 36108 | unknown | 0,14 | 0,29 |
| Intron07 | P2XR7I07A | C-T | 36374 | unknown | 0,07 | - |
| Intron07 | P2XR7I07B | G-A | 36378 | unknown | 0,21 | 0,28 |
| Intron07 | P2XR7I07C | T-A | 36387 | unknown | 0,21 | 0,28 |
| Intron07 | P2XR7I07D | G-C | 36398 | unknown | 0,42 | 0,4 |
| Intron07 | P2XR7I07E | C-T | 37439 | unknown | 0,41 | - |

Table 12. (continued)

| Associated exons or Introns | Variation (SNP or others) | Allele | Position* | Modification | Frequency (Canada) | Frequency (Germany) |
|--------------------------------|------------------------------|-------------------------------|-------------|------------------------------------|-----------------------|------------------------|
| Intron07 | P2XR7I07F | T-C | 37513 | unknown | - | RARE |
| Exon08 | P2XR7E08C | C-T | 37604 | Arg270Cys | RARE | - |
| Exon08 | P2XR7v08A | G-A | 37605 | Arg270His | 0,46 | 0,24 |
| Exon08 | P2XR7v08B | G-A | 37623 | Arg276His | 0,03 | 0,02 |
| Exon08 | P2XR7E08D | C-T | 37633 | Silent Asp279 | RARE | - |
| Intron09 | P2XR7v11A | C-T | 47214 | unknown | 0,08 | 0,03 |
| Exon11 | P2XR7v11B | G-A | 47383 | Ala348Thr | 0,5 | 0,44 |
| Exon11 | P2XR7v11C | C-G | 47411 | Thr357Ser | 0,08 | 0,07 |
| Intron11 | P2XR7I11D | T-C | 47563 | unknown | 0,43 | 0,44 |
| Intron12 | P2XR7I12A | C-T | 54307 | unknown | 0,32 | - |
| Intron12 | P2XR7I12B | G-A | 54308 | unknown | 0,03 | - |
| Exon13 | P2XR7v13F | C-T | 54399 | Ala433Val | 0,13 | - |
| Exon13 | P2XR7v13A | A-G | 54480 | Gln460Arg | 0,13 | 0,17 |
| Exon13 | P2XR7v13B | C-T | 54523 | Silent Pro474 | 0,1 | 0,07 |
| Exon13 | P2XR7v13G | DelCCCTGAGA GCCACAGG TGCCT | 54562-54582 | Del of 7aa 488 to 494 (PESHRCL) | RARE | - |
| Exon13 | P2XR7v13C | A-C | 54588 | Glu496Ala | 0,13 | 0,06 |
| Exon13 | P2XR7v13H | C-G | 54664 | His521Gln | 0,03 | - |
| Exon13 | P2XR7E13D | G-T | 54703 | Silent Leu534 | 0,1 | 0,02 |
| Exon13 | P2XR7E13J | A-T | 54804 | Ile568Asn | - | 0,01 |
| Exon13 | P2XR7v13I | G-A | 54834 | Arg578Gln | - | RARE |
| Exon13 | P2XR7v13E | G-A | 54847 | Silent Pro582 | 0,4 | 0,45 |
| 3'UTR | P2XR7UTR3A | C-A | 55169 | unknown | 0,48 | 0,37 |

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55 50 45 40 35 30 25 20 15 10 5

Table 12. (continued)

| Comparison between polymorphisms in the Saguenay/Lac-St-Jean population and the German population in the human P2X7R gene | | | | | | |
|---|---------------------------|--------|-----------|--------------|--------------------|---------------------|
| Associated exons or Introns | Variation (SNP or others) | Allele | Position* | Modification | Frequency (Canada) | Frequency (Germany) |
| 3'UTR | P2XR7UTR3B | A-C | 55170 | unknown | 0,09 | 0,1 |
| 3'UTR | P2XR7UTR3C | A-C | 55171 | unknown | 0,05 | 0,06 |
| 3'UTR | P2XR7UTR3D | C-T | 55917 | unknown | 0,001 | - |
| 3'UTR | P2XR7UTR3E | G-A | 54925 | unknown | - | 0,01 |

[0219] The position and numbering of the polymorphism corresponds to the human P2X7R gene as defined in SEQ ID NO: 1. To identify the genomic organization of the P2X7R gene, BAC clones were firstly organized using known polymorphic markers, sequence tag sites (STSs), BAC-end sequences and expressed sequence tags (ESTs). Unorientated and unordered DNA regions were reassembled into a sequences using Phrap and reordered the pieces using P2X7R exons as scaffolds. No complete gene organization for P2X7R has been done. There is only a partial gene structure from exon6 to 13, NT_037809. Therefore, this genomic sequence encompassing the P2X7R gene as depicted in SEQ ID NO: 1 could contain some sequence errors, specifically in intronic regions. Primers used for SNP amplification and sequencing are shown in Table 1a and depicted in SEQ ID NOs: 52 to 111.

[0220] Statistical analysis was performed according to the CLUMP method (Sham & Curtis 1995, Ann. Hum. Genet. 59:97-105). Table 13 resumes the allelic and genotypic association studies for SNPs in P2X7 gene.

Table 13. Allelic and genotypic association studies using CLUMP

| Locus | Allele Frequencies* | Effective | | Allele Analysis | Genotype Analysis | |
|------------|------------------------------|-----------|----------|-----------------|-------------------|--------------|
| | | Cases | Controls | p-value (T1) | p-value (T1) | p-value (T3) |
| P2XR7UTR5F | 2(0.23); 4(0.77) | 311 | 217 | 0.109 | 0.319 | 0.339 |
| P2XR7UTR5N | 1(0.001); 3(0.999)** | 314 | 218 | 0.038 | 0.048 | 0.048 |
| P2XR7UTR5G | 2(0.001); 3(0.105); 4(0.894) | 314 | 218 | 0.993 | 0.714 | 0.761 |
| P2XR7UTR5H | 2(0.92); 4(0.08) | 312 | 215 | 0.743 | 0.884 | 0.754 |
| P2XR7UTR5A | 1(0.08); 2(0.92) | 312 | 219 | 0.557 | 0.786 | 0.678 |
| P2XR7UTR5B | 2(0.73); 4(0.27) | 310 | 218 | 0.485 | 0.761 | 0.814 |
| P2XR7UTR5D | 1(0.92); 3(0.08) | 311 | 217 | 0.555 | 0.787 | 0.691 |
| P2XR7v02A | 2(0.09); 4(0.91) | 313 | 218 | 0.501 | 0.729 | 0.591 |
| P2XR7I04A | 1(0.04); 3(0.96) | 314 | 220 | 0.604 | 0.433 | 0.348 |
| P2XR7v05B | 2(0.69); 4(0.31) | 314 | 220 | 0.133 | 0.270 | 0.325 |
| P2XR7E05D | 1(0.03); 3(0.97) | 314 | 220 | 0.842 | 0.827 | 0.827 |
| P2XR7E05E | 1(0.006); 3(0.994)** | 314 | 220 | 0.048 | 0.045 | 0.045 |
| P2XR7v05A | 2(0.60); 4(0.40) | 314 | 220 | 0.038 | 0.144 | 0.219 |
| P2XR7E05C | 2(0.98); 4(0.02) | 314 | 220 | 1.000 | 1.000 | 1.000 |
| P2XR7I07F | 2(0.002); 4(0.98) | 315 | 219 | 1.000 | 1.000 | 1.000 |
| P2XR7v08A | 1(0.23); 3(0.77) | 315 | 219 | 0.454 | 0.673 | 0.634 |
| P2XR7v08B | 1(0.02); 3(0.98) | 315 | 219 | 0.636 | 0.638 | 0.638 |
| P2XR7v11A | 2(0.95); 4(0.05) | 311 | 218 | 0.348 | 0.391 | 0.436 |
| P2XR7v11B | 1(0.45); 3(0.55) | 312 | 218 | 0.605 | 0.803 | 0.790 |
| P2XR7v11C | 2(0.93); 3(0.07) | 312 | 218 | 0.793 | 0.256 | 0.924 |
| P2XR7I11D | 2(0.45); 4(0.55) | 312 | 219 | 0.665 | 0.735 | 0.740 |
| P2XR7v13A | 1(0.87); 3(0.13) | 305 | 215 | 0.017 | <0.001 | <0.001 |
| P2XR7v13B | 2(0.93); 4(0.07) | 305 | 216 | 1.000 | 0.228 | 0.677 |
| P2XR7V13C | 1(0.91); 2(0.09) | 305 | 216 | 0.151 | 0.006 | 0.008 |
| P2XR7E13D | 3(0.94); 4(0.06) | 315 | 219 | 0.402 | 0.429 | 0.474 |
| P2XR7E13J | 1(0.01); 4(0.99) | 315 | 219 | 0.618 | 0.603 | 0.603 |
| P2XR7E13I | 1(0.004); 3(0.996) | 315 | 219 | 0.999 | 1.000 | 1.000 |
| P2XR7v13E | 1(0.46); 3(0.54) | 314 | 219 | 0.699 | 0.866 | 0.845 |
| P2XR7UTR3A | 1(0.518); 2(0.482) | 314 | 219 | 0.617 | 0.850 | 0.875 |
| P2XR7UTR3B | 1(0.966); 2(0.034) | 313 | 219 | 0.522 | 0.850 | 0.643 |
| P2XR7UTR3C | 1(0.979); 2(0.021) | 313 | 219 | 0.636 | 0.505 | 0.382 |
| P2XR7UTR3E | 1(0.02); 3(0.98) | 315 | 219 | 0.147 | 0.161 | 0.161 |

* The column Allele Frequencies presents the allele for each SNP (A=1, C=2, G=3, T=4) and their respective frequency.

** For this SNP we observed a zero cell in both (allele and genotype) 2X2 contingency tables. p-value <0.045 was observed exact Fisher test.

[0221] For the SNP analysis, the Hardy-Weinberg (HW) equilibrium was controlled in the control samples. The Hardy-Weinberg principle (HWP) may be stated as follow: In a large, randomly mating population, in which there is no migration, or selection against a particular genotype and the mutation rate remains constant, the proportions of the various genotypes will remain unchanged from one generation to another. Take a two allele system with alleles A and a. If the proportion of A in the population is represented as p and the proportion of a as q, then p plus q represent the sum total of alleles at this locus, that is $p+q=1$. The HWP is useful to evaluate some population problems like marital assortment, Inbreeding, population stratification, admixture, decreased viability of a particular genotype. The SNP P2XR7v13A did not respect the Hardy-Weinberg equilibrium.

[0222] The association hypothesis was also tested using an allele positivity table known to be suitable for the detection of susceptibility alleles showing a dominant mode of inheritance (Ohashi and Tokunaga, J. Hum. Genet. 44 (1999), 246-248; Ohashi et al., Ann. Hum. Genet. 65 (2001), 197-206). Similar results were obtained using this method as those obtained using the allele frequency tables, with the exception of P2XR7v05A where the p-values were 0.253. Thus, P2XR7v05A presented a less significant association in this analysis. This difference can be attributed to the mode of inheritance.

[0223] The proportion of unipolar individuals in analysis of the German population is quite important since the American Psychiatric Association (Diagnostic and Statistical Manual of Mental Disorders-4th Edition Text Revision (DMS-IV-TR), American Psychiatric Press, 2000) has reported an increase in susceptibility for unipolar disorders in female groups. To determine whether the sexual variable could influence the association analysis, additional association studies were performed by controlling the sexual parameter. Normal individuals in the German population without gender information were omitted from the study. Then, a logistic regression model was derived by including the sex as factor. In order to obtain a model that is as stable as possible, the regression model was minimised by using the difference between loglikelihood's for models with or without interaction (Hosmer, and Lemeshow, "Applied logistic regression", John Wiley and Sons, 1989). The strategy used for handling the zero cells from contingency tables was to eliminate associated category completely. Calculations were done with SAS v8.0 SAS is a statistical software package that allows the user to manipulate and analyze data in many different ways. Because of its capabilities, this software package is used in many disciplines, including medical sciences, biological sciences, and social sciences.

[0224] The introduction of a sexual parameter did not perturb the association already observed in previous analysis. Moreover, this analysis model revealed additional results: a potential allele association with P2XR7v05B ($p=0.064$), and a genotypic association for P2XR7v08A ($p=0.042$) was observed.

[0225] Association studies using pooled samples was performed by merging individuals from the samples of the Saguenay/Lac St-Jean with those of the German population. Results are illustrated in table 14. The aim of this analysis is to highlight common features between both populations. However, according to differences between both samples (mainly the phenotype of affected individuals i.e. bipolar disorder in the Saguenay/Lac St-Jean samples, versus mostly unipolar disorder in the German population) some parameters were controlled, including sex and ethnicity. The modelling strategy for logistic regressions was described above.

Table 14.

| Association studies using pooled samples from both populations | | | | |
|--|-----------------|-----------------|-------------------|-----------------|
| Locus | Allele analysis | | Genotype analysis | |
| | p-value for SNP | p-value for sex | p-value for SNP | p-value for sex |
| P2XR7v02A | 0.8254 | 0.0085 | 0.8650 | 0.4531 |
| P2XR7v05B | 0.1751 | 0.3714 | 0.2034 | 0.5110 |
| P2XR7v05A | 0.3808 | 0.0266 | 0.0885 | 0.1392 |
| P2XR7v08A | 0.0452 | 0.0041 | 0.1021 | 0.3452 |
| P2XR7v08B | 0.3471 | 0.0040 | 0.3413 | 0.3617 |
| P2XR7v11A | 0.3559 | 0.0136 | 0.5888 | 0.4404 |
| P2XR7v11 B | 0.5902 | 0.0093 | 0.3897 | 0.4302 |
| P2XR7v11C | 0.3731 | 0.0094 | 0.7648 | 0.4615 |
| P2XR7v13A | 0.0047 | 0.0209 | <0.0001 | 0.4814 |
| P2XR7v13B | 0.5129 | 0.2352 | 0.9584 | 0.4092 |
| P2XR7v13C | 0.2466 | 0.0284 | 0.2225 | 0.4228 |

Table 14. (continued)

| Association studies using pooled samples from both populations | | | | |
|--|-----------------|-----------------|-------------------|-----------------|
| Locus | Allele analysis | | Genotype analysis | |
| | p-value for SNP | p-value for sex | p-value for SNP | p-value for sex |
| P2XR7v13E | 0.8168 | 0.0159 | 0.3713 | 0.4990 |

[0226] An allelic and genotypic association was observed for the P2XR7v13A locus ($p=0.0047$) which was stronger than in the separate analyses. A significant allelic association was also noted for the P2XR7v08A locus ($p=0.0452$). In addition, the present analysis also demonstrate the potential relationship between SNP P2XR7v05A and the origin with a p -value= 0.0515 (not shown in the table) which is in agreement with previous association analysis done in both samples separately (see Table 13).

[0227] The haplotype analysis was performed using the German population. The PHASE program (Stephens et al., Am. J. Hum. Genet. 68 (2001), 978-989) was used to estimate SNPs haplotypes within exons of the P2XR7R gene. Haplotypes were created for each exon having more than one associated SNP (see Table 15 for exon-associated SNPs). Case groups varied from 218-220 individuals, whereas control groups varied between 312-316 individuals. Association hypothesis was tested with the CLUMP method since many haplotypes were created for each exon. T1 and T3 statistic tests performed as described above. T2 and T4 statistics were also calculated owing to the presence of small effective cells in the contingency tables. T2 statistic is the usual chi-squared statistic applied on the contingency table obtained after collapsing columns with small expected values. T4 statistic is the largest chi-squared statistic obtained by comparing one column of the original table against the total of the other columns. One thousand simulations were used to estimate p -values. The resulting data was analyzed with the logistic regression model (describe above) using SAS V8.0 in order to consider the sexual parameter (for these tests the sample was reduced by 14 normal individuals). However, this analysis method is limited by the reliability of reconstructed haplotypes.

Table 15.

| Exon-associated SNPs | |
|----------------------|---|
| Exons | Associated SNPs |
| 5 | P2XR7E05D P2XR7E05E P2XR7v05A P2XR7E05C |
| 8 | P2XR7v08A P2XR7v08B |
| 11 | P2XRv11B P2XRv11C |
| 13 | P2XR7v13A P2XR7v13B P2XR7v13C P2XR7E13D P2XR7E13J P2XR7v13I P2XR7v13E |

Table 16.

| Genotypic association with haplotypes in exon 13 of P2X7R | | | | | | |
|---|--|--------------|----------------|---|--------------|----------------|
| Exon (haplotype) | Allele analysis | | | Genotype analysis | | |
| | Clump* | p-value(sex) | p-value(haplo) | Clump | p-value(sex) | p-value(haplo) |
| 5(5) | T1:0.032 T2:0.068 T3:0.054 T4:0.059 | 0.3133 | 0.1947 | T1:0.193 T2:0.159 T3:0.099 T4:0.304 | 0.460 | 0.5355 |
| 8(3) | T1:0.551 T2:0.585 T3:0.646 T4:0.646 | 0.3813 | 0.3064 | T1:0.812 T2:0.689 T3:0.644 T4:0.756 | 0.5428 | 0.6652 |
| 11(3) | T1:0.750 T2:0.786 T3:0.726 T4:0.726 | 0.0886 | 0.7396 | T1:0.625 T2:0.919 T3:0.929 T4:0.921 | 0.2305 | 0.9494 |
| 13(15**) | T1:0.088 T2:0.079 T3:0.147 T4:0.072 | 0.1871 | 0.1264 | T1:0.001 T2:0.002 T3:0.057 T4:<0.001 | 0.4610 | 0.019 |

*T1 test should not be considered because of contingency tables with zero cells.

**Among these 15 haplotypes, we observed 8 haplotypes where case cells have less than 3 individuals.

[0228] Table 16 illustrates a genotypic association with haplotypes in exon 13 of the P2X7R genes. Interestingly, many haplotypes for the exon 13 were observed. The differences between statistics in exon 13 (T3 less significant) can be explained by the involvement of more than one genotype of haplotypes in the disease. A potential allelic association was also noted with haplotypes in exon 5 of the P2X7R gene.

[0229] The following are clinical results illustrating the functional consequences of polymorphisms in P2X7R.

The development and course of depression is causally linked to impairments in the central regulation of the hypothalamic-pituitary-adrenocortical (HPA) axis. Abnormalities in the HPA axis can be measured using the dexamethasone-suppression test (DST) or the combined dexamethasone/corticotropin-releasing hormone (Dex/CRH) test. Changes in cortisol and/or adrenocorticotrophic hormone (ACTH) measurements during the DST or Dex/CRH test are indicative of HPA dysfunction in depressed patients (Heuser et al, J. Psychiat. Res. 28 (1994) 341-356; Rybakowski and Twardowska, J. Psychiat. Res. 33 (1999) 363-370; Zobel et al, J. Psychiat. Res. 35 (2001) 83-94; Künzel et al, Neuropsychopharmacology 28 (2003) 2169-2178). In order to demonstrate that P2X7R SNPs associated with affective disorders also correlate with changes in the HPA axis, cortisol and ACTH levels in response to the DST and Dex/CRH test were measured for the P2XR7v13A and P2XR7v13C SNPs. P2XR7v13A consist of an A to G nucleotide change resulting in a Gln460Arg modification in the P2X7R protein. The P2XR7v13C SNP corresponds to an A to C nucleotide change resulting in a Glu496Ala modification that has been shown to drastically reduce protein activity (Wiley et al, Drug Dev. Res. 53 (2001) 72-76).

[0230] Methods and conditions for performing the DST and Dex/CRH test are well known in the art, see for example Heuser et al, J. Psychiat. Res. 28 (1994) 341-356; Künzel et al, Neuropsychopharmacology 28 (2003) 2169-2178. Briefly, individuals were pre-treated at 23:00 with an oral administration of 1.5 mg dexamethasone. For the DST test, a blood sample was drawn at 8:00 prior to dexamethasone administration (i.e. pre-dexamethasone) and at 8:00 the morning following dexamethasone administration (i.e. post-dexamethasone). For the Dex/CRH test, a venous catheter was inserted at 14:30 the day following dexamethasone administration and blood was collected at 15:00, 15:30, 15:45, 16:00, and 16:15 into tubes containing EDTA and trasylol (Bayer Inc., Germany). At 15:02, 100 mg of human CRH (Ferring Inc., Germany) was administered intravenously. Measurement of plasma cortisol concentrations was done using a commercial radioimmunoassay kit (ICN Biomedicals, USA) while plasma ACTH concentrations was measured using a commercial immunometric assay (Nichols Institute, USA). Both assays were performed according to the manufacturer specifications.

[0231] For the P2XR7v13A SNP, a decrease in basal cortisol levels was seen at admission in individuals with an AG or GG allele when compared to individuals with the AA allele (Figure 1f). During the Dex/CRH test, a reduction in cortisol and ATCH response was measured in individuals with the GG allele when compared to individuals with an AA or AG allele (Figures 1g and 1h).

[0232] Furthermore, response to antidepressant treatment was delayed in GG individuals (figure 1i).

[0233] For the P2XR7v13C SNP, an increase in basal cortisol levels was measured post-dexamethasone administration (Figure 1j). During the Dex/CRH test, individuals with the CC allele displayed elevated cortisol response (Figure 1k), but reduced ATCH response (Figure 1l) when compared to AA and AC individuals. These results are indicative of dysregulation of the HPA axis.

[0234] Thus, SNPs in P2XR7R correlate with dysfunction in the HPA axis and demonstrate the functional and clinical consequences of polymorphisms in P2XR7R.

EXAMPLE 4

P2XR7R gene structure and mRNA expression and transcript sequence

[0235] A 1700 bp nucleotide sequence corresponding to the human P2XR7R promoter was analyzed by using MatInspector V2.2 and Transfac 4.0 algorithms. This analysis showed that the P2XR7R gene does not contain a standard TATA box, but has SP1 sites that can make up for transcriptional initiation. Besides the SP1 sequences, there are binding sites for the transcription factors GATA, Oct and Ikarus. These sites are thought to provide tissue specificity. Interestingly, the P2XR7R promoter has binding sites that suggest responsiveness to different cytokines such as AP-1, NFAT and CEBPB.

[0236] P2XR7R possesses 13 exons and 12 introns (Buell et al., Receptors Channels 5 (1998), 347), providing a basis for alternative splicing that would yield in theory different transcripts and produce different isoforms with possible different functions. No alternatively spliced variant was clearly identified. However, experiments of EST clustering allowed the description of three splicing variants. One is defined by the lack of the exon 5. This P2XR7v02 variant corresponds to the clone IMAGE: 3628076 isolated from brain-derived cell lines. The P2XR7v02 lacking the exon 5 produces a frame shift, thus generating a shorter polypeptide. The second splicing variant, P2XR7v03, is characterized by the presence of the short intron 10 into the mRNA. This variant is supported by two high quality sequences, the cDNA clone BRAMY2008977 (AC number: AK090866) from human amygdala and the EST clone dbEST:7339877 derived from an unknown human tumor. The last variant, P2XR7v04, is defined by the lack of the first exon that suggests an alternative promoter usage closed to the exon 2. A high quality EST clone dbEST:4782844 derived from a head and neck tumor supports this variant. These variants are shown in Figures 16a to 16e.

P2X7 variants.

| | | |
|----|---------|--|
| 5 | P2X7v01 | MPACCSCSDVFQYETNKVTRIQSMNYGTIKWFFHVIIFS YVCFALVSDKLYQRKEPVISS |
| | P2X7v04 | MPPVD-----AFPCLPFS---FALVSDKLYQRKEPVISS |
| | P2X7v02 | MPACCSCSDVFQYETNKVTRIQSMNYGTIKWFFHVIIFS YVCFALVSDKLYQRKEPVISS |
| | P2X7v03 | MPACCSCSDVFQYETNKVTRIQSMNYGTIKWFFHVIIFS YVCFALVSDKLYQRKEPVISS 1.....10.....20.....30.....40.....50 |
| 10 | P2X7v01 | VHTKVKGIAEVKKEIIVENGVKLVHSVFDTADYTFPLQGNSEFFVMTNFLKTEGQEQRCLCP |
| | P2X7v04 | VHTKVKGIAEVKKEIIVENGVKLVHSVFDTADYTFPLQGNSEFFVMTNFLKTEGQEQRCLCP |
| | P2X7v02 | VHTKVKGIAEVKKEIIVENGVKLVHSVFDTADYTFPLQGNSEFFVMTNFLKTEGQEQRCLCP |
| | P2X7v03 | VHTKVKGIAEVKKEIIVENGVKLVHSVFDTADYTFPLQGNSEFFVMTNFLKTEGQEQRCLCP 61.....70.....80.....90.....100.....110 |
| 15 | P2X7v01 | EYPTRRITLCSSDRGCKKGWMDPQSKGIQTGRCVVHEGNQKTCEVSAWCPIEAVEEAPRPA |
| | P2X7v04 | EYPTRRITLCSSDRGCKKGWMDPQSKGIQTGRCVVHEGNQKTCEVSAWCPIEAVEEAPRPA |
| | P2X7v02 | EYPTRRITLCSSDRGCKKGWMDPQSKGLLS----- |
| | P2X7v03 | EYPTRRITLCSSDRGCKKGWMDPQSKGIQTGRCVVHEGNQKTCEVSAWCPIEAVEEAPRPA 121.....130.....140.....150.....160.....170 |
| 20 | P2X7v01 | LLNSAENFTVLIKNNIDFPGHNYTTRNILPGLNITCTFHKTQNPQCFIFRLGDI FRETGD |
| | P2X7v04 | LLNSAENFTVLIKNNIDFPGHNYTTRNILPGLNITCTFHKTQNPQCFIFRLGDI FRETGD |
| | P2X7v02 | ----- |
| | P2X7v03 | LLNSAENFTVLIKNNIDFPGHNYTTRNILPGLNITCTFHKTQNPQCFIFRLGDI FRETGD 181.....190.....200.....210.....220.....230 |
| 25 | P2X7v01 | NFSDVAIQGGIMGIEIYWCNLDWRFHCHPKYSFRRLDDKTTNVS LYPGYNFRYAKYYK |
| | P2X7v04 | NFSDVAIQGGIMGIEIYWCNLDWRFHCHPKYSFRRLDDKTTNVS LYPGYNFRYAKYYK |
| | P2X7v02 | ----- |
| | P2X7v03 | NFSDVAIQGGIMGIEIYWCNLDWRFHCHPKYSFRRLDDKTTNVS LYPGYNFRYAKYYK 241.....250.....260.....270.....280.....290 |
| 30 | P2X7v01 | ENNVEKRTLIKVFGRFDILVFGTGKFDIIQLVVYIGSTLSYFGLAAVDFIDFLIDTYSS |
| | P2X7v04 | ENNVEKRTLIKVFGRFDILVFGTGKFDIIQLVVYIGSTLSYFGLAAVDFIDFLIDTYSS |
| | P2X7v02 | ----- |
| | P2X7v03 | ENNVEKRTLIKVFGRFDILVFGTGKFDIIQLVVYIGSTLSYFGLVDRSLFHALGKWFG 301.....310.....320.....330.....340.....350 |
| 35 | P2X7v01 | NCCRSHIYPWCKCCQPCVNVNEYYYRKKCESIVEPKPTLKYSVFDESHIRMVNQQLLGRS |
| | P2X7v04 | NCCRSHIYPWCKCCQPCVNVNEYYYRKKCESIVEPKPTLKYSVFDESHIRMVNQQLLGRS |
| | P2X7v02 | ----- |
| | P2X7v03 | EGSD----- 361.....370.....380.....390.....400.....410 |
| 40 | P2X7v01 | LQDVKGQEVPRPAMDFTDLSRLPLALHDTTPPIPGQPEEIQLLRKEATPRSRDSPVWCQCG |
| | P2X7v04 | LQDVKGQEVPRPAMDFTDLSRLPLALHDTTPPIPGQPEEIQLLRKEATPRSRDSPVWCQCG |
| | P2X7v02 | ----- |
| | P2X7v03 | ----- 421.....430.....440.....450.....460.....470 |
| 45 | P2X7v01 | SCLPSQLPESHRCLEELCCRKKPGACITTSelfrklvLSRHVLQFLLLYQEPLALDVDS |
| | P2X7v04 | SCLPSQLPESHRCLEELCCRKKPGACITTSelfrklvLSRHVLQFLLLYQEPLALDVDS |
| | P2X7v02 | ----- |
| | P2X7v03 | ----- 481.....490.....500.....510.....520.....530 |
| 50 | P2X7v01 | TNSRLRHCA YRCYATWRFSGQDMADFAILPSCCRWRIRKEFPKSEGQYSGFKSPY |
| | P2X7v04 | TNSRLRHCA YRCYATWRFSGQDMADFAILPSCCRWRIRKEFPKSEGQYSGFKSPY |
| | P2X7v02 | ----- |
| | P2X7v03 | ----- 541.....550.....560.....570.....580.....590 |

[0237] Therefore the transcriptional and translational start sequences of the human P2X7R were analyzed using Blast, Genescan and HMMgene computer software. This analysis indicated that P2X7R possesses with high probability only one translation start site. Most P2X7R expression sequence tags (ESTs; Unique cluster Hs. 193470) having a reliable 5' end showed identical transcriptional start site. None of the ESTs showed any indication of alternative splicing. Therefore, in silico analysis suggests that there is a low probability to find different transcripts produced by alternative splicing or alternative promoter usage.

[0238] The above mentioned in silico data were confirmed by RT-PCR analysis spanning the whole predicted human

P2X7R coding sequence using 14 and 19 bases (5'-ATGCCGGCTTGCTG-3'; 5'-GTAGGGATACTTGAAGCCA-3') oligonucleotides corresponding to the beginning and end of the coding sequence, respectively. Total RNA from whole brain, different dissected brain areas, thymus, spleen and kidney were isolated and analyzed for P2X7R expression. RT-PCR reactions were performed using the C. Therm One Step polymerase system (Roche Applied Science) and a protocol for touch down PCR with hot start. Briefly, Reverse Transcription was performed at 52°C according to the manufacturer's conditions. PCR reactions were executed with an annealing temperatures of 64°C for the first five cycles and of 54°C for the next 30 cycles.

[0239] A single specific band of the size of 1785 bp corresponding to the complete coding sequence of P2X7R was detected. P2X7R mRNA was detected in the whole brain, hippocampus, cerebellum, leukocytes and thymus but not in cerebral cortex, hypothalamus, spleen and kidney (Figure 2). All PCR products were cloned using the pGEM-T-Easy plasmid (Promega), selected in Top-10 bacteria (Invitrogen) by blue-white selection and tested by EcoRI digestion. Clones having fragments of the expected size were amplified and purified for sequencing. The sequence confirmed the identity of the 1785 bp clones as the complete coding sequence of wild-type P2X7R. Therefore, in all the tissues tested, wild-type P2X7R is expressed as a single transcript which includes the complete coding sequence. The presence of tissue specific isoforms is unlikely. These studies provide useful information about the P2X7R mRNA expression and transcript processing. This information can be used to synthesize riboprobes for in situ hybridization, Northern and Southern blot as well as engineering cells for the overexpression of P2X7R.

EXAMPLE 5

P2X7R expression in the mouse brain

[0240] The expression of P2X7R was further studied by immunohistochemistry of serial sections of complete mouse brains using a polyclonal antibody directed against an internal peptide of P2X7R (Santa Cruz Biotechnology). The brains from stress-free mice were shock frozen, cut into 16 µm slices and fixed with paraformaldehyde for 5 minutes. The sections were blocked for 30 minutes at room temperature with 1:10 horse serum. All antibodies were diluted in TBST buffer (Tris-buffered saline with 0.05% Tween-20). The first antibody was used in a dilution 1:200 and incubated overnight. All washes were performed with TBST buffer. As a secondary antibody, an anti-goat IgG biotinylated (Vector Laboratories) was used and detection was performed using the streptavidin-biotin-horse-radish peroxidase complex (Vector Laboratories) in combination with diaminobenzidine. Slides were counterstained with toluidine blue using standard procedures. The same procedure in the absence of the primary antibody was performed as a negative control. As a positive control to test the Preservation of the tissue was verified with an antibody specific for the protein Patched1 (Santa Cruz Biotechnology). Patched1 was used as positive control since it stains all relevant brain structures and is not affected by stress or antidepressants. Very specific staining pattern was detected, consistent with the specific subcellular localization of P2X7R in brain cells. Negative controls were completely devoid of signal. Positive control with Patched1 showed identical signal intensity and distribution in all samples, indicating that all tissues were equally well preserved and processed.

[0241] Proceeding from frontal to caudal, P2X7R protein was observed in the glomerular layer of the olfactory bulb at low levels (Figure 3). P2X7R was also present at very low levels in a restricted area of the periventricular hypothalamic nucleus (figure 3). Ependymal cells surrounding the lateral ventricles also showed a faint staining (Figure 3). A stronger signal was detected in restricted areas of the hippocampus, where the signal was present in single cells of the polymorph layer, the lacunosum moleculare and the oriens layer (Figure 4). In more posterior areas of the hippocampus, the signal was present in the molecular layer, stratum radiatum and near the CA3. In a further caudal position, P2X7R was expressed in the subcomisural organ (Figure 4). Therefore, the basal P2X7R expression in the brain of stress-free mice is restricted to areas that had been previously associated with depression, stress, learning and memory.

EXAMPLE 6

P2X7R is modulated in mice treated with an antidepressant

[0242] Further validation of role of P2X7R in affective disorders was performed by examining its expression pattern in response to stress and treatment with antidepressant drugs. A treatment schedule which has been proven to produce antidepressant effects on the behavioural level was administered to mice which were characterized as antidepressant responsive by using a variety of behavioural paradigms suitable to detect anxiolytic and antidepressant effects of classical antidepressants like the selective serotonin reuptake inhibitor paroxetine. Paroxetine was delivered by gavage to naive male mice over a time period of 28 days at a dosage of 10 mg/kg bodyweight twice per day. In parallel, a control group of mice was given vehicle solution (i.e. without paroxetine) using the same treatment regiment while a

second control group of mice was left undisturbed and stress-free (i.e. untreated) during the same period of the experiments. At the end of the long-term treatment, part of the mice of each experimental group were tested in the dark/light box (test of anxiety behaviour) and in the Porsolt's forced swim test (test of depressive-like behaviour) to confirm the effectiveness of the treatment (Figure 5). Passive stress coping behaviour decreased after long-term treatment with the antidepressant paroxetine. The other part of the experimental groups (i.e. mice without test experience) were decapitated, brains rapidly removed and frozen at -80°C until usage.

[0243] The expression of P2X7R in the brains of mice under stress-free conditions, and mice under mild stress produced by the vehicle application, and mice under paroxetine treatment was evaluated using three different brains from each group. Serial slides from each group of animals were analyzed in parallel by immunohistochemistry using the same materials in order to produce completely comparable results. No significant change in P2X7R expression in the olfactory bulb was seen in response to stress or to paroxetine treatment (Figure 6). However, in the periventricular nucleus of the hypothalamus, paroxetine produced a slight inhibition of P2X7R expression (Figure 7). No significant change was observed in the ependymal cells from different brain areas (Figure 8). The most dramatic changes were observed in the hippocampus, where P2X7R was strongly inhibited by stressful handling whereas paroxetine treatment produced a marked stimulation above basal levels (Figures 9, 10 and 11). This effect was observed all along the hippocampus but was more evident in the polymorph layer near the dentate gyrus. In the subcommissural organ, P2X7R expression remained unchanged by the different treatments. Therefore, P2X7R expression is strongly regulated in two specific brain areas involved in depression and stress. Other brain areas, which showed low levels of P2X7R and are not directly involved in depression, did not show changes.

[0244] In the samples from mice treated with paroxetine and showing a strong P2X7R expression, it was possible to analyze the distribution of P2X7R in more detail (Figures 10 and 11). The P2X7R protein was not only present in cell bodies but also was clearly detected in projections innervating the granular layer of the dentate gyrus (Figure 12). This subcellular localization of P2X7R is consistent with a role in neurotransmitter release and long term potentiation.

[0245] Since some reports (Muria et al., *Biochem. J.* 288 (1992), 897-901; Ferrari et al., *FEBS Lett.* 447 (1999), 71-75) suggest that chronic and high dose stimulation of P2X7R may cause apoptosis in some cell types, the hippocampus of the above described animals were analyzed for the co-localization of apoptotic cells and P2X7R expressing cells, in consecutive sections, using TUNNEL staining and immunohistochemistry. In correlative sections, only few apoptotic cells were detected and they were present along the granular layers of the hippocampus where no P2X7R expression was observed (Figure 13). No significant differences in the numbers of apoptotic cells were observed between the different treatment conditions. Therefore, the location and number of apoptotic cells did not correlate with the location and number of cells expressing P2X7R and rules out an involvement of P2X7R in the induction of apoptosis in the hippocampus.

[0246] Thus, P2X7R expression is considerably restricted to specific brain areas involved in depression. Moreover, P2X7R expression is inhibited by stress and strongly stimulated by antidepressant treatment in these specific areas. Therefore, P2X7R fulfils all criteria required for the actions of antidepressants according to the highest standards in the field of depression research. In addition, these results suggest that modulation of function of P2X7R is associated with chronic stress, which serves as a model for several aspects of affective disorders.

EXAMPLE 7

The behavioural effect of P2X7R inhibition in mice

[0247] To demonstrate that P2X7R inhibition acts as a causative agent for affective disorders, P2X7R function was specifically inhibited in distinct regions of the brain without affecting any other brain function. This was achieved by delivering double stranded small interference RNA molecules (siRNA) into restricted areas of the brain.

[0248] According to the observed expression pattern of P2X7R in the hippocampus (Figures 9, 10, and 11) and the known involvement of the hippocampus in depression, the dentate gyrus (hippocampus) was selected as target region for siRNA application. Male, naive mice were bilaterally implanted with a guide cannulae (23 gauge, length 8 mm) by means of a stereotactic instrument. The coordinates, in relation to bregma, were -2.0 mm posterior, ± 1.0 mm lateral, and -1.0 mm ventral. Following a recovery period of 5 days, the mice were divided into three experimental groups: vehicle (veh), control double stranded RNA (control), and P2X7R specific double stranded siRNA (siRNA). Sequences used for P2X7R siRNA are 5'-GUGGGUCUUGCACAUGAUCTT-3' and 5'-GAUCAUGUGCAAGACCCACTT-3'. Both sequences were annealed and injected together as a double stranded RNA. On day 6 after surgery, mice were slightly anaesthetized with Isofluran and injections of siRNA were carried out. The concentration of the control and siRNA was 0.1 nmol/ μ l, and a volume of 1 μ l per side was infused using specifically adapted injection systems (30 gauge, length 9 mm). The anaesthesia for the infusion was of short duration and the mice were awake immediately or few seconds after the manipulation.

[0249] Once delivered into the brain the siRNA molecules specific for P2X7R were taken up by brain cells and spe-

cifically induce the degradation of the complementary P2X7R mRNA with high efficiency. As a result, P2X7R function was specifically inhibited for a short period without affecting any other brain function. In this regard, injection of vehicle or control siRNA did not result in any obvious changes in normal behaviour, i.e., food and water intake, or motor behaviour in the home cage.

[0250] The effects of P2X7R inhibition on depressive-like behaviour was assessed 24 hours and 48 hours after infusion of siRNA, control or vehicle according to the standard test paradigm, the Porsolt's forced swim test (Porsolt et al., Arch. Int. Pharmacodyn. 229 (1977), 327-336; Porsolt, Rev. Neurosci. 11 (2000), 53-58). The parameter used to evaluate depressive-like behaviour is the time the animal is floating in the water, a behaviour which is associated with behavioural despair as the animal does not make any effort to actively cope with the stressful situation. Compared to vehicle application, no influence of control double stranded RNA (5'-CAACUUCUUCUUCUACGCGTT-3') on floating behaviour (passive stress coping) was detected. In contrast, compared to controls, mice infused with P2X7R specific siRNA showed a significant increase in passive behaviour, which is construed as depressive-like behaviour (Figure 14). This interpretation becomes moreover evident when the effects of antidepressants on passive stress coping behaviour in the forced swim test are visualized (Figure 5). Passive stress coping behaviour increased after acute intrahippocampal injection (bilateral, dentate gyrus) of siRNA targeting P2X7R. The Porsolt's forced swim test is a standard test used to assess the effectiveness of antidepressants and it has been proven by many studies that the test is selectively sensitive for these effects, given that the right animal model is used. The paradigm has been widely used to test pharmaceutical compounds and to validate animal models of depression, which show an increase in passive behaviour as do the mice where P2X7R has been inhibited (siRNA).

[0251] At the end of the experiment, the mice were sacrificed and the brains were examined to confirm the location and efficiency of the siRNA injections. For this purpose the brains were cut into sections and the slides were stained by immunohistochemistry using the above mentioned protocols. Brains from mice injected with the specific double stranded siRNA, with control double stranded RNA and with vehicle were examined in parallel. Under these conditions, the specific siRNA directed against P2X7R injected near the dentate gyrus induced on average an 80% inhibition of P2X7R protein expression as compared to the samples from mice injected with vehicle or with control double stranded RNA. Both the number of cells expressing P2X7R as well as the intensity of the expression were strongly reduced (Figure 15). The injections with siRNA did not produce any sign of local inflammation or infiltration at the hippocampus. Thus, P2X7R expression is specifically and locally inhibited by siRNA application in vivo. This inhibition produced behavioural changes indicating a causative role for P2X7R in affective disorders. These results in combination with those mentioned above support and confirm the observation of mutations in P2X7R being associated with affective diseases in humans and that modulation of P2X7R activity has antidepressive effects.

EXAMPLE 8

Drug screening assay

[0252] Methods for identifying P2X7R agonists were established using an immortalised mouse hippocampal cell line expressing the endogenous P2X7 gene. Briefly, the expression of P2X7 was confirmed by culturing the cells at 37°C/5% CO₂ in DMEM with 10% foetal calf serum (Gibco). Upon reaching 80 % confluence, cells were collected in PBS and homogenized by repeated passage through a syringe (18G needle). The amount of total protein was measured by the Bradford assay (Sigma; diluted 1:5, O.D. measured at 595 nm) according to the manufacturer's recommendation. Protein homogenates were then mixed with an equal volume of loading buffer (50 mM Tris-Cl pH 6.8; 25% glycerol; 7,2 mM bromophenol blue; 2% SDS; 200 nM β -mercaptoethanol) and subsequently denatured in boiling water for 10 minutes. 20 mg of each sample were loaded onto a 10% polyacrylamide gel containing 0,4 % SDS. Electrophoresis and Western blot transfer were performed according to conventional protocols described, for example, in Sambrook, Russell "Molecular Cloning, A Laboratory Manual", Cold Spring Harbor Laboratory, N.Y. (2001). Membranes were then blocked with 5 % dry milk and incubated with an antibody against P2X7R (1:1000 dilution; Santa Cruz Biotech) followed by incubation with a horse anti-goat peroxidase-coupled secondary antibody (1: 10000 dilution; Santa Cruz Biotech). Membranes were then incubated for 1 hour at 37°C in Lumi-Light Western Blotting Substrate (Roche Applied Science) followed by a 10 minute exposure on a BioMax MR Film (Kodak).

[0253] A 70 kD band corresponding to the expected size of the P2X7R protein was detected in HT-22 cells demonstrating expression of the endogenous mouse P2X7 gene (Figure 17). A second mouse hippocampal cell line (HT-39) did not express P2X7.

[0254] Since P2X7R is an ATP-gated ion channel which allows the entry of calcium and sodium ions into cells, a method for identifying P2X7R agonist was established by monitoring calcium influx into HT-22 cells. Cells were first loaded with the fluorescent dye Oregon green AM ester (Molecular Probes) for 30 minutes at room temperature, washed 2 times with DMEM/10% foetal calf serum to remove excess dye and cultured for 15 minutes in the presence of 100 μ M 2- and 2'-3'-O-(4-Benzoylbenzoyl)adenosine 5'-triphosphate (BzATP: C₂₄H₂₄N₅O₁₅P₃). BzATP is a known agonist

of P2X7R (North and Surprenant, Annu. Rev. Pharmacol. Toxicol. 40 (2000), 563-580). Calcium movement into the cells was visualised under a fluorescent microscope with a fluorescein filter (wavelength 492/517 nm). Oregon green AM ester is a fluorescent dye that binds to intracellular calcium. Accordingly, an increase in green fluorescence was observed in cells treated with BzATP (Figure 18) signalling an activation of P2X7R which results in an influx of calcium

into the cells and an increase binding of Oregon green dye to intracellular calcium.
 [0255] Alternatively, Oregon green AM ester can be replaced by Fluo-3, fluo-4, fluo-5F, fluo-5N, fluo-4FF, Fluo-4 dextran, Fluo-3 AM, Fluo-4 AM, Fluo-5F AM, Fluo-5N AM and Fluo-4FF AM (Molecular Probes). Calcium influx in HT-22 cells can also be measured in 96-well and 384-well microplate using the Calcium Plus Assay Kit (Molecular Device) or FLIPR® Calcium Assay Kit for Fluorometric Imaging Plate Reader Systems (Molecular Device). HT-22 cells can be replaced by any cells expressing P2X7R, including cells that have been genetically modified by introducing an exogenous P2X7 gene.

[0256] The specificity of the P2X7R agonist on calcium influx was confirmed by pretreatment of HT-22 cells with 100 mM Oxidized ATP (oATP; Sigma) for 1 hour before the addition of BzATP. oATP is an irreversible inhibitor of the receptor (Chen et al., J. Biol. Chem., 268 (1993), 8199-8203). Activation of P2X7R by the agonist was inhibited by oATP (Figure 18) as illustrated by the absence of green fluorescence in the cells.

[0257] Yet another method of measuring P2X7R activity involves the entry of ethidium bromide into P2X7R expressing cells. Activation of P2X7R by an agonist allows the entry of ethidium bromide which binds nuclear DNA and emits a fluorescence signal. Alternatively, the propidium dye YOPRO-1 can be substituted for ethidium bromide. An increase in fluorescence can be used as a measure of P2X7 receptor activation. Therefore, the assay can be used to test and quantify the effect of an agent or compound with agonist properties on P2X7R. In the present example, 10^3 HT-22 cells were seeded per well in a 96-well flat bottom microtitre plates and incubated at 37°C/5%CO₂ in DMEM medium containing 10% FCS until the cells attached to the culture surface. Once attached, cells were incubated for 60 minutes in DMEM medium containing 10%FCS, 10⁻⁴M ethidium bromide and increasing concentrations of BzATP (1 µM, 10 µM, 100 µM, 500µM, 1 mM). The number of fluorescent cells which have integrated the ethidium bromide to the DNA can then be counted using a fluorescent microscope (Zeiss, Germany). Concentrations above 100µM BzATP increased the number of fluorescent nuclei signalling activation of P2X7R (Figure 19a). Alternatively, ethidium bromide fluorescence can be measured using a Perkin-Elmer fluorescent plate reader (excitation 520 nm, emission 595 nm, slit widths: Ex 15 nm, Em 20 nm). From the readings obtained, a pIC50 figure can be calculated for each candidate agent or compound. Accordingly, a P2X7R agonist is defined as an agent or a compound with an EC50 equal or below 300 micromolar, whereas the term EC 50 is defined as the concentration eliciting 50% of maximal response to an agonist (North and Surprenant, Annu. Rev. Pharmacol. Toxicol. 40 (2000), 563-580). The specificity of an agonist for P2X7R can be evaluated by pre-incubation of the cells for 60 minutes with 100 µM o-ATP before adding the agonist and ethidium bromide dye. Under these conditions, activation of P2X7R by the agonist is inhibited by oATP resulting in a reduction in the number of fluorescent cells (Figure 19b).

[0258] Yet another method for identifying P2X7R agonists was devised by generating a immortalised mouse cell line that overexpresses the human P2X7R gene under the control of the human cytomegalovirus (CMV) early promoter/enhancer region. The human P2X7R cDNA was inserted into the pcDNA3.1 vector (Invitrogen) and transfected into the mouse hippocampal cell line HT-22 using Lipofectamine (Invitrogen) according to the manufacturer's specifications. One day after transfection, culture medium containing 500 µg/ml G418 was added to the cells. Resistant clones were separately isolated and cultured 14 days after applying the selection medium.

[0259] The agonistic activity of a compound was evaluated by measuring calcium entry in the cells that overexpress the human P2X7R. Cells were cultured in 96 well plates and incubated at 37°C with 5% CO₂ DMEM with 10% foetal calf serum (Gibco) until they reached confluence. Cells were then loaded for one hour with 10 µM of Fluo-4 AM (Molecular Probes). Fluo-4 AM is a fluorescent dye that binds to intracellular calcium. After loading, cells were washed once with a buffer containing 0.5 mM CaCl₂ and 20 mM Hepes and were treated with 20 µM BzATP or 50 µM tenidap. Agonist activity was detected by measuring an increase in calcium influx which results in increased binding to Fluo-4 AM and increased fluorescence. Changes in fluorescence signal are measured using a Fluostar Optima plate reader (BMG biotech). Both BzATP and tenidap produced a rapid increase in fluorescence intensity which declined slowly over time (Figure 19c). Thus, both compound stimulated the activity of P2X7R which results in an influx of ions into the cells.

EXAMPLE 9

Activation of P2X7R with agonists has antidepressive effects

[0260] To demonstrate that activation of P2X7R has therapeutic effects on affective disorders, the P2X7R agonist BzATP (2'-3'-O-(4-Benzoylbenzoyl)adenosine 5'-triphosphate (C₂₄H₂₄N₅O₁₅P₃)) was administered to a selected DBA/2Ola mouse strain that displays characteristics of being highly anxious, responding to antidepressants, and showing

anxiolysis after subchronic antidepressant treatment (Lucki et al., *Psychopharmacology* 155 (2001), 315-322). BzATP is a compound with strong specificity to P2X7R (North and Surprenant, *Annu. Rev. Pharmacol. Toxicol.* 40 (2000), 563-580). In the present example, the P2X7R agonist was directly injected into the hippocampus of mice. However, a P2X7R agonist agent or compound could also be delivered orally, subcutaneously, intravenously, intra-arterial, intranasally, intramedullary, intrathecal, intraventricular, intranasally, intrabronchial, transdermally, intrarectally, intraperitoneally, intramuscularly, intrapulmonary, vaginally, rectally, or intraocularly.

[0261] Four months old male mice were bilaterally implanted with guide cannulae (23 gauge, length 8 mm) by means of a stereotaxic instrument (David Kopf Instruments). The coordinates, in relation to bregma, were -2.0 mm posterior, ± 1.0 mm lateral, and -1.0 mm ventral. After surgery, the mice were allowed to recover for 10 to 12 days. Following this recovery period, mice were injected with 1 μ l vehicle solution (0.5% DMSO, Sigma) or 50 μ M BzATP (Sigma, prepared in 0.5% DMSO) in each side of the brain over a period of 60 seconds. Injections were performed using a 9 mm-30 gauge needle inserted into the guide cannulae and connected via tubing to a 10 μ l Hamilton syringe.

[0262] The behaviour of individual mice was assessed using the Porsolt's forced swim test 24 hours after injection of vehicle solution or BzATP. A pre-exposure of 5 minutes to the test was done 10-15 minutes after vehicle or BzATP injection. The forced swim test is a standard test that measures primary stress-induced reductions in avoidance or escape, termed behavioural despair. The test is used to determine the effectiveness of antidepressants, test new pharmaceutical compounds and validate animal models of depression (Porsolt et al., *Arch. Int. Pharmacodyn.* 229 (1977), 327-336; Porsolt, *Rev. Neurosci.* 11 (2000), 53-58; R  n  ric et al., *Behav. Brain Res.* 136 (2002), 521-532; Page et al., *Psychopharmacology* 165 (2003), 194-201; Kelliher et al., *Psychoneuroendocrinology* 28 (2003), 332-347). The test consists of placing a mouse for a period of 5 minutes into a glass cylinder containing water. Under such circumstances, the mouse cannot touch the bottom of the cylinder and is thus forced to swim. Time, latency and frequency of struggling versus floating are scored as behavioural parameters. Floating (i.e. movements made only for keeping balance and breath) is a passive behaviour associated with despair and represents a depressive-like symptom since the animal does not make any effort to actively cope with the stressful situation. Increased struggling (i.e. active attempts to escape) indicates active coping behaviour that can be interpreted as an improvement of depression-like symptoms. For example, treatment with serotonergic antidepressants reduce the total time spent floating (Borsini, *Neurosci. Biobehav. Rev.* 19 (1995), 377-395; Redrobe and Bourin, *Psychopharmacology* 138 (1998), 198-206, and in parallel increases the time of active behaviour (i.e. swimming or struggling; Lucki et al., *Psychopharmacology* 155 (2001), 315-322).

[0263] The P2X7R agonist BzATP was found to increase active escape attempts (i.e. increase in time and frequency of struggling, decrease in latency of struggling) while a decrease in passive behaviour (i.e. decrease in time and frequency of floating, increase in latency of floating) was measured when compared to control mice injected with vehicle solution (Figure 20). Observed results were verified statistically using Mann-Whitney U and one-way MANOVA tests. The differences in time struggling, latency of floating and frequency of floating were found to be statistically significant. While latency and frequency of struggling and time floating results were not supported statistically, they still represented a tendency towards improvement in stress coping behaviour. These results demonstrate that a P2X7R agonist can lead to improvements in depressive-like symptoms.

[0264] Since conclusions drawn from the forced swim test can be influenced by unspecific effects of an agent or compound on animal activity (i.e. increase in struggling behaviour can be the result of hyperactivity instead of increased active coping behaviour), the potential effect of BzATP on locomotor activity was assessed by the open field test (Crawley, "What's wrong with my mouse: Behavioral phenotyping of transgenic and knockout mice", Wiley-Liss (2000)). Locomotor activity in mice treated with control vehicle solution or 50 μ M BzATP was assessed 24 hours after injection by placing individual animal in a dark-grey wooden box (30x30x40 cm). Locomotor activity was monitored for a period of 30 minutes using a video camera. Overall distance travelled by the animals during the testing period was then analysed by means of VideoMot2 computer software (TSE GmbH, Bad Homburg). No difference in locomotor activity was measured between mice treated with control vehicle solution and BzATP (Figure 21). Therefore, the application of BzATP did not induce hyperactivity. These results confirm that activation of P2X7R by an agonist agent or compound leads to improvements in depressive-like symptoms and is not the result of an unspecific effect on animal activity per se.

[0265] Several reports suggest that activation of P2X7R can induce apoptosis and cell death in vitro (Di Virgilio et al., *Cell Death Differ.* 5 (1998), 191-199; Virginio et al., *J. Physiol.* 519 (1999), 335-346). To test whether P2X7R activation in the hippocampus resulted in cell death, apoptosis levels were quantified in the brain of the mice treated with BzATP. Mice were sacrificed at the end of the behavioural experiments, the brains were removed, shock frozen and sectioned into 16 μ m slices. Brain sections were then studied for apoptosis using the DeadEnd fluorometric TUNEL system according to the manufacturer's recommendation (Promega Corporation). The TUNEL system measures the fragmented DNA of apoptotic cells. Positive control for the assay are made by pre-treating brain sections for 10 minutes with 1 unit/ml of DNase I.

[0266] Very few apoptotic cells (i.e. less than one cell per brain section) were observed in brains of mice treated with control vehicle or the P2X7R agonist (Figure 22) when compared to positive control sections pre-treated with DNase.

Moreover, no significant differences in the numbers of apoptotic cells was observed between the control animals and mice treated with BzATP, indicating that activation of P2X7R did not result in cerebral cell death in vivo.

Example 10

P2X7R antagonists have no antidepressive effects

[0267] The P2X7R antagonists KN-62 (1-(N,O-bis[5-isoquinolinesulphonyl]-N-methyl-L-tyrosyl)-4-phenylpiperazine) and oxidized ATP (oATP) were administered to DBA/2O1a mice (Harlan Winkelmann, Germany) that exhibit the behavioural characteristic of being highly anxious. KN-62 has been shown to be a non competitive antagonist of P2X7R (Chessel et al., Brit. J. Pharmacol., 124 (1998), 1314-1320) while oATP acts as an irreversible inhibitor of P2X7R (Chen et al., J. Biol. Chem., 268 (1993), 8199-8203).

[0268] In the present example, the P2X7R antagonists were directly injected into the dentate gyrus region of the hippocampus. Briefly, three months old male mice were bilaterally implanted with guide cannulae (23 gauge, length 8 mm) by means of a stereotactic instrument (David Kopf Instruments). The coordinates, in relation to bregma, were -1.5 mm posterior, ± 1.0 mm lateral, and -0.8 mm ventral. Mice were allowed to recover for 10 to 13 days after surgery. Following this recovery period, mice were injected with 1 μ l vehicle solution (0,01% DMSO, Sigma), or 100nM KN-62 (Sigma, prepared in 0,01% DMSO), or 10 μ M oATP (Sigma, prepared in PBS) in each side of the brain over a period of 60 seconds. All injections were performed using a 9 mm-31 gauge needle inserted into the guide cannulae and connected via tubing to a 10 μ l Hamilton syringe.

[0269] The behaviour of individual mice was assessed using the Porsolt's forced swim test 24 hours after injection of vehicle solution, KN-62, or oATP. A pre-exposure of 5 minutes to the test was performed 15-17 minutes after administration of vehicle, KN-62, or oATP. A description of the Porsolt's forced swim test is given in example 9. In the present example, no changes in active escape attempts (i.e. time, frequency, latency of struggling) or in passive behaviour (i.e. time, frequency, latency of floating) was measured between vehicle, KN-62 or oATP treated mice (figure 23). Observed results were verified statistically using one-way MANOVA test. The differences seen in the different parameters between vehicle, KN-62 or oATP treated mice were not supported statistically. These results demonstrate that P2X7R antagonists do not improve depressive-like symptoms and have no antidepressive action.

[0270] Since conclusions drawn from the forced swim test can be influenced by unspecific effects of an agent or compound on animal activity (i.e. increase in struggling behaviour can be the result of hyperactivity instead of increased active coping behaviour), the potential effect of the P2X7R antagonist oATP on locomotor activity was assessed by performing the open field test. Locomotor activity in mice treated with control vehicle solution, 10 μ M oATP, or 50 μ M oATP was assessed 15 minutes after injection by placing individual animal in a dark-grey wooden box (30x30x40 cm). Locomotor activity was monitored for a period of 30 minutes using a video camera. Overall distance travelled by the animals during the testing period was then analysed by means of VideoMot2 computer software (TSE GmbH, Bad Homburg). No difference in locomotor activity was measured between mice treated with control vehicle solution and oATP (Figure 24). Therefore, the application of a P2X7R antagonist did not induce hypo- or hyperactivity in the animals.

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Glu Gly Asn Gln Lys Thr Cys Glu Val Ser Ala Trp Cys Pro Ile Glu
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Thr Thr Arg Asn Ile Leu Pro Gly Leu Asn Ile Thr Cys Thr Phe His
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| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
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| 15 | gct | gtg | ttc | atc | gac | ttc | ctc | atc | gac | act | tac | tcc | agt | aac | tgc | tgt | 1167 |
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| 20 | cgc | tcc | cat | att | tat | ccc | tgg | tgc | aag | tgc | tgt | cag | ccc | tgt | gtg | gtc | 1215 |
| | Arg | Ser | His | Ile | Tyr | Pro | Trp | Cys | Lys | Cys | Cys | Gln | Pro | Cys | Val | Val | |
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| | aac | gaa | tac | tac | tac | agg | aag | aag | tgc | gag | tcc | att | gtg | gag | cca | aag | 1263 |
| | Asn | Glu | Tyr | Tyr | Tyr | Arg | Lys | Lys | Cys | Glu | Ser | Ile | Val | Glu | Pro | Lys | |
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| 25 | ccg | aca | tta | aag | tat | gtg | tcc | ttt | gtg | gat | gaa | tcc | cac | att | agg | atg | 1311 |
| | Pro | Thr | Leu | Lys | Tyr | Val | Ser | Phe | Val | Asp | Glu | Ser | His | Ile | Arg | Met | |
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| | gtg | aac | cag | cag | cta | cta | ggg | aga | agt | ctg | caa | gat | gtc | aag | ggc | caa | 1359 |
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| 30 | gaa | gtc | cca | aga | cct | gcg | atg | gac | ttc | aca | gat | ttg | tcc | agg | ctg | ccc | 1407 |
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| | Leu | Ala | Leu | His | Asp | Thr | Pro | Pro | Ile | Pro | Gly | Gln | Pro | Glu | Glu | Ile | |
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| 35 | cag | ctg | ctt | aga | aag | gag | gcg | act | cct | aga | tcc | agg | gat | agc | ccc | gtc | 1503 |
| | Gln | Leu | Leu | Arg | Lys | Glu | Ala | Thr | Pro | Arg | Ser | Arg | Asp | Ser | Pro | Val | |
| | | 460 | | | | 465 | | | | | 470 | | | | | 475 | |
| | tgg | tgc | cag | tgt | gga | agc | tgc | ctc | cca | tct | caa | ctc | cct | gag | agc | cac | 1551 |
| | Trp | Cys | Gln | Cys | Gly | Ser | Cys | Leu | Pro | Ser | Gln | Leu | Pro | Glu | Ser | His | |
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| | agg | tgc | ctg | gag | gag | ctg | tgc | tgc | cgg | aaa | aag | ccg | ggg | gcc | tgc | atc | 1599 |
| | Arg | Cys | Leu | Glu | Glu | Leu | Cys | Cys | Arg | Lys | Lys | Pro | Gly | Ala | Cys | Ile | |
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| | Gln | Phe | Leu | Leu | Leu | Tyr | Gln | Glu | Pro | Leu | Leu | Ala | Leu | Asp | Val | Asp | |
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| | tgg | cgc | ttc | ggc | tcc | cag | gac | atg | gct | gac | ttt | gcc | atc | ctg | ccc | agc | 1791 |
| | Trp | Arg | Phe | Gly | Gly | Gln | Asp | Met | Ala | Asp | Phe | Ala | Ile | Leu | Pro | Ser | |
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Cys Cys Arg Trp Arg Ile Arg Lys Glu Phe Pro Lys Ser Glu Gly Gln
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5 tac agt ggc ttc aag agt cct tac tgaagccagg caccgtggct cacgtctgta 1893
Tyr Ser Gly Phe Lys Ser Pro Tyr 595

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gcctgggctaa caaggcgaaa tcctgtctgt actaaaaata caaaaatcag ccagacatgg 2013

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Lys Leu Tyr Gln Arg Lys Glu Pro Val Ile Ser Ser Val His Thr Lys
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30 Val Lys Gly Ile Ala Glu Val Lys Glu Glu Ile Val Glu Asn Gly Val
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Lys Lys Leu Val His Ser Val Phe Asp Thr Ala Asp Tyr Thr Phe Pro
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Gly Gln Glu Gln Arg Leu Cys Pro Glu Tyr Pro Thr Arg Arg Thr Leu
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40 Cys Ser Ser Asp Arg Gly Cys Lys Lys Gly Trp Met Asp Pro Gln Ser
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45 Lys Gly Ile Gln Thr Gly Arg Cys Val Val His Glu Gly Asn Gln Lys
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Thr Cys Glu Val Ser Ala Trp Cys Pro Ile Glu Ala Val Glu Glu Ala
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50 Pro Arg Pro Ala Leu Leu Asn Ser Ala Glu Asn Phe Thr Val Leu Ile
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55 Lys Asn Asn Ile Asp Phe Pro Gly His Asn Tyr Thr Thr Arg Asn Ile
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 10 Tyr Trp Asp Cys Asn Leu Asp Arg Trp Phe His His Cys His Pro Lys
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 Tyr Ser Phe Arg Arg Leu Asp Asp Lys Thr Thr Asn Val Ser Leu Tyr
 275 280 285
 15 Pro Gly Tyr Asn Phe Arg Tyr Ala Lys Tyr Tyr Lys Glu Asn Asn Val
 290 295 300
 20 Glu Lys Arg Thr Leu Ile Lys Val Phe Gly Ile Arg Phe Asp Ile Leu
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 Val Phe Gly Thr Gly Gly Lys Phe Asp Ile Ile Gln Leu Val Val Tyr
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 25 Ile Gly Ser Thr Leu Ser Tyr Phe Gly Leu Ala Ala Val Phe Ile Asp
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 Phe Leu Ile Asp Thr Tyr Ser Ser Asn Cys Cys Arg Ser His Ile Tyr
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 370 375 380
 Arg Lys Lys Cys Glu Ser Ile Val Glu Pro Lys Pro Thr Leu Lys Tyr
 385 390 395 400
 Val Ser Phe Val Asp Glu Ser His Ile Arg Met Val Asn Gln Gln Leu
 405 410 415
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 420 425 430
 Ala Met Asp Phe Thr Asp Leu Ser Arg Leu Pro Leu Ala Leu His Asp
 435 440 445
 45 Thr Pro Pro Ile Pro Gly Gln Pro Glu Glu Ile Gln Leu Leu Arg Lys
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 Glu Ala Thr Pro Arg Ser Arg Asp Ser Pro Val Trp Cys Gln Cys Gly
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 55 Leu Cys Cys Arg Lys Lys Pro Gly Ala Cys Ile Thr Thr Ser Glu Leu
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Phe Arg Lys Leu Val Leu Ser Arg His Val Leu Gln Phe Leu Leu Leu
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5 Tyr Gln Glu Pro Leu Leu Ala Leu Asp Val Asp Ser Thr Asn Ser Arg
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10 Gln Asp Met Ala Asp Phe Ala Ile Leu Pro Ser Cys Cys Arg Trp Arg
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Lys Leu Tyr Gln Arg Lys Glu Pro Val Ile Ser Ser Val His Thr Lys
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Val Lys Gly Ile Ala Glu Val Lys Glu Glu Ile Val Glu Asn Gly Val
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5 Lys Lys Leu Val His Ser Val Phe Asp Thr Ala Asp Tyr Thr Phe Pro
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Leu Gln Gly Asn Ser Phe Phe Val Met Thr Asn Phe Leu Lys Thr Glu
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10 Gly Gln Glu Gln Arg Leu Cys Pro Glu Tyr Pro Thr Arg Arg Thr Leu
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15 Lys Gly Ile Gln Thr Gly Arg Cys Val Val His Glu Gly Asn Gln Lys
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Thr Cys Glu Val Ser Ala Trp Cys Pro Ile Glu Ala Val Glu Glu Ala
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25 Lys Asn Asn Ile Asp Phe Pro Gly His Asn Tyr Thr Thr Arg Asn Ile
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30 Gln Cys Pro Ile Phe Arg Leu Gly Asp Ile Phe Arg Glu Thr Gly Asp
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Asn Phe Ser Asp Val Ala Ile Gln Gly Gly Ile Met Gly Ile Glu Ile
245 250 255

35 Tyr Trp Asp Cys Asn Leu Asp Arg Trp Phe His His Cys Arg Pro Lys
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40 Tyr Ser Phe Arg Arg Leu Asp Asp Lys Thr Thr Asn Val Ser Leu Tyr
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Pro Gly Tyr Asn Phe Arg Tyr Ala Lys Tyr Tyr Lys Glu Asn Asn Val
290 295 300

45 Glu Lys Arg Thr Leu Ile Lys Val Phe Gly Ile Arg Phe Asp Ile Leu
305 310 315 320

Val Phe Gly Thr Gly Gly Lys Phe Asp Ile Ile Gln Leu Val Val Tyr
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50 Ile Gly Ser Thr Leu Ser Tyr Phe Gly Leu Ala Ala Val Phe Ile Asp
340 345 350

Phe Leu Ile Asp Thr Tyr Ser Ser Asn Cys Cys Arg Ser His Ile Tyr
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Pro Trp Cys Lys Cys Cys Gln Pro Cys Val Val Asn Glu Tyr Tyr Tyr
370 375 380

5 Arg Lys Lys Cys Glu Ser Ile Val Glu Pro Lys Pro Thr Leu Lys Tyr
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Val Ser Phe Val Asp Glu Ser His Ile Arg Met Val Asn Gln Gln Leu
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10 Leu Gly Arg Ser Leu Gln Asp Val Lys Gly Gln Glu Val Pro Arg Pro
420 425 430

Ala Met Asp Phe Thr Asp Leu Ser Arg Leu Pro Leu Ala Leu His Asp
435 440 445

15 Thr Pro Pro Ile Pro Gly Gln Pro Glu Glu Ile Gln Leu Leu Arg Lys
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20 Glu Ala Thr Pro Arg Ser Arg Asp Ser Pro Val Trp Cys Gln Cys Gly
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Ser Cys Leu Pro Ser Gln Leu Pro Glu Ser His Arg Cys Leu Glu Glu
485 490 495

25 Leu Cys Cys Arg Lys Lys Pro Gly Ala Cys Ile Thr Thr Ser Glu Leu
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Phe Arg Lys Leu Val Leu Ser Arg His Val Leu Gln Phe Leu Leu Leu
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30 Tyr Gln Glu Pro Leu Leu Ala Leu Asp Val Asp Ser Thr Asn Ser Arg
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Leu Arg His Cys Ala Tyr Arg Cys Tyr Ala Thr Trp Arg Phe Gly Ser
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35 Gln Asp Met Ala Asp Phe Ala Ile Leu Pro Ser Cys Cys Arg Trp Arg
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| | Val Lys Gly Ile Ala Glu Val Lys Glu Glu Ile Val Glu Asn Gly Val 65 70 75 80 | | |
| 10 | Lys Lys Leu Val His Ser Val Phe Asp Thr Ala Asp Tyr Thr Phe Pro 85 90 95 | | |
| | Leu Gln Gly Asn Ser Phe Phe Val Met Thr Asn Phe Leu Lys Thr Glu 100 105 110 | | |
| 15 | Gly Gln Glu Gln Trp Leu Cys Pro Glu Tyr Pro Thr Arg Arg Thr Leu 115 120 125 | | |
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| 20 | Lys Gly Ile Gln Thr Gly Arg Cys Val Val His Glu Gly Asn Gln Lys 145 150 155 160 | | |
| | Thr Cys Glu Val Ser Ala Trp Cys Pro Ile Glu Ala Val Glu Glu Ala 165 170 175 | | |
| 25 | Pro Arg Pro Ala Leu Leu Asn Ser Ala Glu Asn Phe Thr Val Leu Ile 180 185 190 | | |
| | Lys Asn Asn Ile Asp Phe Pro Gly His Asn Tyr Thr Thr Arg Asn Ile 195 200 205 | | |
| 30 | Leu Pro Gly Leu Asn Ile Thr Cys Thr Phe His Lys Thr Gln Asn Pro 210 215 220 | | |
| 35 | Gln Cys Pro Ile Phe Arg Leu Gly Asp Ile Phe Arg Glu Thr Gly Asp 225 230 235 240 | | |
| | Asn Phe Ser Asp Val Ala Ile Gln Gly Gly Ile Met Gly Ile Glu Ile 245 250 255 | | |
| 40 | Tyr Trp Asp Cys Asn Leu Asp Arg Trp Phe His His Cys Arg Pro Lys 260 265 270 | | |
| | Tyr Ser Phe Arg Arg Leu Asp Asp Lys Thr Thr Asn Val Ser Leu Tyr 275 280 285 | | |
| 45 | Pro Gly Tyr Asn Phe Arg Tyr Ala Lys Tyr Tyr Lys Glu Asn Asn Val 290 295 300 | | |
| | Glu Lys Arg Thr Leu Ile Lys Val Phe Gly Ile Arg Phe Asp Ile Leu 305 310 315 320 | | |
| 50 | Val Phe Gly Thr Gly Gly Lys Phe Asp Ile Ile Gln Leu Val Val Tyr 325 330 335 | | |
| 55 | Ile Gly Ser Thr Leu Ser Tyr Phe Gly Leu Ala Ala Val Phe Ile Asp | | |

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| | Pro Trp Cys Lys Cys Cys Gln Pro Cys Val Val Asn Glu Tyr Tyr Tyr 370 375 380 | | |
| 10 | Arg Lys Lys Cys Glu Ser Ile Val Glu Pro Lys Pro Thr Leu Lys Tyr 385 390 395 400 | | |
| | Val Ser Phe Val Asp Glu Ser His Ile Arg Met Val Asn Gln Gln Leu 405 410 415 | | |
| 15 | Leu Gly Arg Ser Leu Gln Asp Val Lys Gly Gln Glu Val Pro Arg Pro 420 425 430 | | |
| | Ala Met Asp Phe Thr Asp Leu Ser Arg Leu Pro Leu Ala Leu His Asp 435 440 445 | | |
| 20 | Thr Pro Pro Ile Pro Gly Gln Pro Glu Glu Ile Gln Leu Leu Arg Lys 450 455 460 | | |
| | Glu Ala Thr Pro Arg Ser Arg Asp Ser Pro Val Trp Cys Gln Cys Gly 465 470 475 480 | | |
| 25 | Ser Cys Leu Pro Ser Gln Leu Pro Glu Ser His Arg Cys Leu Glu Glu 485 490 495 | | |
| | Leu Cys Cys Arg Lys Lys Pro Gly Ala Cys Ile Thr Thr Ser Glu Leu 500 505 510 | | |
| 30 | Phe Arg Lys Leu Val Leu Ser Arg His Val Leu Gln Phe Leu Leu Leu 515 520 525 | | |
| | Tyr Gln Glu Pro Leu Leu Ala Leu Asp Val Asp Ser Thr Asn Ser Arg 530 535 540 | | |
| 35 | Leu Arg His Cys Ala Tyr Arg Cys Tyr Ala Thr Trp Arg Phe Gly Ser 545 550 555 560 | | |
| 40 | Gln Asp Met Ala Asp Phe Ala Ile Leu Pro Ser Cys Cys Arg Trp Arg 565 570 575 | | |
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 Phe His Val Ile Ile Phe Ser Tyr Val Cys Phe Ala Leu Val Ser Asp
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 10 Lys Leu Tyr Gln Arg Lys Glu Pro Val Ile Ser Ser Val His Thr Lys
 50 55 60
 Val Lys Gly Ile Ala Glu Val Lys Glu Glu Ile Val Glu Asn Gly Val
 65 70 75 80
 15 Lys Lys Leu Val His Ser Val Phe Asp Thr Ala Asp Tyr Thr Phe Pro
 85 90 95
 Leu Gln Gly Asn Ser Phe Phe Val Met Thr Asn Phe Leu Lys Thr Glu
 100 105 110
 20 Gly Gln Glu Gln Arg Leu Cys Pro Glu Tyr Pro Thr Arg Arg Thr Leu
 115 120 125
 Cys Ser Ser Asp Arg Gly Cys Lys Lys Gly Trp Met Asp Pro Gln Ser
 130 135 140
 25 Lys Gly Ile Gln Thr Arg Arg Cys Val Val His Glu Gly Asn Gln Lys
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 Thr Cys Glu Val Ser Ala Trp Cys Pro Ile Glu Ala Val Glu Glu Ala
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 35 Lys Asn Asn Ile Asp Phe Pro Gly His Asn Tyr Thr Thr Arg Asn Ile
 195 200 205
 Leu Pro Gly Leu Asn Ile Thr Cys Thr Phe His Lys Thr Gln Asn Pro
 210 215 220
 40 Gln Cys Pro Ile Phe Arg Leu Gly Asp Ile Phe Arg Glu Thr Gly Asp
 225 230 235 240
 Asn Phe Ser Asp Val Ala Ile Gln Gly Gly Ile Met Gly Ile Glu Ile
 245 250 255
 45 Tyr Trp Asp Cys Asn Leu Asp Arg Trp Phe His His Cys Arg Pro Lys
 260 265 270
 Tyr Ser Phe Arg Arg Leu Asp Asp Lys Thr Thr Asn Val Ser Leu Tyr
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Val Phe Gly Thr Gly Gly Lys Phe Asp Ile Ile Gln Leu Val Val Tyr
325 330 335

5 Ile Gly Ser Thr Leu Ser Tyr Phe Gly Leu Ala Ala Val Phe Ile Asp
340 345 350

Phe Leu Ile Asp Thr Tyr Ser Ser Asn Cys Cys Arg Ser His Ile Tyr
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10 Pro Trp Cys Lys Cys Cys Gln Pro Cys Val Val Asn Glu Tyr Tyr Tyr
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Arg Lys Lys Cys Glu Ser Ile Val Glu Pro Lys Pro Thr Leu Lys Tyr
385 390 395 400

Val Ser Phe Val Asp Glu Ser His Ile Arg Met Val Asn Gln Gln Leu
405 410 415

20 Leu Gly Arg Ser Leu Gln Asp Val Lys Gly Gln Glu Val Pro Arg Pro
420 425 430

Ala Met Asp Phe Thr Asp Leu Ser Arg Leu Pro Leu Ala Leu His Asp
435 440 445

25 Thr Pro Pro Ile Pro Gly Gln Pro Glu Glu Ile Gln Leu Leu Arg Lys
450 455 460

Glu Ala Thr Pro Arg Ser Arg Asp Ser Pro Val Trp Cys Gln Cys Gly
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30 Ser Cys Leu Pro Ser Gln Leu Pro Glu Ser His Arg Cys Leu Glu Glu
485 490 495

Leu Cys Cys Arg Lys Lys Pro Gly Ala Cys Ile Thr Thr Ser Glu Leu
500 505 510

Phe Arg Lys Leu Val Leu Ser Arg His Val Leu Gln Phe Leu Leu Leu
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40 Tyr Gln Glu Pro Leu Leu Ala Leu Asp Val Asp Ser Thr Asn Ser Arg
530 535 540

Leu Arg His Cys Ala Tyr Arg Cys Tyr Ala Thr Trp Arg Phe Gly Ser
545 550 555 560

45 Gln Asp Met Ala Asp Phe Ala Ile Leu Pro Ser Cys Cys Arg Trp Arg
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35 40 45

Lys Leu Tyr Gln Arg Lys Glu Pro Val Ile Ser Ser Val His Thr Lys
50 55 60

15 Val Lys Gly Ile Ala Glu Val Lys Glu Glu Ile Val Glu Asn Gly Val
65 70 75 80

20 Lys Lys Leu Val His Ser Val Phe Asp Thr Ala Asp Tyr Thr Phe Pro
85 90 95

Leu Gln Gly Asn Ser Phe Phe Val Met Thr Asn Phe Leu Lys Thr Glu
100 105 110

25 Gly Gln Glu Gln Arg Leu Cys Pro Glu Tyr Pro Thr Arg Arg Thr Leu
115 120 125

Cys Ser Ser Asp Arg Gly Cys Lys Lys Gly Trp Met Asp Pro Gln Ser
130 135 140

30 Lys Gly Ile Gln Thr Gly Arg Cys Val Val His Glu Gly Asn Gln Lys
145 150 155 160

35 Thr Cys Glu Val Ser Ala Trp Cys Pro Ile Glu Ala Val Glu Glu Ala
165 170 175

Pro Arg Pro Ala Leu Leu Asn Ser Ala Lys Asn Phe Thr Val Leu Ile
180 185 190

40 Lys Asn Asn Ile Asp Phe Pro Gly His Asn Tyr Thr Thr Arg Asn Ile
195 200 205

Leu Pro Gly Leu Asn Ile Thr Cys Thr Phe His Lys Thr Gln Asn Pro
210 215 220

45 Gln Cys Pro Ile Phe Arg Leu Gly Asp Ile Phe Arg Glu Thr Gly Asp
225 230 235 240

Asn Phe Ser Asp Val Ala Ile Gln Gly Gly Ile Met Gly Ile Glu Ile
245 250 255

50 Tyr Trp Asp Cys Asn Leu Asp Arg Trp Phe His His Cys Arg Pro Lys
260 265 270

55 Tyr Ser Phe Arg Arg Leu Asp Asp Lys Thr Thr Asn Val Ser Leu Tyr
275 280 285

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| | | | | |
|----|---|-----|-----|-----|
| | Pro Gly Tyr Asn Phe Arg Tyr Ala Lys Tyr Tyr Lys Glu Asn Asn Val | 290 | 295 | 300 |
| 5 | Glu Lys Arg Thr Leu Ile Lys Val Phe Gly Ile Arg Phe Asp Ile Leu | 305 | 310 | 315 |
| | Val Phe Gly Thr Gly Gly Lys Phe Asp Ile Ile Gln Leu Val Val Tyr | | 325 | 330 |
| 10 | Ile Gly Ser Thr Leu Ser Tyr Phe Gly Leu Ala Ala Val Phe Ile Asp | | 340 | 345 |
| | Phe Leu Ile Asp Thr Tyr Ser Ser Asn Cys Cys Arg Ser His Ile Tyr | | 355 | 360 |
| 15 | Pro Trp Cys Lys Cys Cys Gln Pro Cys Val Val Asn Glu Tyr Tyr Tyr | | 370 | 375 |
| | Arg Lys Lys Cys Glu Ser Ile Val Glu Pro Lys Pro Thr Leu Lys Tyr | | 385 | 390 |
| 20 | Val Ser Phe Val Asp Glu Ser His Ile Arg Met Val Asn Gln Gln Leu | | 405 | 410 |
| | Leu Gly Arg Ser Leu Gln Asp Val Lys Gly Gln Glu Val Pro Arg Pro | | 420 | 425 |
| 25 | Ala Met Asp Phe Thr Asp Leu Ser Arg Leu Pro Leu Ala Leu His Asp | | 435 | 440 |
| | Thr Pro Pro Ile Pro Gly Gln Pro Glu Glu Ile Gln Leu Leu Arg Lys | | 450 | 455 |
| 30 | Glu Ala Thr Pro Arg Ser Arg Asp Ser Pro Val Trp Cys Gln Cys Gly | | 465 | 470 |
| | Ser Cys Leu Pro Ser Gln Leu Pro Glu Ser His Arg Cys Leu Glu Glu | | 485 | 490 |
| 35 | Leu Cys Cys Arg Lys Lys Pro Gly Ala Cys Ile Thr Thr Ser Glu Leu | | 500 | 505 |
| | Phe Arg Lys Leu Val Leu Ser Arg His Val Leu Gln Phe Leu Leu Leu | | 515 | 520 |
| 40 | Tyr Gln Glu Pro Leu Leu Ala Leu Asp Val Asp Ser Thr Asn Ser Arg | | 530 | 535 |
| | Leu Arg His Cys Ala Tyr Arg Cys Tyr Ala Thr Trp Arg Phe Gly Ser | | 545 | 550 |
| 45 | Gln Asp Met Ala Asp Phe Ala Ile Leu Pro Ser Cys Cys Arg Trp Arg | | 565 | 570 |
| | Ile Arg Lys Glu Phe Pro Lys Ser Glu Gly Gln Tyr Ser Gly Phe Lys | | 580 | 585 |
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Ser Pro Tyr
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Lys Val Thr Arg Ile Gln Ser Met Asn Tyr Gly Thr Ile Lys Trp Phe
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15 Phe His Val Ile Ile Phe Ser Tyr Val Cys Phe Ala Leu Val Ser Asp
35 40 45

Lys Leu Tyr Gln Arg Lys Glu Pro Val Ile Ser Ser Val His Thr Lys
50 55 60

20 Val Lys Gly Ile Ala Glu Val Lys Glu Glu Ile Val Glu Asn Gly Val
65 70 75 80

25 Lys Lys Leu Val His Ser Val Phe Asp Thr Ala Asp Tyr Thr Phe Pro
85 90 95

Leu Gln Gly Asn Ser Phe Phe Val Met Thr Asn Phe Leu Lys Thr Glu
100 105 110

30 Gly Gln Glu Gln Arg Leu Cys Pro Glu Tyr Pro Thr Arg Arg Thr Leu
115 120 125

Cys Ser Ser Asp Arg Gly Cys Lys Lys Gly Trp Met Asp Pro Gln Ser
130 135 140

35 Lys Gly Ile Gln Thr Gly Arg Cys Val Val His Glu Gly Asn Gln Lys
145 150 155 160

Thr Cys Glu Val Ser Ala Trp Cys Pro Ile Glu Ala Val Glu Glu Ala
165 170 175

40 Pro Arg Pro Ala Leu Leu Asn Ser Ala Glu Asn Phe Thr Val Pro Ile
180 185 190

45 Lys Asn Asn Ile Asp Phe Pro Gly His Asn Tyr Thr Thr Arg Asn Ile
195 200 205

Leu Pro Gly Leu Asn Ile Thr Cys Thr Phe His Lys Thr Gln Asn Pro
210 215 220

50 Gln Cys Pro Ile Phe Arg Leu Gly Asp Ile Phe Arg Glu Thr Gly Asp
225 230 235 240

Asn Phe Ser Asp Val Ala Ile Gln Gly Gly Ile Met Gly Ile Glu Ile
245 250 255

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Tyr Trp Asp Cys Asn Leu Asp Arg Trp Phe His His Cys Arg Pro Lys
 260 265 270
 5 Tyr Ser Phe Arg Arg Leu Asp Asp Lys Thr Thr Asn Val Ser Leu Tyr
 275 280 285
 Pro Gly Tyr Asn Phe Arg Tyr Ala Lys Tyr Tyr Lys Glu Asn Asn Val
 290 295 300
 10 Glu Lys Arg Thr Leu Ile Lys Val Phe Gly Ile Arg Phe Asp Ile Leu
 305 310 315 320
 Val Phe Gly Thr Gly Gly Lys Phe Asp Ile Ile Gln Leu Val Val Tyr
 325 330 335
 15 Ile Gly Ser Thr Leu Ser Tyr Phe Gly Leu Ala Ala Val Phe Ile Asp
 340 345 350
 Phe Leu Ile Asp Thr Tyr Ser Ser Asn Cys Cys Arg Ser His Ile Tyr
 355 360 365
 20 Pro Trp Cys Lys Cys Cys Gln Pro Cys Val Val Asn Glu Tyr Tyr Tyr
 370 375 380
 Arg Lys Lys Cys Glu Ser Ile Val Glu Pro Lys Pro Thr Leu Lys Tyr
 385 390 395 400
 25 Val Ser Phe Val Asp Glu Ser His Ile Arg Met Val Asn Gln Gln Leu
 405 410 415
 30 Leu Gly Arg Ser Leu Gln Asp Val Lys Gly Gln Glu Val Pro Arg Pro
 420 425 430
 Ala Met Asp Phe Thr Asp Leu Ser Arg Leu Pro Leu Ala Leu His Asp
 435 440 445
 35 Thr Pro Pro Ile Pro Gly Gln Pro Glu Glu Ile Gln Leu Leu Arg Lys
 450 455 460
 Glu Ala Thr Pro Arg Ser Arg Asp Ser Pro Val Trp Cys Gln Cys Gly
 465 470 475 480
 40 Ser Cys Leu Pro Ser Gln Leu Pro Glu Ser His Arg Cys Leu Glu Glu
 485 490 495
 45 Leu Cys Cys Arg Lys Lys Pro Gly Ala Cys Ile Thr Thr Ser Glu Leu
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 Phe Arg Lys Leu Val Leu Ser Arg His Val Leu Gln Phe Leu Leu Leu
 515 520 525
 50 Tyr Gln Glu Pro Leu Leu Ala Leu Asp Val Asp Ser Thr Asn Ser Arg
 530 535 540
 Leu Arg His Cys Ala Tyr Arg Cys Tyr Ala Thr Trp Arg Phe Gly Ser
 545 550 555 560
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Gln Asp Met Ala Asp Phe Ala Ile Leu Pro Ser Cys Cys Arg Trp Arg
565 570 575

5 Ile Arg Lys Glu Phe Pro Lys Ser Glu Gly Gln Tyr Ser Gly Phe Lys
580 585 590

Ser Pro Tyr
595

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Lys Val Thr Arg Ile Gln Ser Met Asn Tyr Gly Thr Ile Lys Trp Phe
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Phe His Val Ile Ile Phe Ser Tyr Val Cys Phe Ala Leu Val Ser Asp
35 40 45

25 Lys Leu Tyr Gln Arg Lys Glu Pro Val Ile Ser Ser Val His Thr Lys
50 55 60

Val Lys Gly Ile Ala Glu Val Lys Glu Glu Ile Val Glu Asn Gly Val
65 70 75 80

30 Lys Lys Leu Val His Ser Val Phe Asp Thr Ala Asp Tyr Thr Phe Pro
85 90 95

Leu Gln Gly Asn Ser Phe Phe Val Met Thr Asn Phe Leu Lys Thr Glu
100 105 110

35 Gly Gln Glu Gln Arg Leu Cys Pro Glu Tyr Pro Thr Arg Arg Thr Leu
115 120 125

Cys Ser Ser Asp Arg Gly Cys Lys Lys Gly Trp Met Asp Pro Gln Ser
130 135 140

40 Lys Gly Ile Gln Thr Gly Arg Cys Val Val His Glu Gly Asn Gln Lys
145 150 155 160

Thr Cys Glu Val Ser Ala Trp Cys Pro Ile Glu Ala Val Glu Glu Ala
165 170 175

45 Pro Arg Pro Ala Leu Leu Asn Ser Ala Glu Asn Phe Thr Val Leu Ile
180 185 190

Lys Asn Asn Ile Asp Phe Pro Gly His Asn Tyr Thr Thr Arg Asn Ile
195 200 205

50 Leu Pro Gly Leu Asn Ile Thr Cys Thr Phe His Lys Thr Gln Asn Pro
210 215 220

55 Gln Cys Pro Ile Phe Arg Leu Gly Asp Ile Phe Arg Glu Thr Gly Asp

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| | | | | | | | |
|----|---|---|-----------------------------|-----|-----|-----|-----|
| | 225 | | 230 | | 235 | | 240 |
| 5 | Asn Phe Ser Asp | Val Ala Ile Gln Gly | Gly Ile Met Gly Ile Glu Ile | | | | |
| | | 245 | | 250 | | 255 | |
| | Tyr Trp Asp Cys | Asn Leu Asp Arg Trp Phe His His Cys Cys Pro Lys | | | | | |
| | | 260 | | 265 | | 270 | |
| 10 | Tyr Ser Phe Arg Arg Leu Asp Asp Lys Thr Thr Asn Val Ser Leu Tyr | | | | | | |
| | | 275 | | 280 | | 285 | |
| | Pro Gly Tyr Asn Phe Arg Tyr Ala Lys Tyr Tyr Lys Glu Asn Asn Val | | | | | | |
| | | 290 | | 295 | | 300 | |
| 15 | Glu Lys Arg Thr Leu Ile Lys Val Phe Gly Ile Arg Phe Asp Ile Leu | | | | | | |
| | | 305 | | 310 | | 315 | |
| | Val Phe Gly Thr Gly Gly Lys Phe Asp Ile Ile Gln Leu Val Val Tyr | | | | | | |
| | | | 325 | | 330 | | 335 |
| 20 | Ile Gly Ser Thr Leu Ser Tyr Phe Gly Leu Ala Ala Val Phe Ile Asp | | | | | | |
| | | 340 | | 345 | | 350 | |
| | Phe Leu Ile Asp Thr Tyr Ser Ser Asn Cys Cys Arg Ser His Ile Tyr | | | | | | |
| 25 | | 355 | | 360 | | 365 | |
| | Pro Trp Cys Lys Cys Cys Gln Pro Cys Val Val Asn Glu Tyr Tyr Tyr | | | | | | |
| | | 370 | | 375 | | 380 | |
| 30 | Arg Lys Lys Cys Glu Ser Ile Val Glu Pro Lys Pro Thr Leu Lys Tyr | | | | | | |
| | | 385 | | 390 | | 395 | |
| | Val Ser Phe Val Asp Glu Ser His Ile Arg Met Val Asn Gln Gln Leu | | | | | | |
| | | | 405 | | 410 | | 415 |
| 35 | Leu Gly Arg Ser Leu Gln Asp Val Lys Gly Gln Glu Val Pro Arg Pro | | | | | | |
| | | 420 | | 425 | | 430 | |
| | Ala Met Asp Phe Thr Asp Leu Ser Arg Leu Pro Leu Ala Leu His Asp | | | | | | |
| 40 | | 435 | | 440 | | 445 | |
| | Thr Pro Pro Ile Pro Gly Gln Pro Glu Glu Ile Gln Leu Leu Arg Lys | | | | | | |
| | | 450 | | 455 | | 460 | |
| 45 | Glu Ala Thr Pro Arg Ser Arg Asp Ser Pro Val Trp Cys Gln Cys Gly | | | | | | |
| | | 465 | | 470 | | 475 | |
| | Ser Cys Leu Pro Ser Gln Leu Pro Glu Ser His Arg Cys Leu Glu Glu | | | | | | |
| | | | 485 | | 490 | | 495 |
| 50 | Leu Cys Cys Arg Lys Lys Pro Gly Ala Cys Ile Thr Thr Ser Glu Leu | | | | | | |
| | | 500 | | 505 | | 510 | |
| | Phe Arg Lys Leu Val Leu Ser Arg His Val Leu Gln Phe Leu Leu Leu | | | | | | |
| | | 515 | | 520 | | 525 | |
| 55 | Tyr Gln Glu Pro Leu Leu Ala Leu Asp Val Asp Ser Thr Asn Ser Arg | | | | | | |

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| | | | | | | |
|----|-------------------------------------|---------------------------------|-------------------------|-----|-----|--|
| | 530 | | 535 | | 540 | |
| 5 | Leu Arg His Cys Ala Tyr | Arg Cys Tyr Ala Thr | Trp Arg Phe Gly Ser | | | |
| | 545 | 550 | 555 | | 560 | |
| | Gln Asp Met Ala Asp | Phe Ala Ile Leu Pro | Ser Cys Cys Arg Trp Arg | | | |
| | | 565 | 570 | 575 | | |
| 10 | Ile Arg Lys Glu Phe Pro Lys Ser | Glu Gly Gln Tyr Ser Gly | Phe Lys | | | |
| | | 580 | 585 | 590 | | |
| | Ser Pro Tyr | | | | | |
| | | 595 | | | | |
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| | <211> 595 | | | | | |
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| | <213> Homo sapiens | | | | | |
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| | 1 | 5 | 10 | 15 | | |
| | Lys Val Thr Arg Ile Gln Ser Met Asn | Tyr Gly Thr Ile Lys Trp Phe | | | | |
| | | 20 | 25 | 30 | | |
| 25 | Phe His Val Ile Ile Phe Ser Tyr | Val Cys Phe Ala Leu Val Ser Asp | | | | |
| | | 35 | 40 | 45 | | |
| | Lys Leu Tyr Gln Arg Lys Glu Pro | Val Ile Ser Ser Val His Thr Lys | | | | |
| | | 50 | 55 | 60 | | |
| 30 | Val Lys Gly Ile Ala Glu Val Lys Glu | Glu Ile Val Glu Asn Gly Val | | | | |
| | | 65 | 70 | 75 | 80 | |
| | Lys Lys Leu Val His Ser Val Phe Asp | Thr Ala Asp Tyr Thr Phe Pro | | | | |
| | | 85 | 90 | 95 | | |
| | Leu Gln Gly Asn Ser Phe Phe Val Met | Thr Asn Phe Leu Lys Thr Glu | | | | |
| | | 100 | 105 | 110 | | |
| 40 | Gly Gln Glu Gln Arg Leu Cys Pro | Glu Tyr Pro Thr Arg Arg Thr Leu | | | | |
| | | 115 | 120 | 125 | | |
| | Cys Ser Ser Asp Arg Gly Cys Lys Lys | Gly Trp Met Asp Pro Gln Ser | | | | |
| | | 130 | 135 | 140 | | |
| 45 | Lys Gly Ile Gln Thr Gly Arg Cys Val | Val His Glu Gly Asn Gln Lys | | | | |
| | | 145 | 150 | 155 | 160 | |
| | Thr Cys Glu Val Ser Ala Trp Cys Pro | Ile Glu Ala Val Glu Glu Ala | | | | |
| | | 165 | 170 | 175 | | |
| 50 | Pro Arg Pro Ala Leu Leu Asn Ser | Ala Glu Asn Phe Thr Val Leu Ile | | | | |
| | | 180 | 185 | 190 | | |
| 55 | Lys Asn Asn Ile Asp Phe Pro Gly | His Asn Tyr Thr Thr Arg Asn Ile | | | | |
| | | 195 | 200 | 205 | | |

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5 Leu Pro Gly Leu Asn Ile Thr Cys Thr Phe His Lys Thr Gln Asn Pro
 210 215 220
 Gln Cys Pro Ile Phe Arg Leu Gly Asp Ile Phe Arg Glu Thr Gly Asp
 225 230 235 240
 10 Asn Phe Ser Asp Val Ala Ile Gln Gly Gly Ile Met Gly Ile Glu Ile
 245 250 255
 Tyr Trp Asp Cys Asn Leu Asp Arg Trp Phe His His Cys Arg Pro Lys
 260 265 270
 15 Tyr Ser Phe Arg Arg Leu Asp Asp Lys Thr Thr Asn Val Ser Leu Tyr
 275 280 285
 Pro Gly Tyr Asn Phe Arg Tyr Ala Lys Tyr Tyr Lys Glu Asn Asn Val
 290 295 300
 20 Glu Lys Arg Thr Leu Ile Lys Val Phe Gly Ile Arg Phe Asp Ile Leu
 305 310 315 320
 Val Phe Gly Thr Gly Gly Lys Phe Asp Ile Ile Gln Leu Val Val Tyr
 325 330 335
 25 Ile Gly Ser Thr Leu Ser Tyr Phe Gly Leu Ala Ala Val Phe Ile Asp
 340 345 350
 30 Phe Leu Ile Asp Thr Tyr Ser Ser Asn Cys Cys Arg Ser His Ile Tyr
 355 360 365
 Pro Trp Cys Lys Cys Cys Gln Pro Cys Val Val Asn Glu Tyr Tyr Tyr
 370 375 380
 35 Arg Lys Lys Cys Glu Ser Ile Val Glu Pro Lys Pro Thr Leu Lys Tyr
 385 390 395 400
 Val Ser Phe Val Asp Glu Ser His Ile Arg Met Val Asn Gln Gln Leu
 405 410 415
 40 Leu Gly Arg Ser Leu Gln Asp Val Lys Gly Gln Glu Val Pro Arg Pro
 420 425 430
 Ala Met Asp Phe Thr Asp Leu Ser Arg Leu Pro Leu Ala Leu His Asp
 435 440 445
 45 Thr Pro Pro Ile Pro Gly Gln Pro Glu Glu Ile Gln Leu Leu Arg Lys
 450 455 460
 50 Glu Ala Thr Pro Arg Ser Arg Asp Ser Pro Val Trp Cys Gln Cys Gly
 465 470 475 480
 Ser Cys Leu Pro Ser Gln Leu Pro Glu Ser His Arg Cys Leu Glu Glu
 485 490 495
 55 Leu Cys Cys Arg Lys Lys Pro Gly Ala Cys Ile Thr Thr Ser Glu Leu
 500 505 510

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5 Phe Arg Lys Leu Val Leu Ser Arg His Val Leu Gln Phe Leu Leu Leu
 515 520 525
 Tyr Gln Glu Pro Leu Leu Ala Leu Asp Val Asp Ser Thr Asn Ser Arg
 530 535 540
 10 Leu Arg His Cys Ala Tyr Arg Cys Tyr Ala Thr Trp Arg Phe Gly Ser
 545 550 555 560
 Gln Asp Met Ala Asp Phe Ala Asn Leu Pro Ser Cys Cys Arg Trp Arg
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 Ser Pro Tyr
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 30 Phe His Val Ile Ile Phe Ser Tyr Val Cys Phe Ala Leu Val Ser Asp
 35 40 45
 Lys Leu Tyr Gln Arg Lys Glu Pro Val Ile Ser Ser Val His Thr Lys
 50 55 60
 35 Val Lys Gly Ile Ala Glu Val Lys Glu Glu Ile Val Glu Asn Gly Val
 65 70 75 80
 40 Lys Lys Leu Val His Ser Val Phe Asp Thr Ala Asp Tyr Thr Phe Pro
 85 90 95
 Leu Gln Gly Asn Ser Phe Phe Val Met Thr Asn Phe Leu Lys Thr Glu
 100 105 110
 45 Gly Gln Glu Gln Arg Leu Cys Pro Glu Tyr Pro Thr Arg Arg Thr Leu
 115 120 125
 Cys Ser Ser Asp Arg Gly Cys Lys Lys Gly Trp Met Asp Pro Gln Ser
 130 135 140
 50 Lys Gly Ile Gln Thr Gly Arg Cys Val Val His Glu Gly Asn Gln Lys
 145 150 155 160
 55 Thr Cys Glu Val Ser Ala Trp Cys Pro Ile Glu Ala Val Glu Glu Ala
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Pro Arg Pro Ala Leu Leu Asn Ser Ala Glu Asn Phe Thr Val Leu Ile
180 185 190

5 Lys Asn Asn Ile Asp Phe Pro Gly His Asn Tyr Thr Thr Arg Asn Ile
195 200 205

Leu Pro Gly Leu Asn Ile Thr Cys Thr Phe His Lys Thr Gln Asn Pro
210 215 220

10 Gln Cys Pro Ile Phe Arg Leu Gly Asp Ile Phe Arg Glu Thr Gly Asp
225 230 235 240

Asn Phe Ser Asp Val Ala Ile Gln Gly Gly Ile Met Gly Ile Glu Ile
245 250 255

15 Tyr Trp Asp Cys Asn Leu Asp Arg Trp Phe His His Cys Arg Pro Lys
260 265 270

Tyr Ser Phe Arg Arg Leu Asp Asp Lys Thr Thr Asn Val Ser Leu Tyr
275 280 285

20 Pro Gly Tyr Asn Phe Arg Tyr Ala Lys Tyr Tyr Lys Glu Asn Asn Val
290 295 300

25 Glu Lys Arg Thr Leu Ile Lys Val Phe Gly Ile Arg Phe Asp Ile Leu
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Val Phe Gly Thr Gly Gly Lys Phe Asp Ile Ile Gln Leu Val Val Tyr
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30 Ile Gly Ser Thr Leu Ser Tyr Phe Gly Leu Ala Ala Val Phe Ile Asp
340 345 350

Phe Leu Ile Asp Thr Tyr Ser Ser Asn Cys Cys Arg Ser His Ile Tyr
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35 Pro Trp Cys Lys Cys Cys Gln Pro Cys Val Val Asn Glu Tyr Tyr Tyr
370 375 380

40 Arg Lys Lys Cys Glu Ser Ile Val Glu Pro Lys Pro Thr Leu Lys Tyr
385 390 395 400

Val Ser Phe Val Asp Glu Ser His Ile Arg Met Val Asn Gln Gln Leu
405 410 415

45 Leu Gly Arg Ser Leu Gln Asp Val Lys Gly Gln Glu Val Pro Arg Pro
420 425 430

Ala Met Asp Phe Thr Asp Leu Ser Arg Leu Pro Leu Ala Leu His Asp
435 440 445

50 Thr Pro Pro Ile Pro Gly Gln Pro Glu Glu Ile Gln Leu Leu Arg Lys
450 455 460

Glu Ala Thr Pro Arg Ser Arg Asp Ser Pro Val Trp Cys Gln Cys Gly
465 470 475 480

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Ser Cys Leu Pro Ser Gln Leu Glu Glu Leu Cys Cys Arg Lys Lys Pro
 485 490 495
 5 Gly Ala Cys Ile Thr Thr Ser Glu Leu Phe Arg Lys Leu Val Leu Ser
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 Arg His Val Leu Gln Phe Leu Leu Leu Tyr Gln Glu Pro Leu Leu Ala
 515 520 525
 10 Leu Asp Val Asp Ser Thr Asn Ser Arg Leu Arg His Cys Ala Tyr Arg
 530 535 540
 Cys Tyr Ala Thr Trp Arg Phe Gly Ser Gln Asp Met Ala Asp Phe Ala
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 35 35 40 45
 Lys Leu Tyr Gln Arg Lys Glu Pro Val Ile Ser Ser Val His Thr Lys
 50 55 60
 40 Val Lys Gly Ile Ala Glu Val Lys Glu Glu Ile Val Glu Asn Gly Val
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 Lys Lys Leu Val His Ser Val Phe Asp Thr Ala Asp Tyr Thr Phe Pro
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 45 Leu Gln Gly Asn Ser Phe Phe Val Met Thr Asn Phe Leu Lys Thr Glu
 100 105 110
 Gly Gln Glu Gln Arg Leu Cys Pro Glu Tyr Pro Thr Arg Arg Thr Leu
 115 120 125
 50 Cys Ser Ser Asp Arg Gly Cys Lys Lys Gly Trp Met Asp Pro Gln Ser
 130 135 140
 55 Lys Gly Ile Gln Thr Gly Arg Cys Val Val His Glu Gly Asn Gln Lys
 145 150 155 160

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Thr Cys Glu Val Ser Ala Trp Cys Pro Ile Glu Ala Val Glu Glu Ala
165 170 175

5 Pro Arg Pro Ala Leu Leu Asn Ser Ala Glu Asn Phe Thr Val Leu Ile
180 185 190

Lys Asn Asn Ile Asp Phe Pro Gly His Asn Tyr Thr Thr Arg Asn Ile
195 200 205

10 Leu Pro Gly Leu Asn Ile Thr Cys Thr Phe His Lys Thr Gln Asn Pro
210 215 220

Gln Cys Pro Ile Phe Arg Leu Gly Asp Ile Phe Arg Glu Thr Gly Asp
225 230 235 240

15 Asn Phe Ser Asp Val Ala Ile Gln Gly Gly Ile Met Gly Ile Glu Ile
245 250 255

Tyr Trp Asp Cys Asn Leu Asp Arg Trp Phe His His Cys Arg Pro Lys
260 265 270

20 Tyr Ser Phe Arg Arg Leu Asp Asp Lys Thr Thr Asn Val Ser Leu Tyr
275 280 285

25 Pro Gly Tyr Asn Phe Arg Tyr Ala Lys Tyr Tyr Lys Glu Asn Asn Val
290 295 300

Glu Lys Arg Thr Leu Ile Lys Val Phe Gly Ile Arg Phe Asp Ile Leu
305 310 315 320

30 Val Phe Gly Thr Gly Gly Lys Phe Asp Ile Ile Gln Leu Val Val Tyr
325 330 335

Ile Gly Ser Thr Leu Ser Tyr Phe Gly Leu Ala Ala Val Phe Ile Asp
340 345 350

35 Phe Leu Ile Asp Thr Tyr Ser Ser Asn Cys Cys Arg Ser His Ile Tyr
355 360 365

Pro Trp Cys Lys Cys Cys Gln Pro Cys Val Val Asn Glu Tyr Tyr Tyr
370 375 380

40 Arg Lys Lys Cys Glu Ser Ile Val Glu Pro Lys Pro Thr Leu Lys Tyr
385 390 395 400

45 Val Ser Phe Val Asp Glu Ser His Ile Arg Met Val Asn Gln Gln Leu
405 410 415

Leu Gly Arg Ser Leu Gln Asp Val Lys Gly Gln Glu Val Pro Arg Pro
420 425 430

50 Ala Met Asp Phe Thr Asp Leu Ser Arg Leu Pro Leu Ala Leu His Asp
435 440 445

Thr Pro Pro Ile Pro Gly Gln Pro Glu Glu Ile Gln Leu Leu Arg Lys
450 455 460

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| | Glu Ala Thr Pro Arg Ser Arg Asp Ser Pro Val Trp Cys Gln Cys Gly | |
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| 5 | Ser Cys Leu Pro Ser Gln Leu Pro Glu Ser His Arg Cys Leu Glu Glu | |
| | 485 490 495 | |
| | Leu Cys Cys Arg Lys Lys Pro Gly Ala Cys Ile Thr Thr Ser Glu Leu | |
| | 500 505 510 | |
| 10 | Phe Arg Lys Leu Val Leu Ser Arg His Val Leu Gln Phe Leu Leu Leu | |
| | 515 520 525 | |
| | Tyr Gln Glu Pro Leu Leu Ala Leu Asp Val Asp Ser Thr Asn Ser Arg | |
| | 530 535 540 | |
| 15 | Leu Arg His Cys Ala Tyr Arg Cys Tyr Ala Thr Trp Arg Phe Gly Ser | |
| | 545 550 555 560 | |
| | Gln Asp Met Ala Asp Phe Ala Ile Leu Pro Ser Cys Cys Arg Trp Arg | |
| | 565 570 575 | |
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20

Claims

1. A nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of:

(a) a genomic nucleotide sequence encoding an ATP-gated ion channel P2X7R and which contains a mutation in the 5'UTR region corresponding to positions 362, 532, 1100, 1122, 1171 or 1702 of the genomic sequence of the wild-type ATP-gated ion channel P2X7R as depicted in SEQ ID NO: 1, wherein at said position said nucleotide is replaced by another nucleotide;

(b) a nucleic acid sequence encoding a polypeptide which has an amino acid sequence of the ATP-gated ion channel P2X7R, wherein in the exon as indicated in column "Exon" of the following Table A the amino acid residue as indicated in column "Amino acid residue" of Table A corresponding to the position as indicated in column "Position in wild-type" of Table A of the wild-type ATP-gated ion channel P2X7R amino acid sequence as depicted in SEQ ID NO: 3 or 4 is replaced by another amino acid residue

Table A

| Exon | Amino acid residue | Position in wild-type |
|---------|--------------------|-----------------------|
| exon 3 | R (Arg) | 117 |
| exon 5 | G (Gly) | 150 |
| exon 6 | E (Glu) | 186 |
| exon 6 | L (Leu) | 191 |
| exon 8 | R (Arg) | 270 |
| exon 13 | I (Ile) | 568 |
| exon 13 | R (Arg) | 578 |

(c) a nucleotide sequence encoding an ATP-gated ion channel P2X7R and which contains a mutation in exon 5 or 8 corresponding to position 32548 or position 37633 of the wild-type ATP-gated ion channel P2X7R nucleotide sequence as depicted in SEQ ID NO: 1, wherein at said position said nucleotide is replaced by another nucleotide

(d) a nucleic acid sequence encoding a polypeptide which has an amino acid sequence of an ATP-gated ion channel P2X7R, wherein amino acids corresponding to positions 488 to 494 of the wild-type ATP-gated ion channel P2X7R as depicted in SEQ ID NO: 3 or 4 are deleted;

(e) a genomic nucleotide sequence encoding an ATP-gated ion channel P2X7R, wherein in the intron as indicated in column "Intron" of the following Table B the nucleotide as indicated in column "Replaced nucleotide" of Table B corresponding to the position as indicated in column "Position in wild-type" of Table B of the wild-type ATP-gated ion channel P2X7R nucleotide sequence as depicted in SEQ ID NO: 1 is replaced by another nucleotide

Table B

| Intron | Replaced nucleotide | Position in wild-type |
|-----------|---------------------|-----------------------|
| intron 1 | G | 3166 |
| intron 1 | C | 24778 |
| intron 1 | C | 24830 |
| intron 3 | A | 26308 |
| intron 3 | G | 26422 |
| intron 4 | G | 32394 |
| intron 4 | T | 32434 |
| intron 5 | A | 32783 |
| intron 6 | G | 35641 |
| intron 6 | A | 35725 |
| intron 6 | T | 36001 |
| intron 7 | G | 36378 |
| intron 7 | T | 36387 |
| intron 7 | G | 36398 |
| intron 9 | C | 47214 |
| intron 11 | T | 47563 |
| intron 12 | C | 54307 |
| intron 12 | G | 54308 |

(f) a genomic nucleotide sequence encoding an ATP-gated ion channel P2X7R and which contains a mutation in the 3'UTR region corresponding to position 54925, 55169, 55170, 55171 or 55917 of the wild-type ATP-gated ion channel P2X7R nucleotide sequence as depicted in SEQ ID NO: 1, wherein at said position said nucleotide is replaced by another nucleotide;

(g) a nucleotide sequence comprising at least 20 or 21 nucleotides and comprising the mutations or deletions as defined in any one of (a) to (f);

(h) a nucleic acid sequence comprising a nucleotide sequence as shown in any one of SEQ ID NOs: 13 to 51;

(i) a nucleic acid sequence encoding a polypeptide comprising the amino acid sequence of SEQ ID NOs: 5 to 12;

(j) a nucleotide sequence which hybridizes to a nucleotide sequence defined in any one of (a) to (g) or to the nucleotide sequence of (h) and having a mutation as defined in any one of (a) to (f); and

(k) a nucleic acid sequence being degenerate as a result of the genetic code to the nucleic acid sequence as defined in (j).

2. The nucleic acid molecule of claim 1 derived from mouse, rat or human.
3. The nucleic acid molecule of claim 1 or 2 which is DNA, RNA, PNA or phosphorothioates.
4. A vector comprising the nucleic acid molecule of any one of claims 1 to 3.
5. The vector of claim 4 which is an expression vector, a gene targeting vector and/or a gene transfer vector.
6. A host transformed with a vector of claim 4 or 5 or transformed with the nucleic acid molecule of any one of claims 1 to 3.
7. The host of claim 6 which is a mammalian cell, an amphibian cell, a fish, an insect cell, a fungal cell, a plant cell

or a bacterial cell.

8. The host of claim 7, wherein said mammalian cell is selected from the group consisting of CHO cells, HEK293 cells, COS-7 cells or PC12 cells.

9. The host of claim 7, wherein said amphibian cell is an oocyte, preferably a *Xenopus* oocyte.

10. The host of claim 9, wherein said oocyte is a frog oocyte.

11. The host of claim 6 which is a non-human transgenic organism.

12. The host of claim 11, wherein said non-human organism is a mammal, amphibian, a fish, an insect, a fungus or a plant.

13. A method for producing the polypeptide encoded by a nucleic acid molecule of claims 1(b) or 1(d) comprising culturing/raising the host of any one of claims 6 to 11 and isolating the produced polypeptide.

14. A polypeptide encoded by the nucleic acid molecule of claim 1(b) or 1(d) or produced by the method of claim 13.

15. An antibody specifically directed to the polypeptide of claim 14, wherein said antibody specifically reacts with an epitope generated and/or formed by the mutation in the ATP-gated ion channel P2X7R selected from the group consisting of:

(i) an epitope specifically presented by a polypeptide which has an amino acid sequence of an ATP-gated ion channel P2X7R, wherein the R (Arg), G (Gly), E (Glu), L (Leu), R (Arg), I (Ile) or R (Arg) residue corresponding to position 117, 150, 186, 191, 270, 568 or 578 of the wild-type ATP-gated ion channel P2X7R as depicted in SEQ ID NO: 3 or 4 is replaced by another amino acid residue; and

(ii) an epitope specifically presented by a polypeptide which has an amino acid sequence of an ATP-gated ion channel P2X7R, wherein amino acids corresponding to positions 488 to 494 of the wild-type ATP-gated ion channel P2X7R as depicted in SEQ ID NO: 3 or 4 are deleted.

16. The antibody of claim 15 which is a monoclonal antibody.

17. An aptamer specifically binding to a nucleic acid molecule of any one of claims 1 to 3 or to the polypeptide of claim 14.

18. A primer or pair of primers capable of specifically amplifying a nucleic acid molecule as defined in any one of claims 1 to 3.

19. The primer or pair of primers of claim 18, which is selected from the group consisting of SEQ ID NOs.: 52 to 111.

20. A composition comprising the nucleic acid molecule of any one of claims 1 to 3, the vector of claim 4 or 5, the polypeptide of claim 14, the antibody of claim 15 or 16, the aptamer of claim 17 and/or the primer or pair of primers of claim 18 or 19.

21. The composition of claim 20 which is a diagnostic composition.

22. The diagnostic composition of claim 21, optionally further comprising suitable means for detection.

23. Use of the nucleic acid molecule of any one of claims 1 to 3, the vector of claim 4 or 5, the polypeptide of claim 14, the antibody of claim 15 or 16, the aptamer of claim 17 and/or the primer or pair of primers of claim 18 or 19 for the preparation of a diagnostic composition for the detection of an affective disorder.

24. A method of diagnosing an affective disorder or a susceptibility to an affective disorder comprising the step of determining in a sample obtained from an individual whether the P2XR7 protein expressed in the cells of said individual is non-functional, shows an altered ATP-gating in comparison to the wild-type P2XR7 protein or is over- or under-expressed in comparison to the P2XR7 protein level in an unaffected individual.

25. A method for diagnosing an affective disorder or a susceptibility to an affective disorder comprising the step of determining in a sample obtained from an individual whether the P2X7R gene sequence or encoded protein thereof comprises a mutation in comparison to the wild-type P2X7R sequence.

26. The method of claim 25, wherein said mutation is a mutation as defined in claim 1 and/or a nucleotide replacement or deletion selected from the following Table C indicating in column "Region of P2X7R" the region of the P2X7R genomic nucleotide sequence in which the replacement or deletion occurs, in column "Nucleotide" of Table C the nucleotide which is replaced by another nucleotide or the nucleotides which are deleted and in column "Position in wild-type" of Table C the corresponding position in the nucleotide sequence of the wild-type ATP-gated ion channel P2X7R as depicted in SEQ ID NO: 1

Table C

| Region of P2X7R | Nucleotide | Position in wild-type |
|-----------------|------------|-----------------------|
| 5'UTR | T | 362 |
| 5'UTR | T | 532 |
| 5'UTR | A | 1100 |
| 5'UTR | A | 1122 |
| 5'UTR | C | 1171 |
| 5'UTR | T | 1351 |
| 5'UTR | G | 1702 |
| 5'UTR | T | 1731 |
| 5'UTR | C | 1860 |
| 5'UTR | C | 2162 |
| 5'UTR | C | 2238 |
| 5'UTR | A | 2373 |
| 5'UTR | G | 2569 |
| 5'UTR | G | 2702 |
| intron 1 | G | 3166 |
| intron 1 | C | 24778 |
| intron 1 | C | 24830 |
| exon 2 | T | 24942 |
| exon 3 | C | 26188 |
| exon 3 | A | 26308 |
| exon 3 | G | 26422 |
| intron 4 | G | 32394 |
| intron 4 | T | 32434 |
| exon 5 | G | 32493 |
| exon 5 | G | 32506 |
| exon 5 | C | 32507 |
| exon 5 | C | 32548 |
| intron 5 | A | 32783 |
| intron 5 | T | 35309 |
| intron 5 | C | 35374 |

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Table C (continued)

| | Region of P2X7R | Nucleotide | Position in wild-type |
|----|-----------------|-----------------------------------|-----------------------|
| 5 | intron 5 | A | 35378 |
| | exon 6 | G | 35438 |
| | exon 6 | T | 35454 |
| 10 | intron 6 | T | 35549 |
| | intron 6 | G | 35641 |
| | intron 6 | A | 35725 |
| | intron 6 | T | 36001 |
| 15 | intron 6 | A | 36064 |
| | intron 6 | deletion of GTTT | 36091 to 36094 |
| | intron 6 | C | 36108 |
| 20 | intron 7 | C | 36374 |
| | intron 7 | G | 36378 |
| | intron 7 | T | 36387 |
| | intron 7 | G | 36398 |
| 25 | intron 7 | C | 37439 |
| | intron 7 | T | 37513 |
| | exon 8 | C | 37604 |
| 30 | exon 8 | G | 37605 |
| | exon 8 | G | 37623 |
| | exon 8 | C | 37633 |
| | intron 9 | C | 47214 |
| 35 | exon 11 | G | 47383 |
| | exon 11 | C | 47411 |
| | intron 11 | T | 47563 |
| 40 | intron 12 | C | 54307 |
| | intron 12 | G | 54308 |
| | exon 13 | C | 54399 |
| | exon 13 | A | 54480 |
| 45 | exon 13 | C | 54523 |
| | exon 13 | deletion of CCCTGAGAGCCACAGGTGCCT | 54562 to 54582 |
| | exon 13 | A | 54588 |
| 50 | exon 13 | C | 54664 |
| | exon 13 | G | 54703 |
| | exon 13 | A | 54804 |
| | exon 13 | G | 54834 |
| 55 | exon 13 | G | 54847 |
| | 3'UTR | G | 54925 |

Table C (continued)

| Region of P2X7R | Nucleotide | Position in wild-type |
|-----------------|------------|-----------------------|
| 3'UTR | C | 55169 |
| 3'UTR | A | 55170 |
| 3'UTR | A | 55171 |
| 3'UTR | C | 55917 |

27. The method of claim 26, wherein the occurrence of the mutation in the ATP-gated ion channel P2X7R gene is determined by PCR or immunological methods.
28. The composition of claim 20 which is a pharmaceutical composition.
29. The pharmaceutical composition of claim 28, optionally further comprising a pharmaceutically acceptable carrier.
30. A method of treating an affective disorder comprising administering a therapeutically effective amount of the nucleic acid molecule as defined in any one of claims 1 to 3 or a therapeutically effective amount of the polypeptide of claim 14 to a subject suffering from said disorder.
31. Use of the nucleic acid molecule of any one of claims 1 to 3, the vector of claim 4 or 5, the polypeptide of claim 14, the antibody of claim 15 or 16 and/or the aptamer of claim 17 for the preparation of a pharmaceutical composition for the treatment of an affective disorder.
32. A pharmaceutical composition comprising a nucleic acid molecule comprising a nucleotide sequence which encodes a functional ATP-gated ion channel P2X7R and which is selected from the group consisting of:
- (a) a nucleotide sequence encoding a polypeptide comprising the amino acid sequence as depicted in SEQ ID NO: 3 or 4;
 - (b) a nucleotide sequence comprising the nucleotide sequence as depicted in SEQ ID NO: 1 or 2;
 - (c) a nucleotide sequence which hybridizes to the nucleotide sequence of
 - (a) or (b); and
 - (d) a nucleotide sequence which is degenerated as a result of the genetic code to the nucleotide sequence of (c).
33. A pharmaceutical composition comprising a compound the administration of which to cells leads to an increase of the expression of a nucleic acid encoding an ATP-gated ion channel P2X7R in the cells or comprising a nucleic acid molecule the expression of which in cells or the administration of which to cells leads to an increase of the expression of a nucleic acid encoding an ATP-gated ion channel P2X7R in the cells.
34. A method of treating an affective disorder comprising administering a therapeutically effective amount of the nucleic acid molecule as defined in claim 32 or 33 or a therapeutically effective amount of the polypeptide encoded thereof to a subject suffering from said disorder.
35. Use of the nucleic acid molecule as defined in claim 32 or 33 for the preparation of a pharmaceutical composition for treating an affective disorder.
36. Use of a modulator of P2X7R activity for the preparation of a pharmaceutical composition for treating an affective disorder.
37. The use of claim 36, wherein said modulator is an agonist.
38. The use of claim 37, wherein said agonist is selected from the group consisting of ATP, ATP-4 and BzATP (2'-3'-O-(4-Benzoylbenzoyl)adenosine 5'-triphosphate (C₂₄H₂₄N₅O₁₅P₃)).

39. Use of tenidap ($C_{15}H_{11}ClN_2O_2S$) or a derivative thereof or 3-substituted-2-oxindole-1-carboxamides for the preparation of a pharmaceutical composition for treating an affective disorder.
- 5 40. The use of any one of claims 35 to 39 or the method of claim 34, wherein said pharmaceutical composition optionally further comprises a β -adrenergic receptor modulator.
41. The use or the method of claim 40, wherein said β -adrenergic receptor modulator is a β -adrenergic receptor antagonist selected from the group consisting of DL-propanolol, D-propanolol and labetalol.
- 10 42. The use of any one of claims 23, 30 or 35 to 41 or the method of any one of claims 24 to 27 or 34, wherein said affective disorder is selected from the group consisting of major depression, generalized anxiety disorder and bipolar disorder.
- 15 43. The use or the method of claim 42, wherein said major depression is selected from the group consisting of major depression, dysthymia, atypical depression, premenstrual dysphoric disorder and seasonal affective disorder.
- 20 44. The use or the method of claim 42, wherein said generalized anxiety disorder is selected from the group consisting of panic disorder, phobias, agoraphobia, social phobia, specific phobia, obsessive-compulsive disorder, post-traumatic stress disorder, separation anxiety disorder, mania, hypomania and cyclothymic disorder.
- 25 45. The use or the method of claim 42, wherein said bipolar disorder is bipolar disorder type I or bipolar disorder type II.
46. A kit comprising the nucleic acid molecule of any one of claims 1 to 3, a vector of claim 4 or 5, a host of any one of claims 6 to 11, a polypeptide of claim 14, an antibody of claim 15 or 16, an aptamer of claim 17 and/or a primer or pair of primers of claim 18 or 19.
- 30 47. A method for identifying compounds which are capable of specifically interacting with the polypeptide of claim 14, comprising the steps of
 - (a) contacting a polypeptide of claim 14 with a compound or a candidate mixture of compounds to be tested; and
 - (b) determining whether said compound or a candidate mixture of compounds is capable of specifically interacting with said polypeptide.
- 35 48. A method for the characterization of compounds which are capable of altering characteristics of the polypeptide of claim 14, comprising the steps of
 - (a) contacting a polypeptide of claim 14 with a compound or a candidate mixture; and
 - (b) determining whether the compound or a candidate mixture alters a characteristic of the polypeptide of claim 14.
- 40 49. A method of screening for compounds which are capable of interacting with the polypeptide of claim 14, comprising the steps of
 - (a) contacting a polypeptide of claim 14 with a compound or a candidate mixture of compounds;
 - 45 (b) measuring and/or detecting a response; and
 - (c) comparing said response to a standard response as measured in the absence of said candidate molecule.
- 50 50. A method for the production of a pharmaceutical composition comprising the steps of the method of any one of claims 47 to 49 and comprising a further step, wherein a derivative of said identified, characterized and/or screened molecule is generated.
- 55 51. A method for the production of a pharmaceutical composition comprising the steps of the method of any one of claims 47 to 50 and formulating the molecules identified, characterized, screened and/or derivatized in pharmaceutically acceptable form.
52. The method of claim 51, wherein the pharmaceutical composition to be produced further comprises neuroprotective substances, nootropic substances, brilliant blue, piperidine or piperazine derivatives thereof, adamantane derivatives, substituted phenyl compounds, oxidized ATP, 2-O-(4-benzoylbenzoyl)adenosine-5-triphosphate,

3-O-(4-benzoylbenzoyl)adenosine-5-triphosphate or β -adrenergic receptor modulators.

53. The method of any one of claims 47 to 52, wherein said compound(s) or candidate mixture(s) of compounds
5 comprise(s) antagonist(s), partial antagonist(s), partial agonist(s) and/or agonist(s) for an altered ATP-gated ion
channel P2X7R.

54. A method for diagnosing an affective disorder of an individual comprising:

- 10 (a) isolating DNA from cells obtained from an individual;
(b) determining all or part of the nucleotide composition of the P2X7R gene; and
(c) analyzing said nucleotide composition of P2X7R for the presence of one or more polymorphism(s) mutation
or allelic variation.

55. A method for diagnosing an affective disorder of an individual comprising:

- 15 (a) isolating RNA from cells obtained from an individual;
(b) converting said RNA into cDNA;
(c) determining all or part of the nucleotide composition of the P2X7R gene; and
20 (d) analyzing said nucleotide composition of P2X7R for the presence of one or more polymorphism(s), mutation
or allelic variation.

56. A method for diagnosing an affective disorder of an individual comprising:

- 25 (a) isolating RNA or protein from cells obtained from an individual ;
(b) determining the levels of P2X7R RNA or protein; and
(c) comparing the levels of P2X7R RNA or protein with the corresponding levels from a normal individual not
afflicted with an affective disorder.

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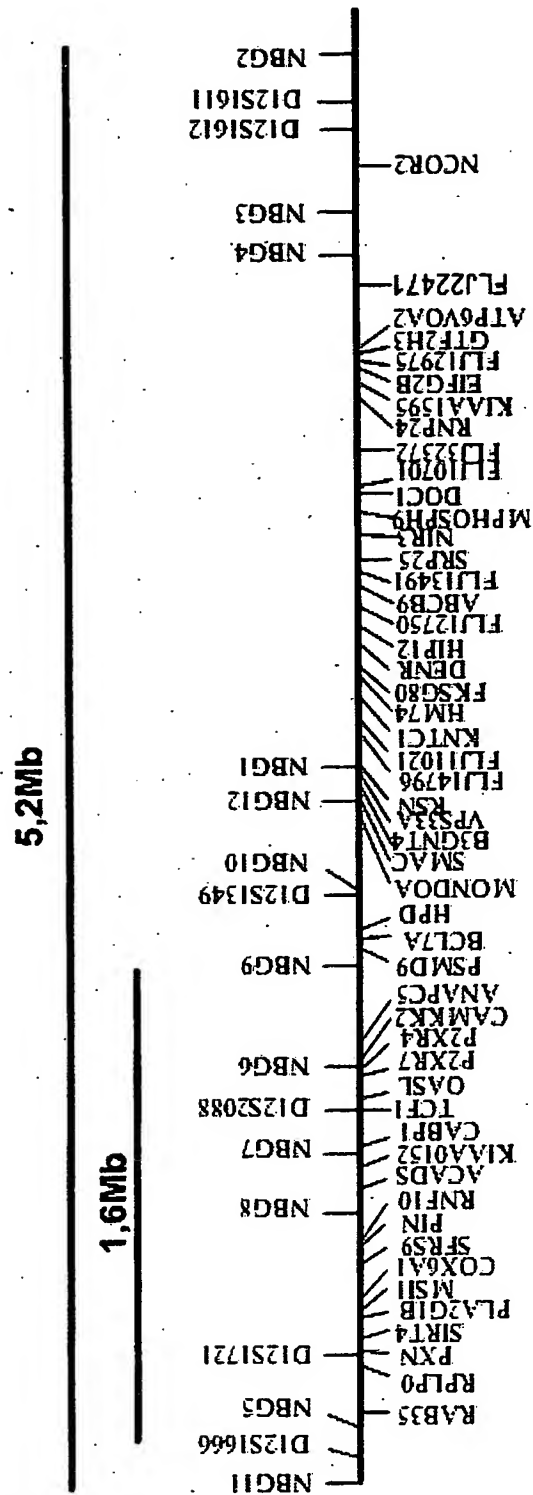


Figure 1a

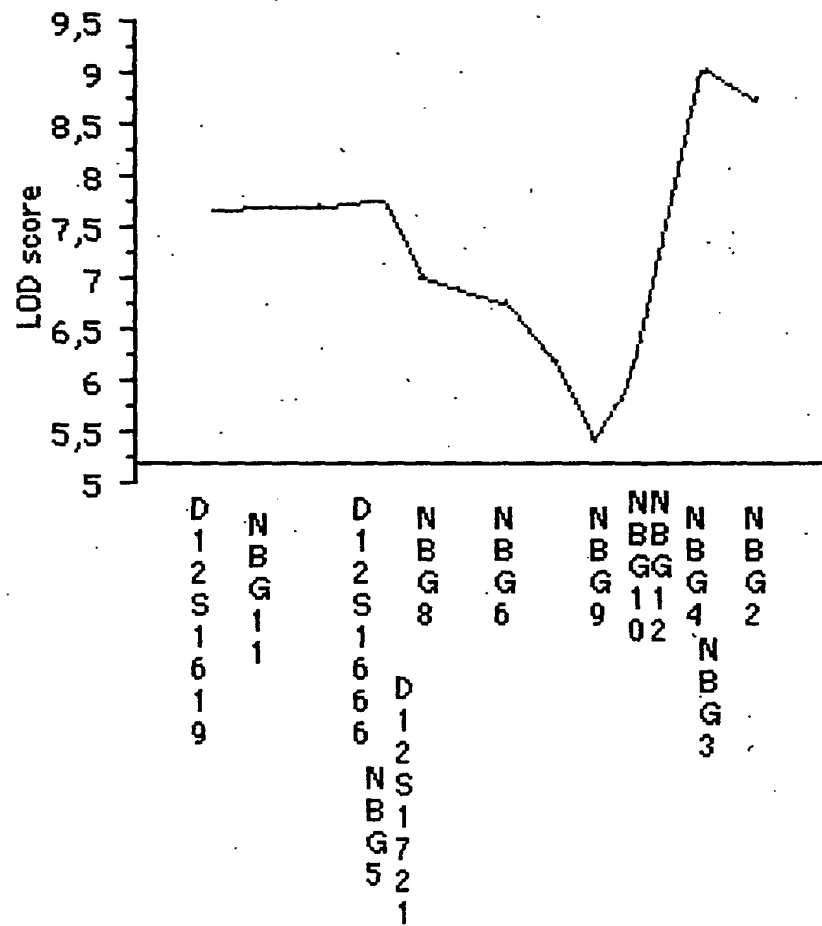


Figure 1b

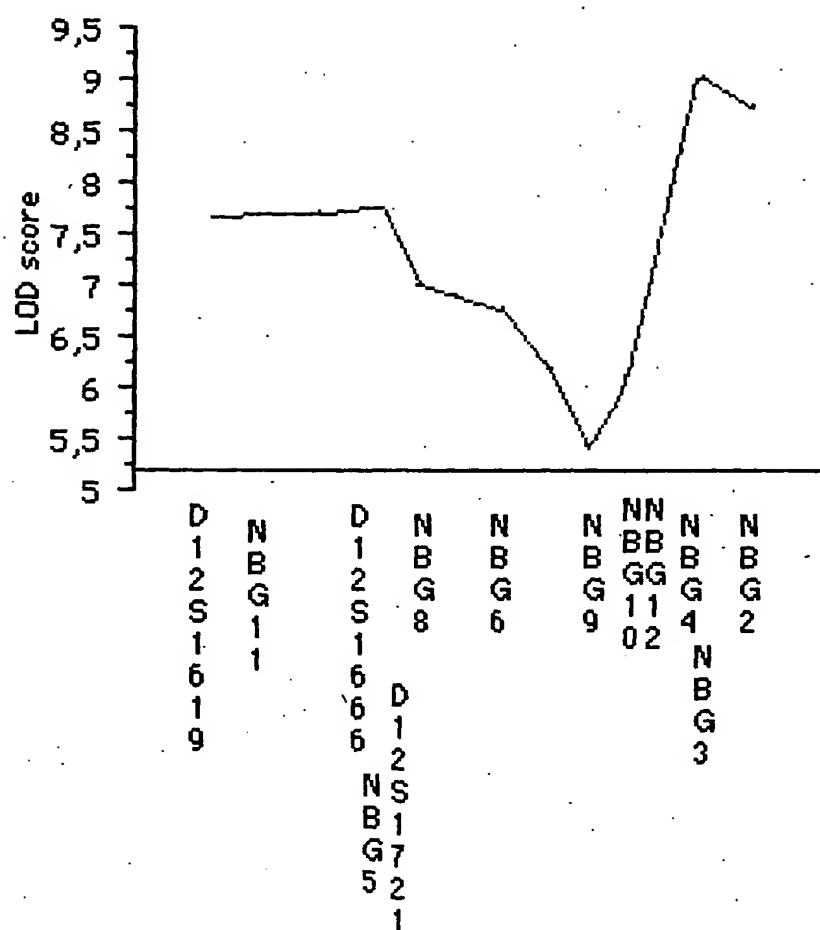


Figure 1c

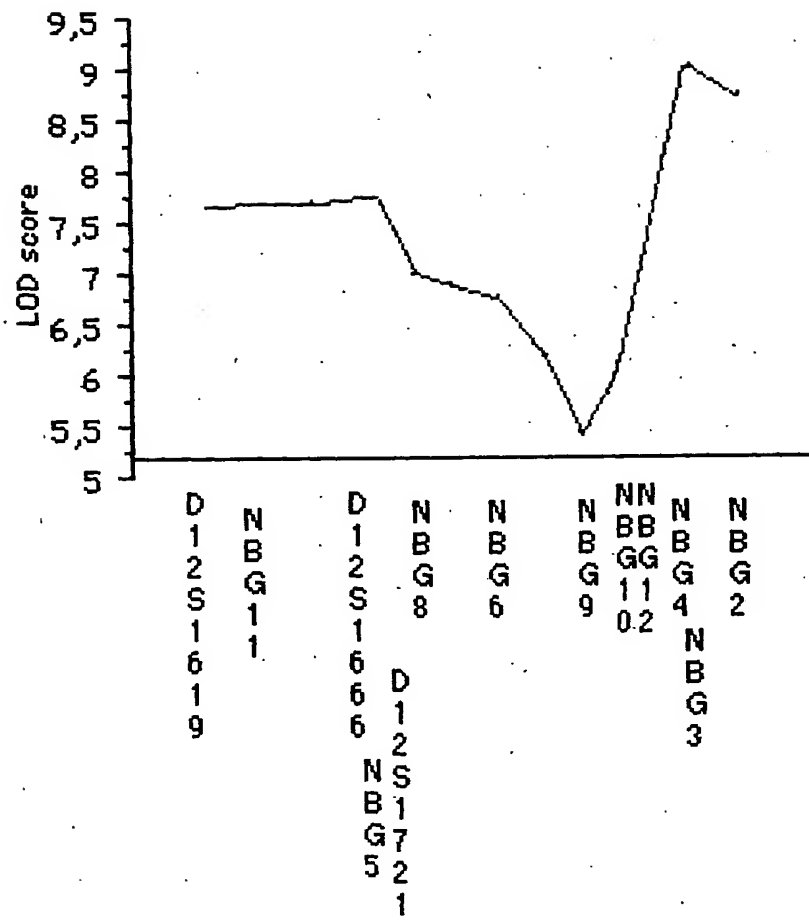


Figure 1d

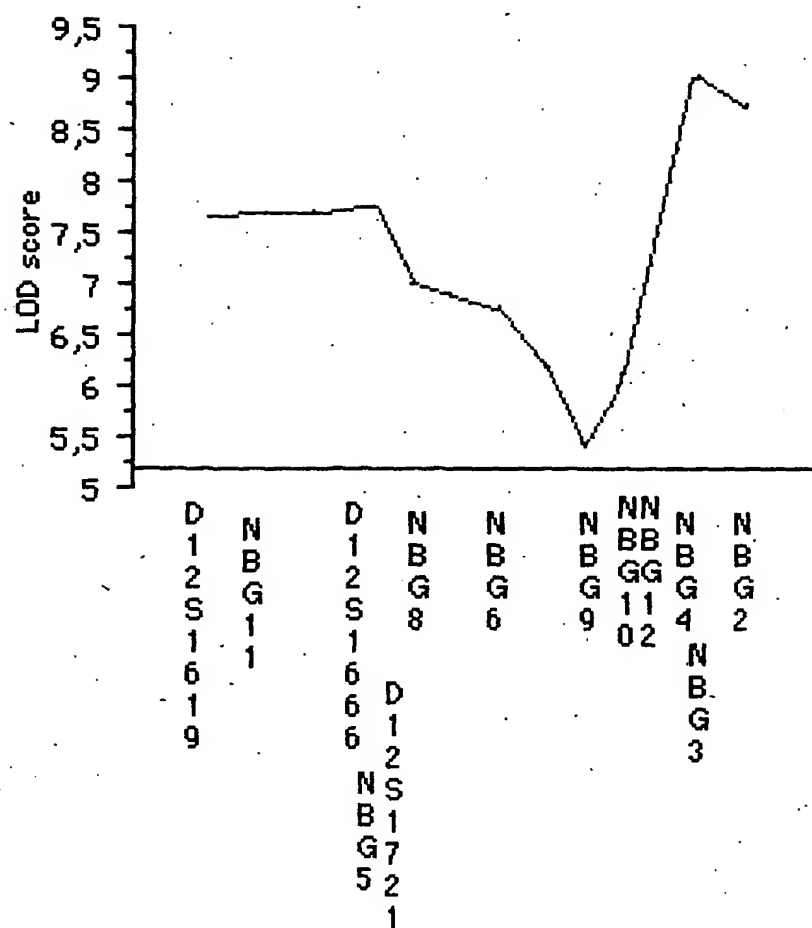


Figure 1e

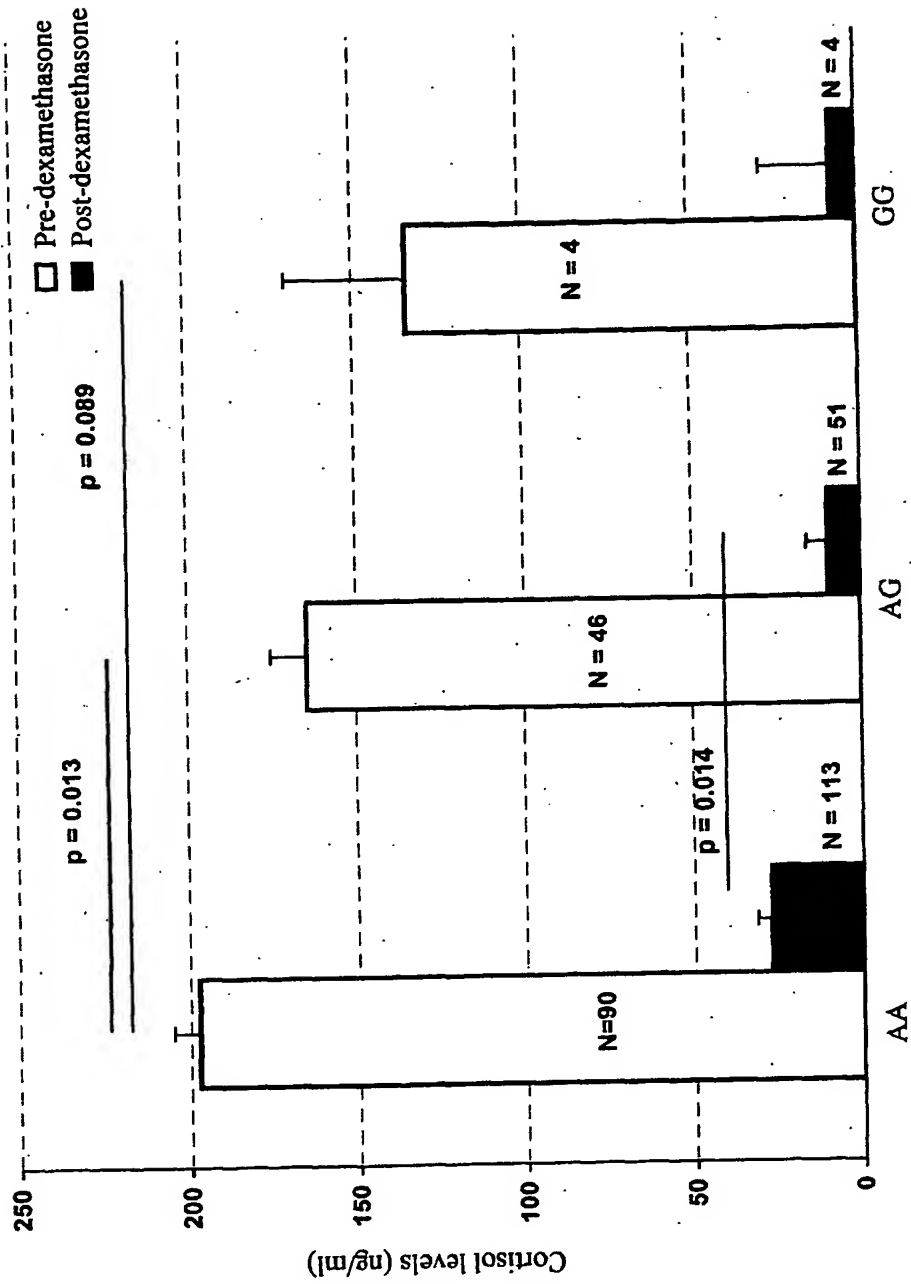


Figure 1f

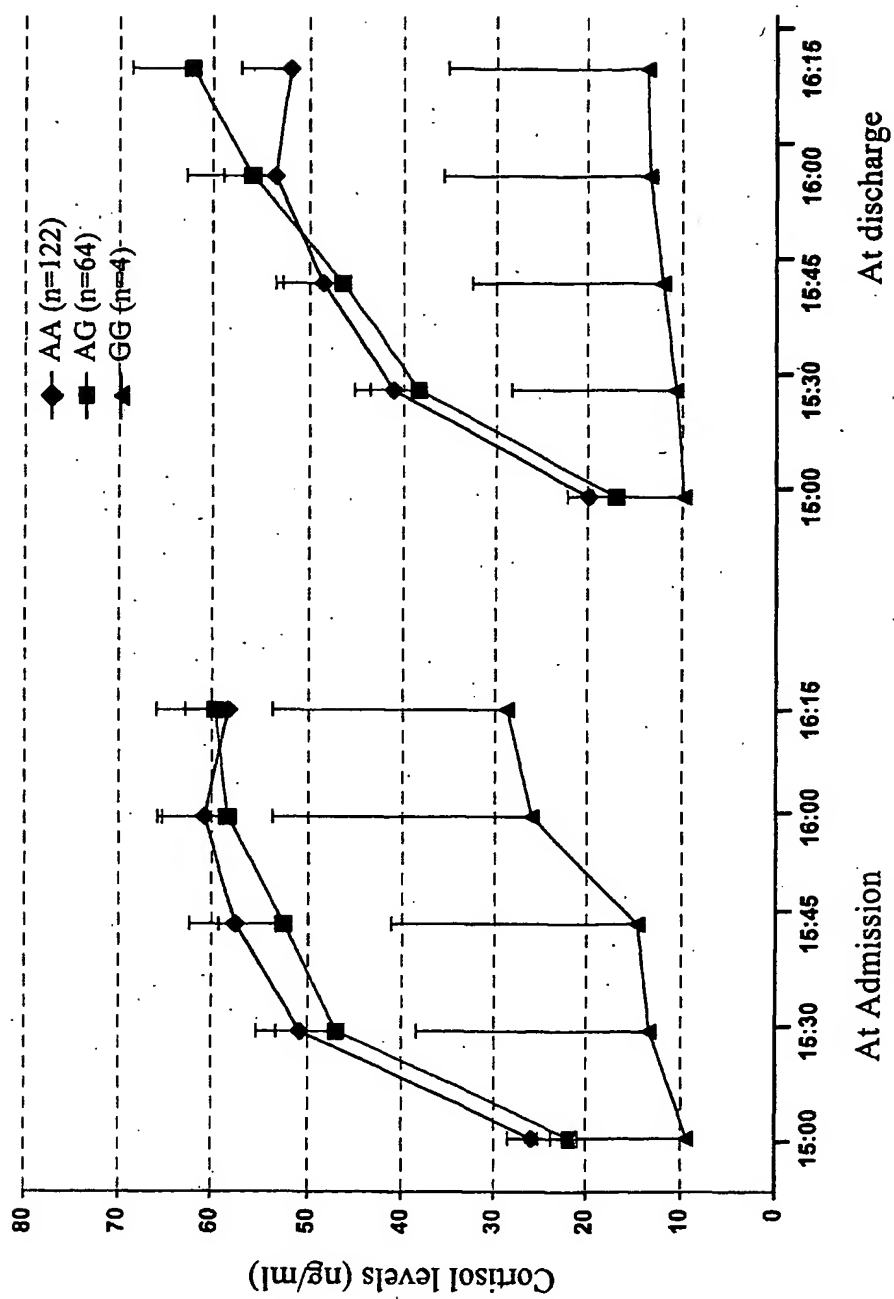


Figure 1g

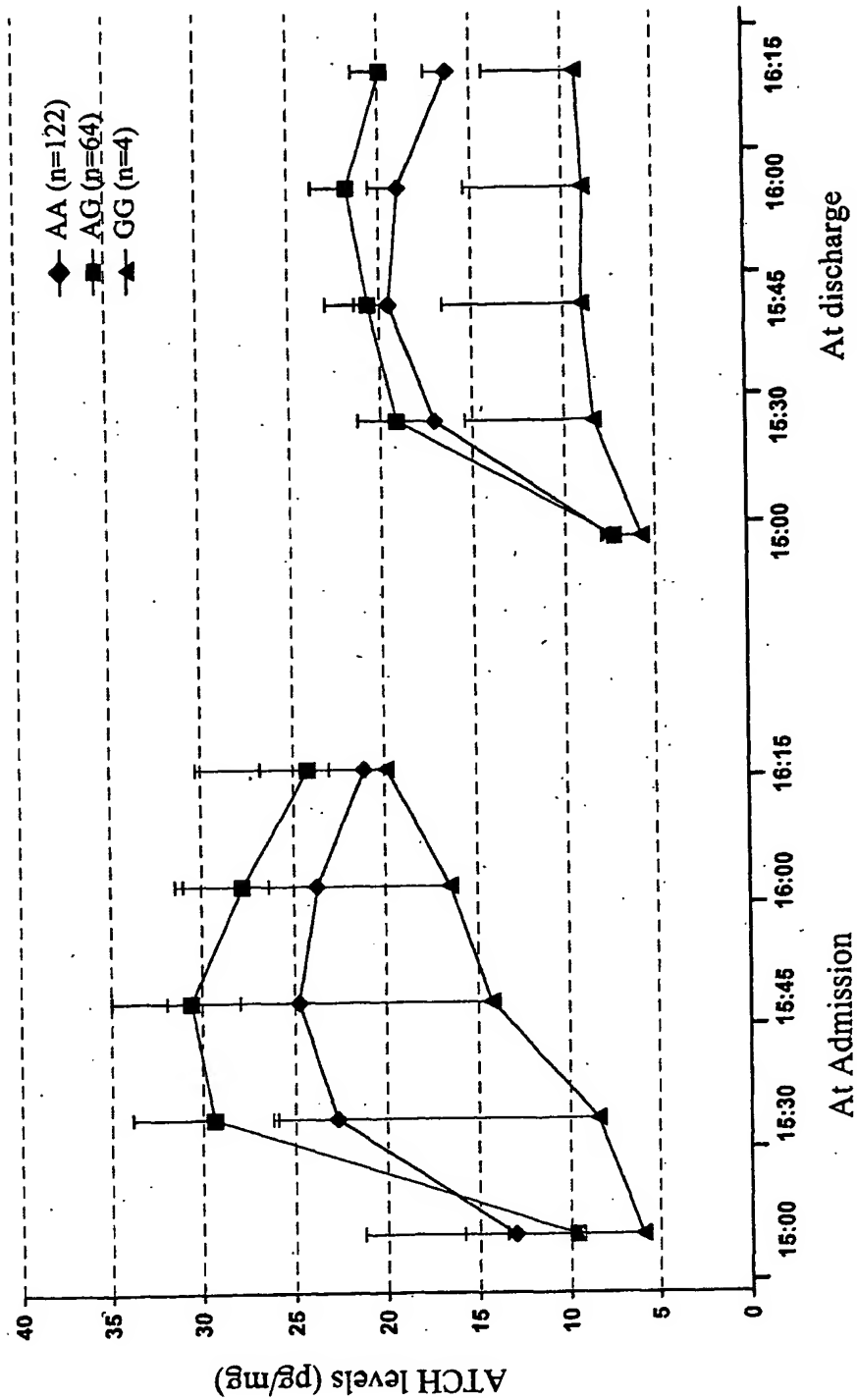


Figure 1h

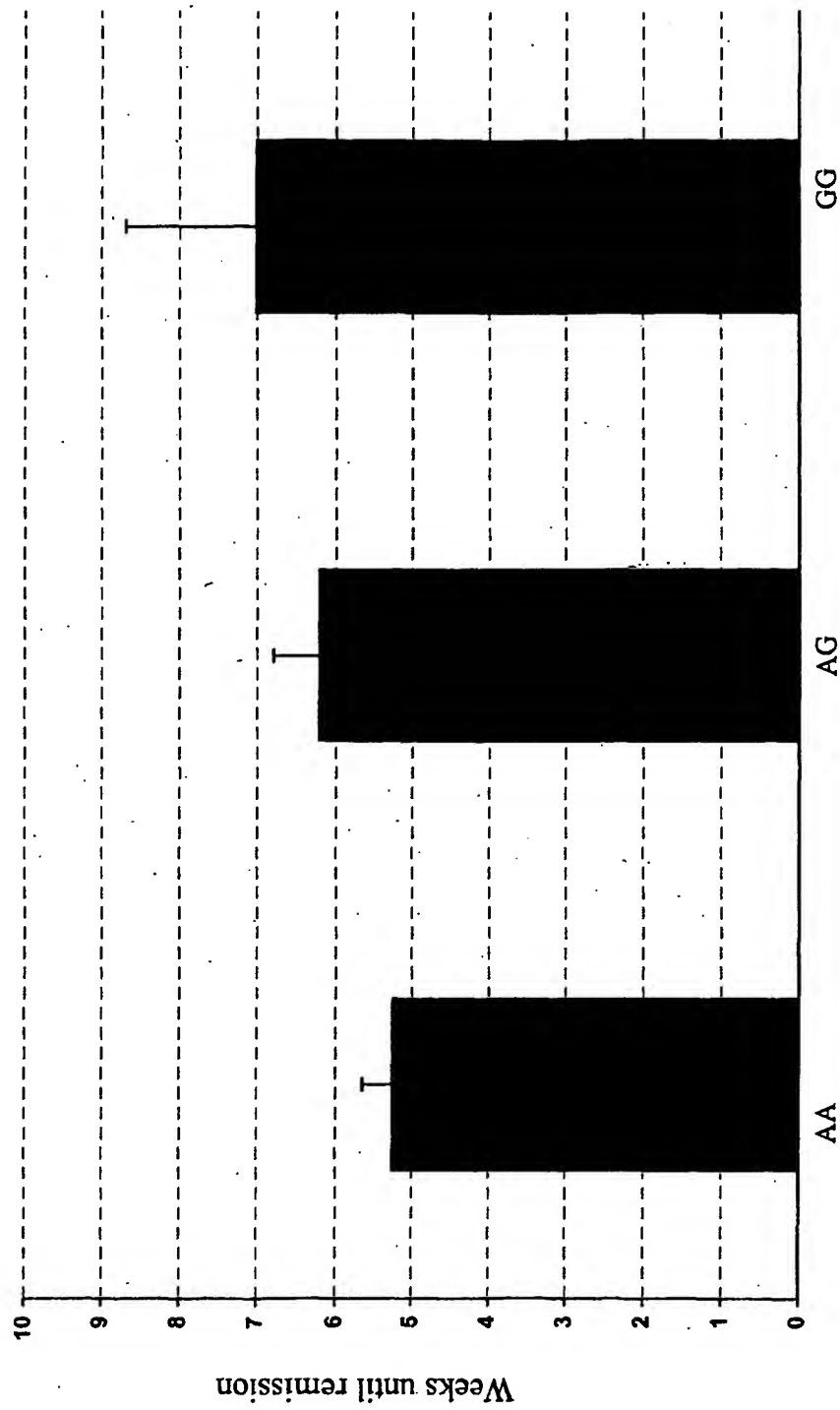


Figure 1i

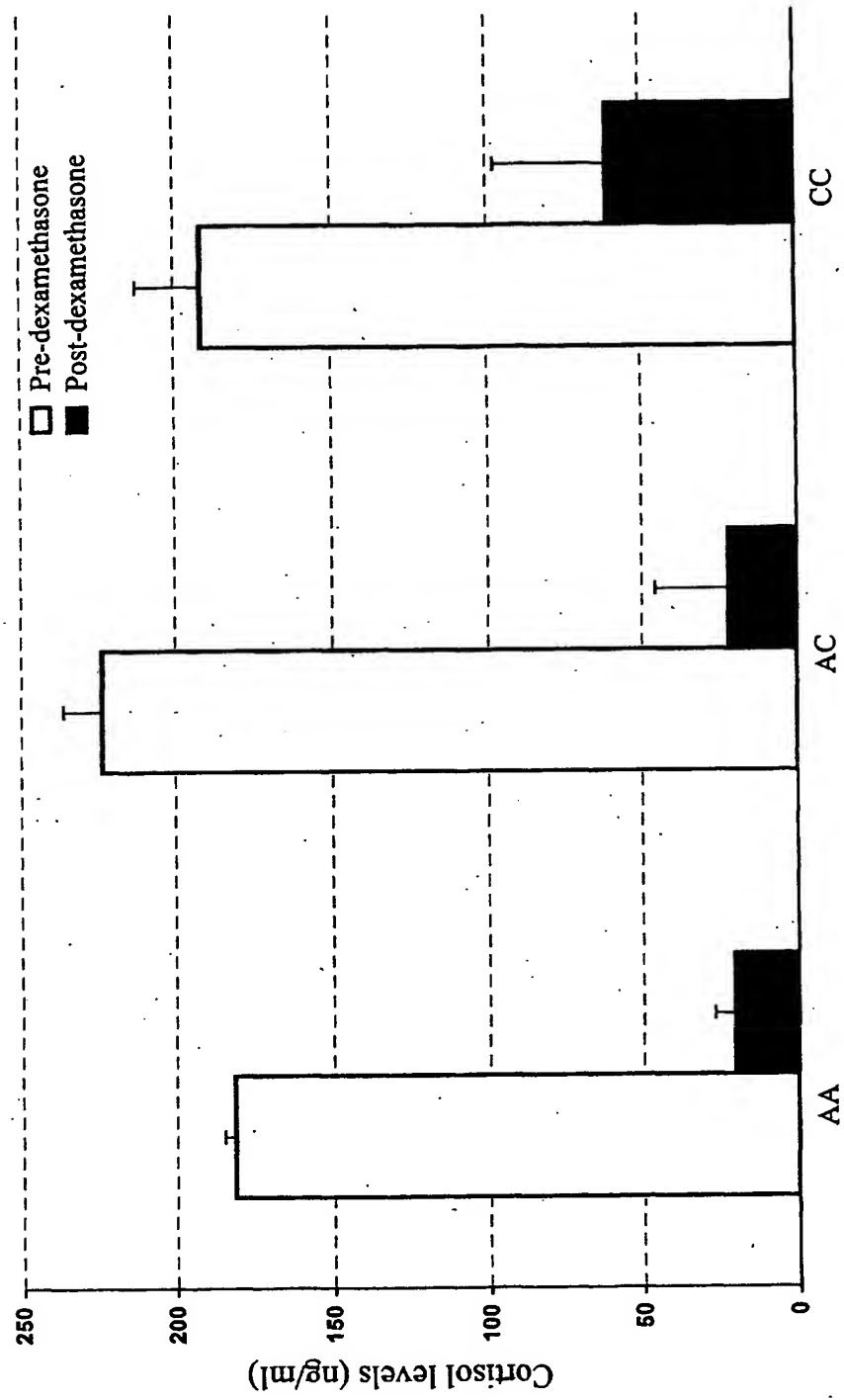


Figure 1j

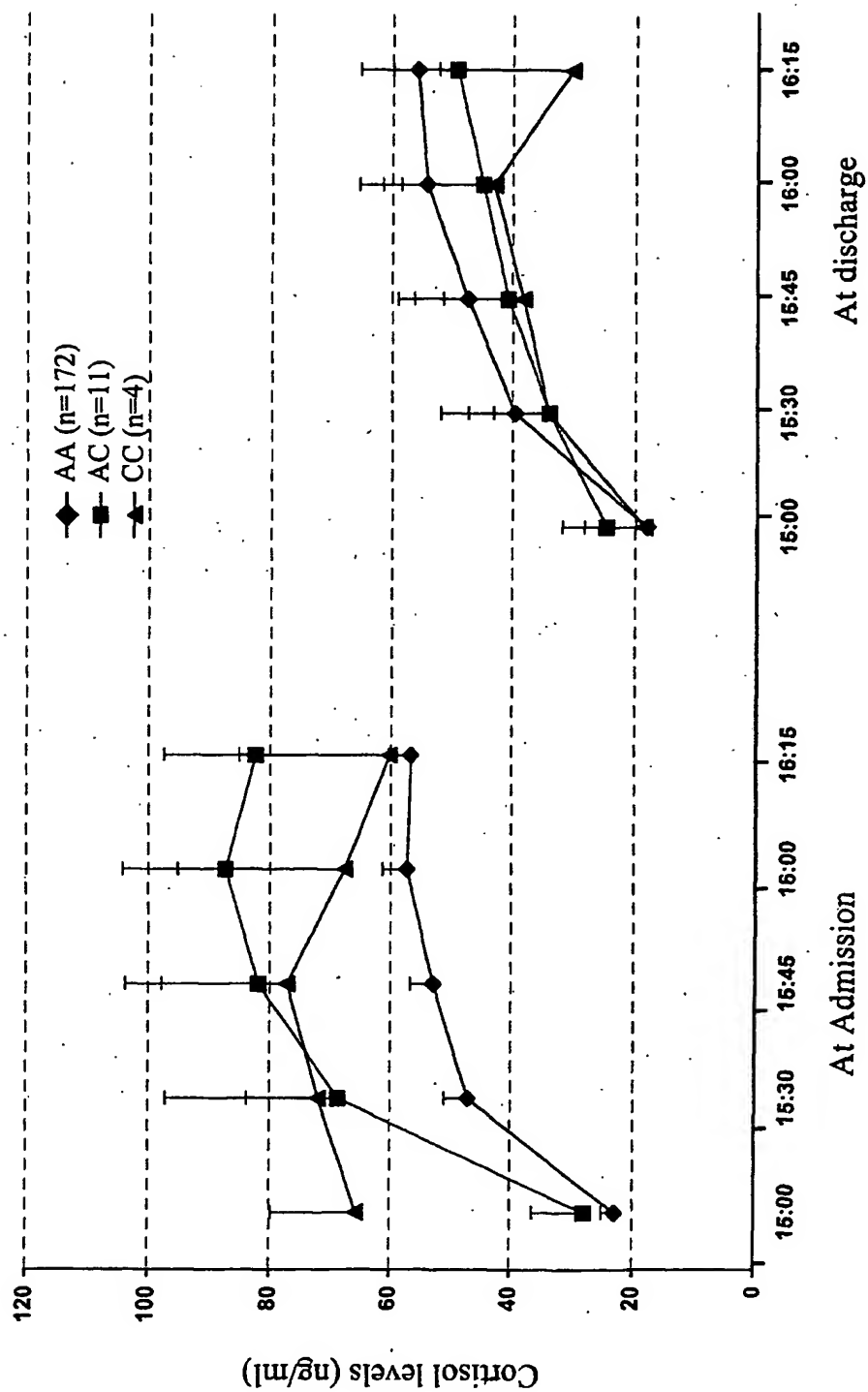


Figure 1k

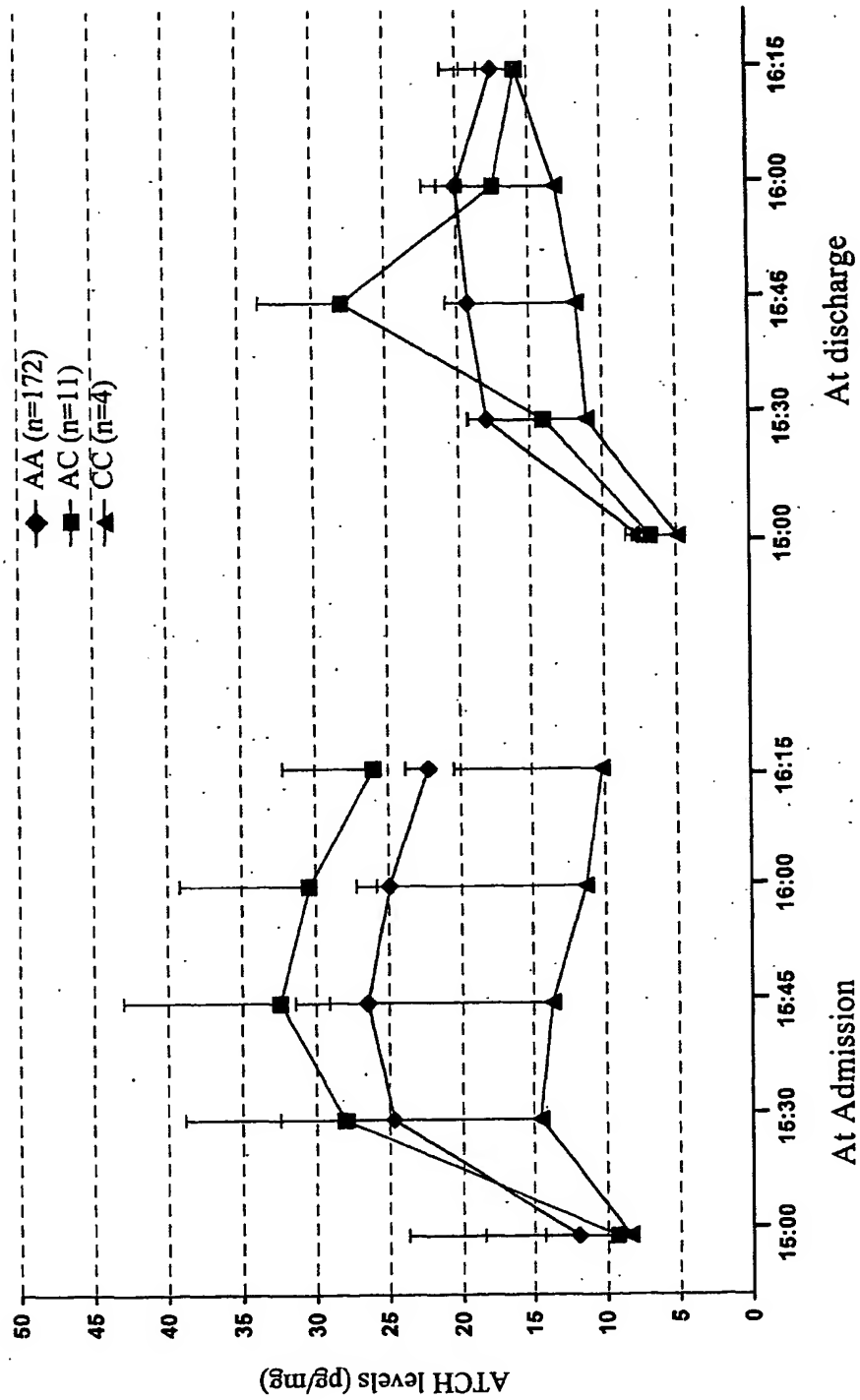


Figure 11

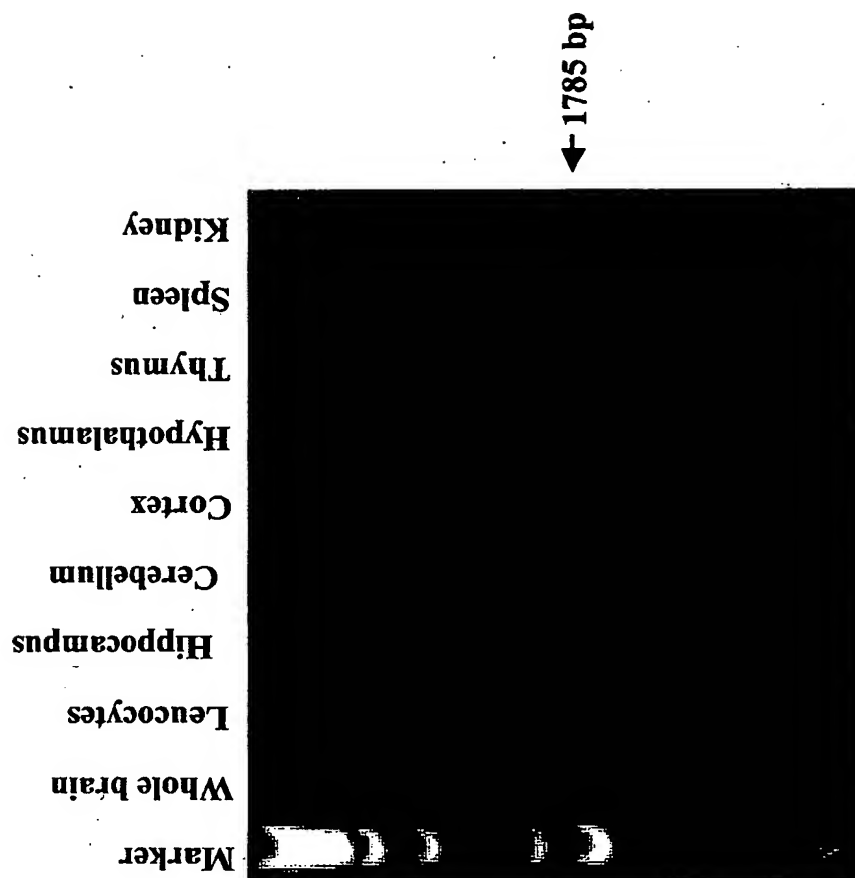


Figure 2

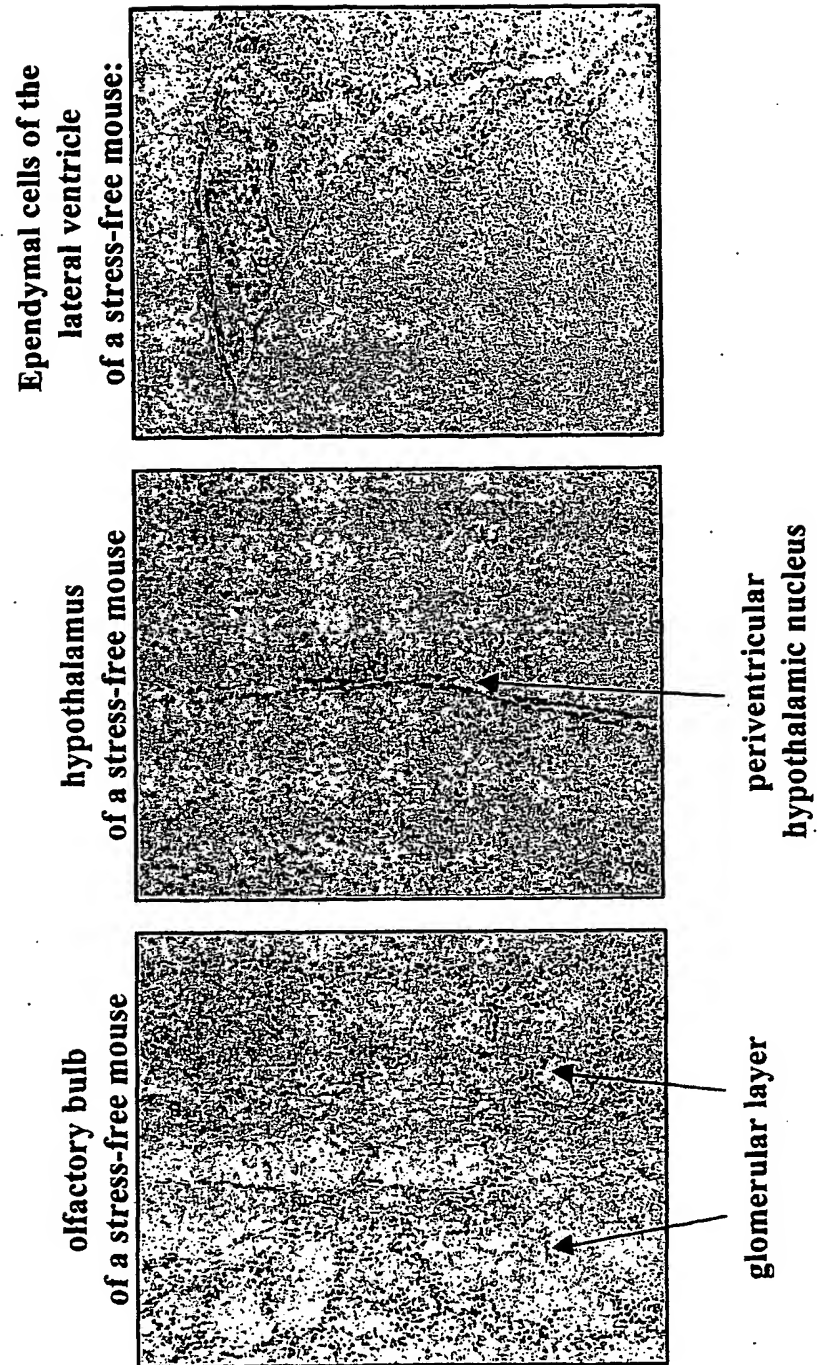


Figure 3

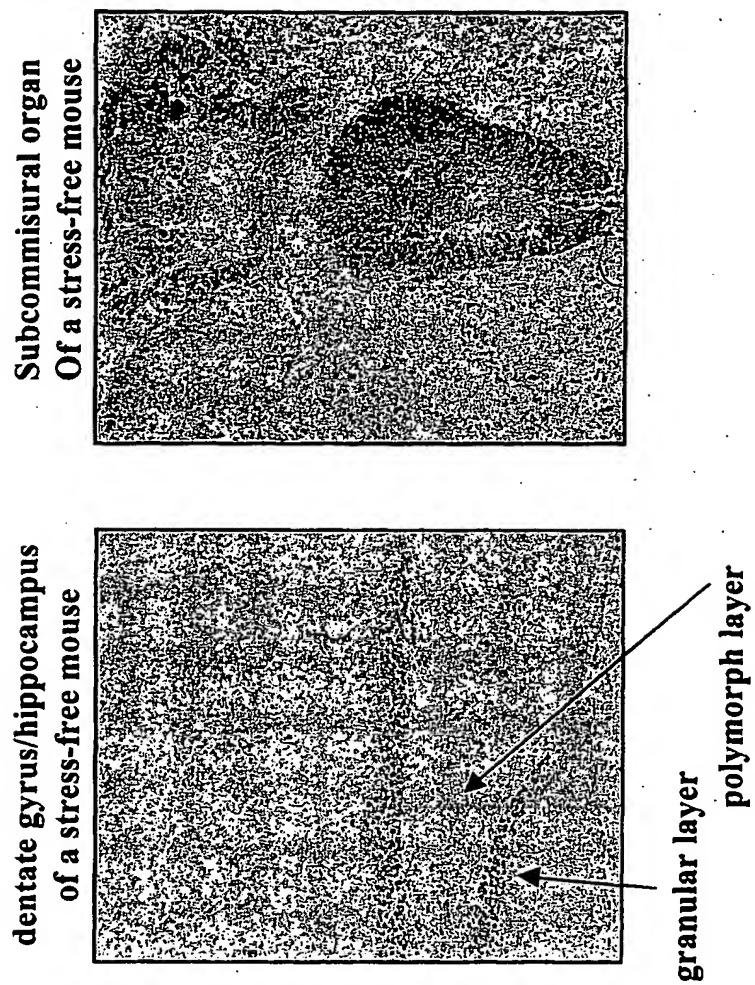


Figure 4

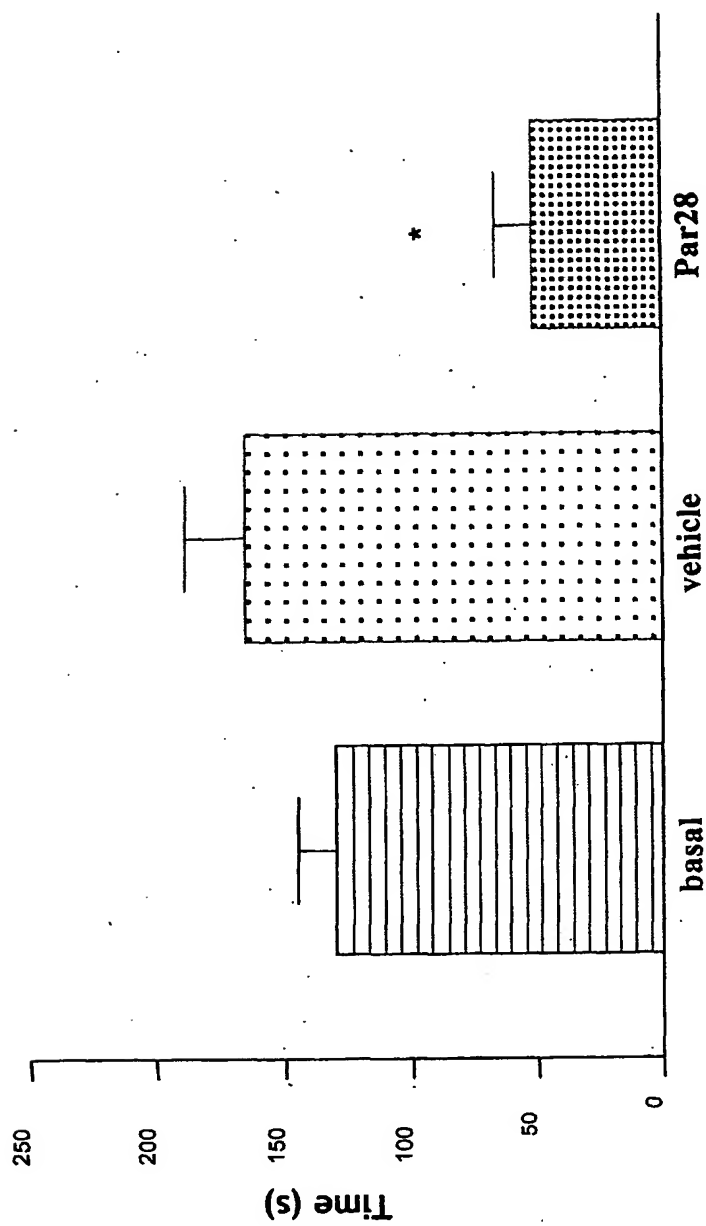


Figure 5

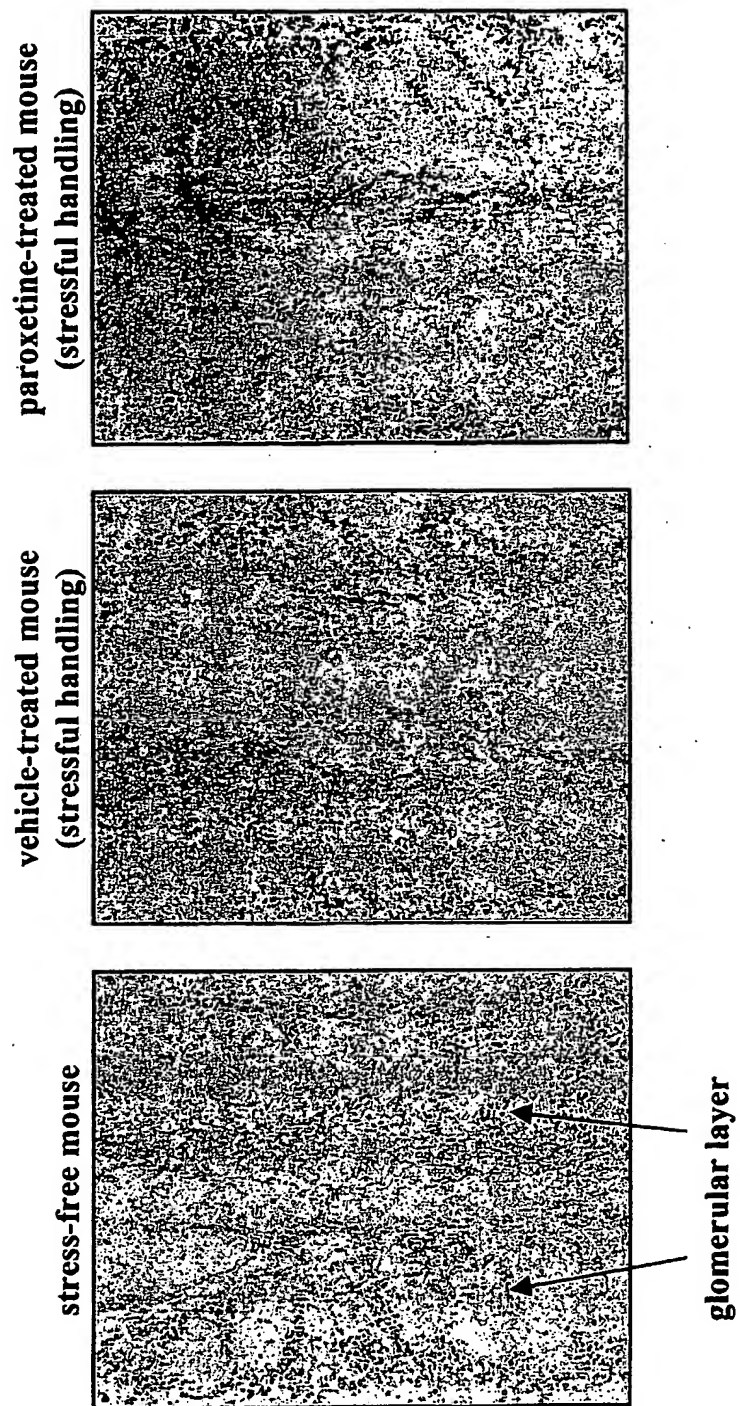


Figure 6

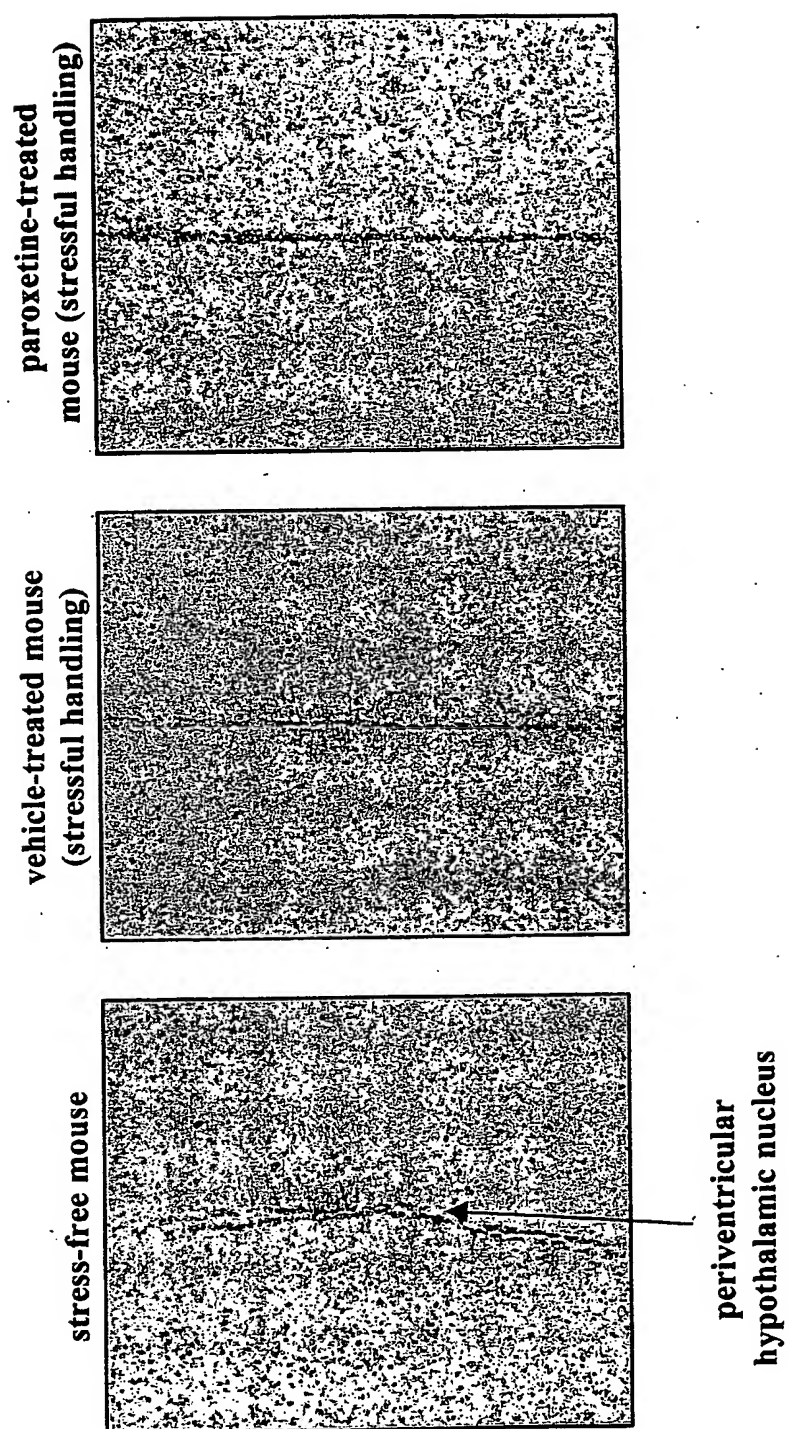


Figure 7

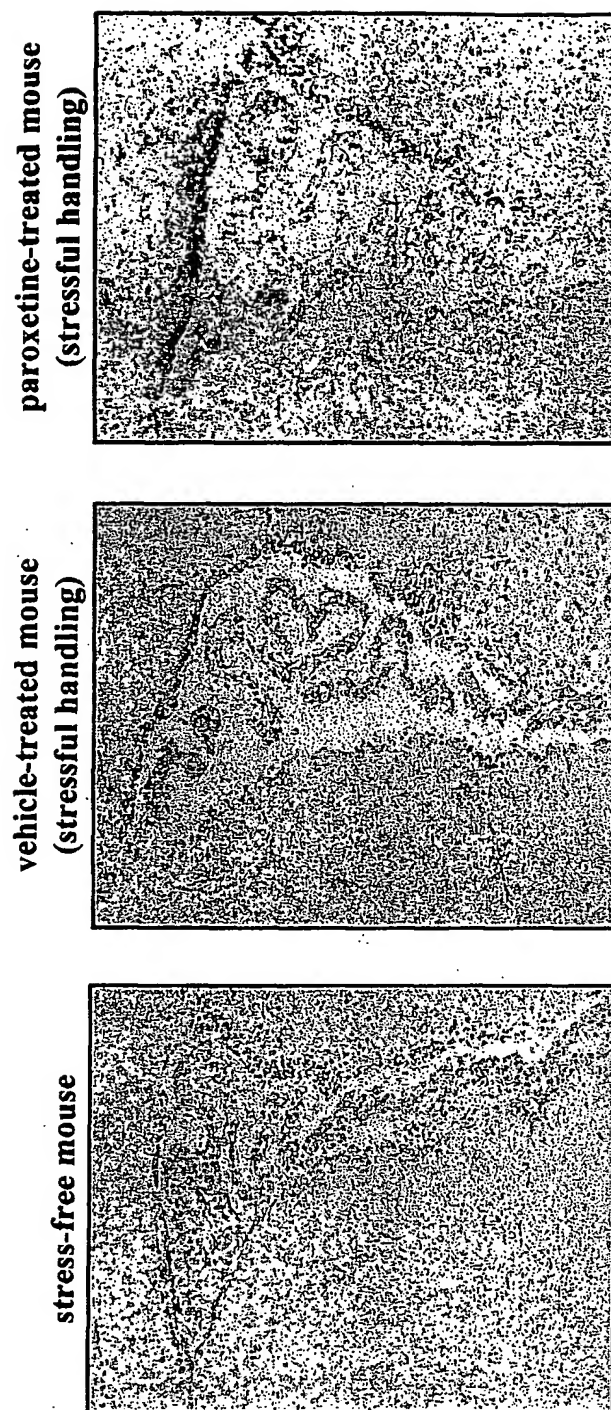


Figure 8

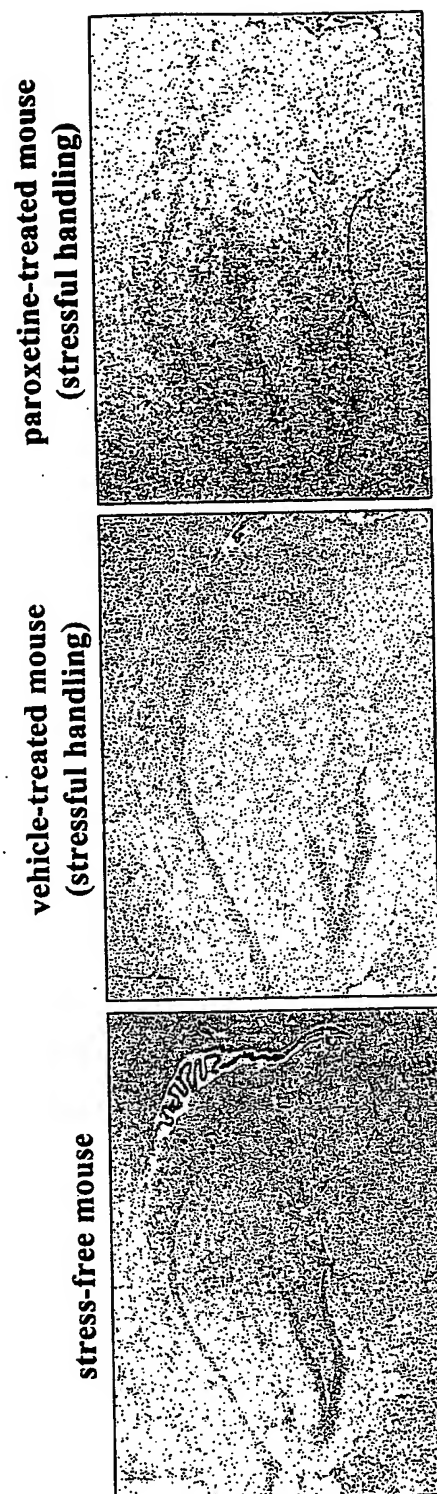


Figure 9

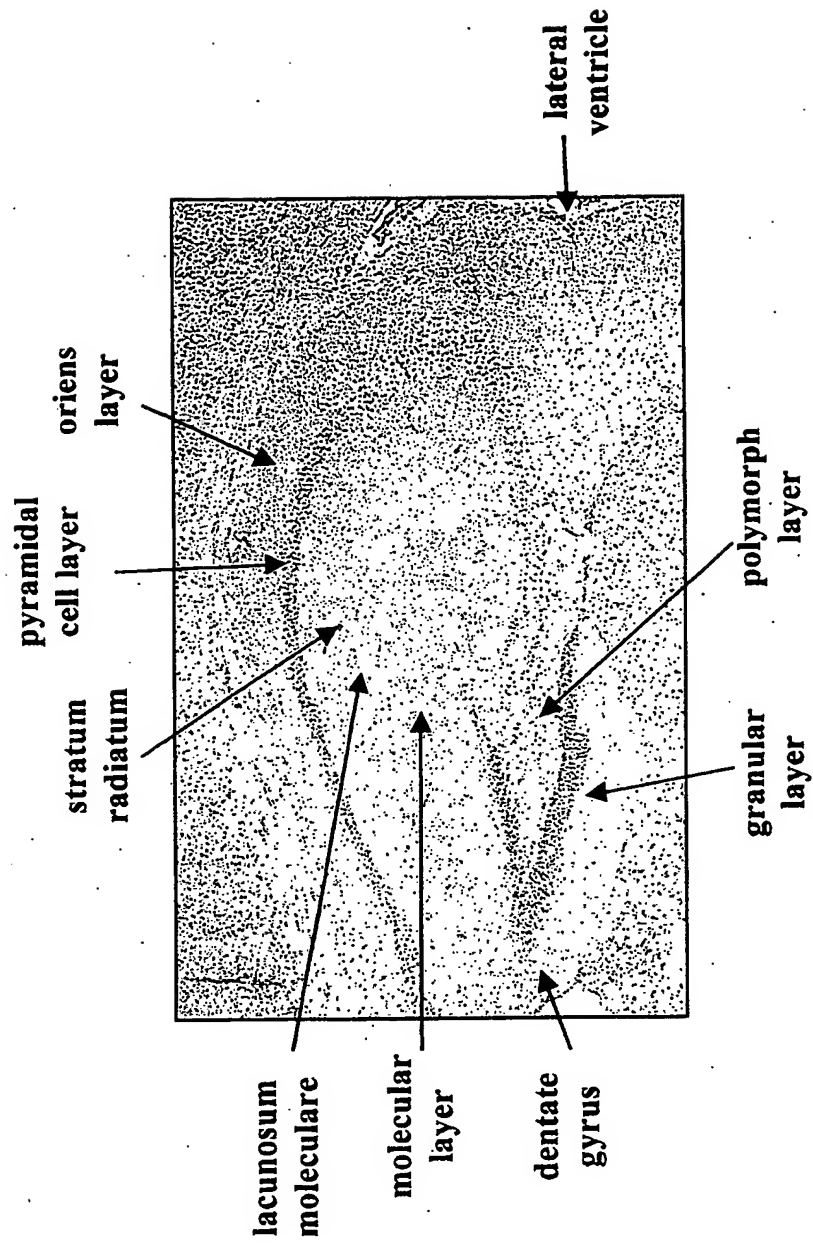


Figure 10

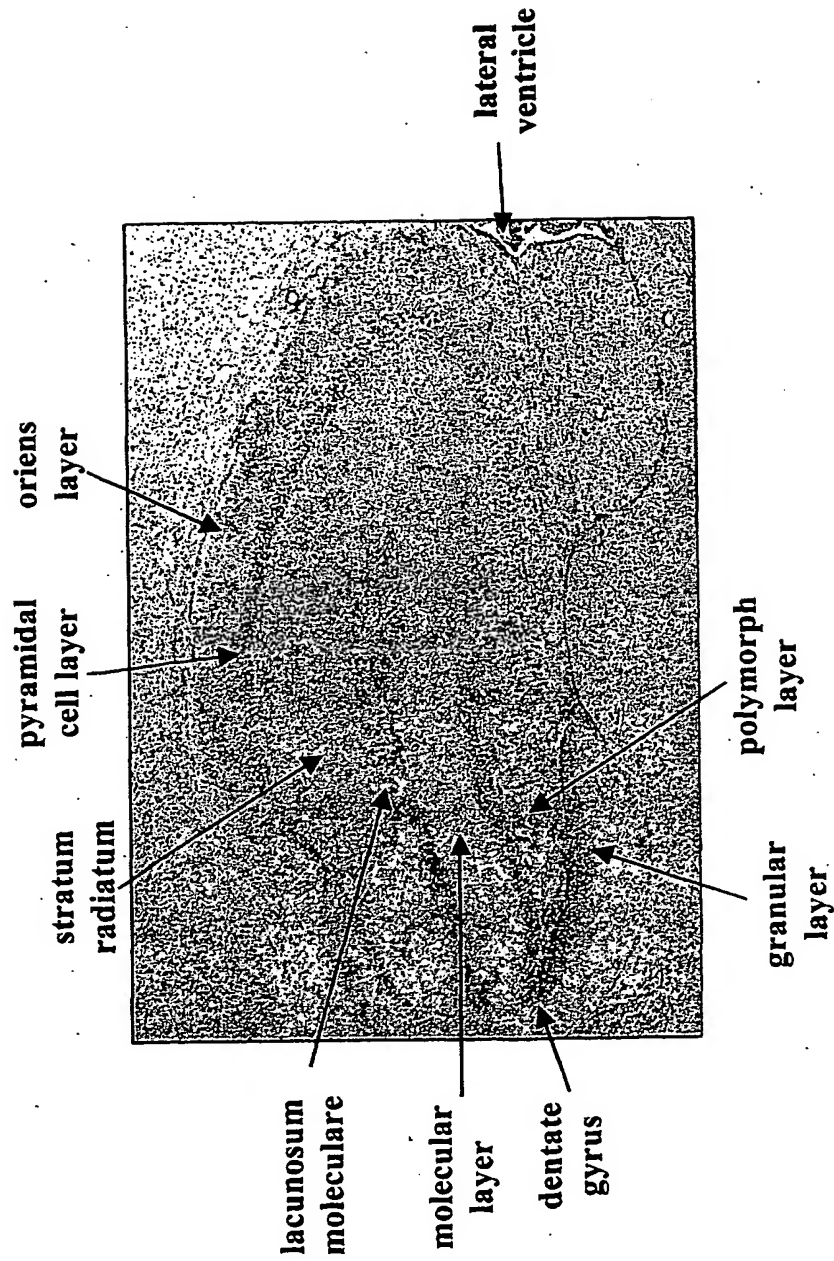


Figure 11

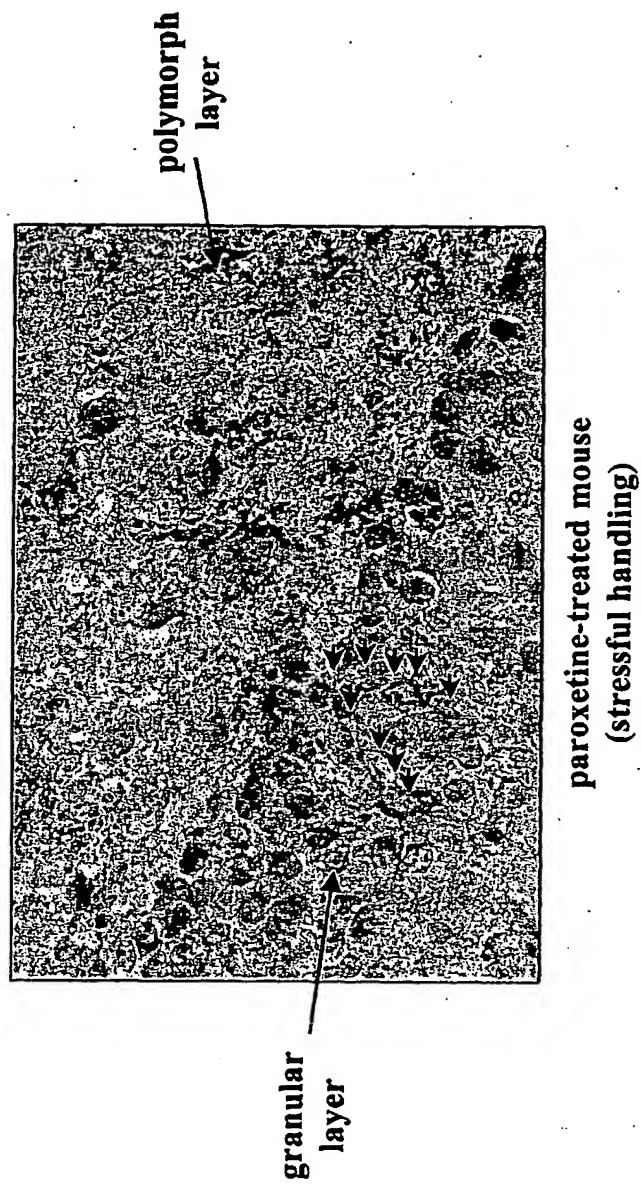


Figure 12

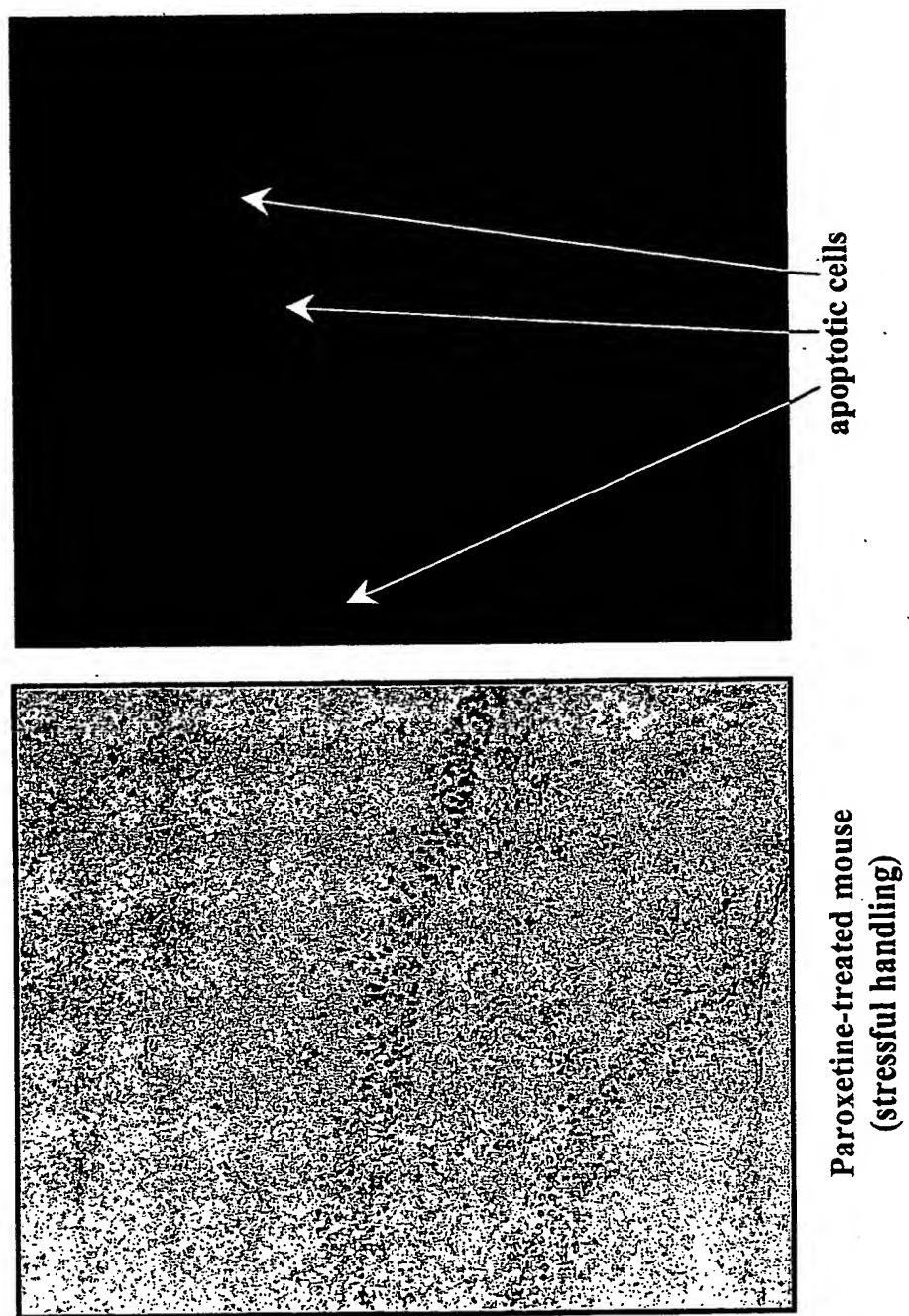


Figure 13

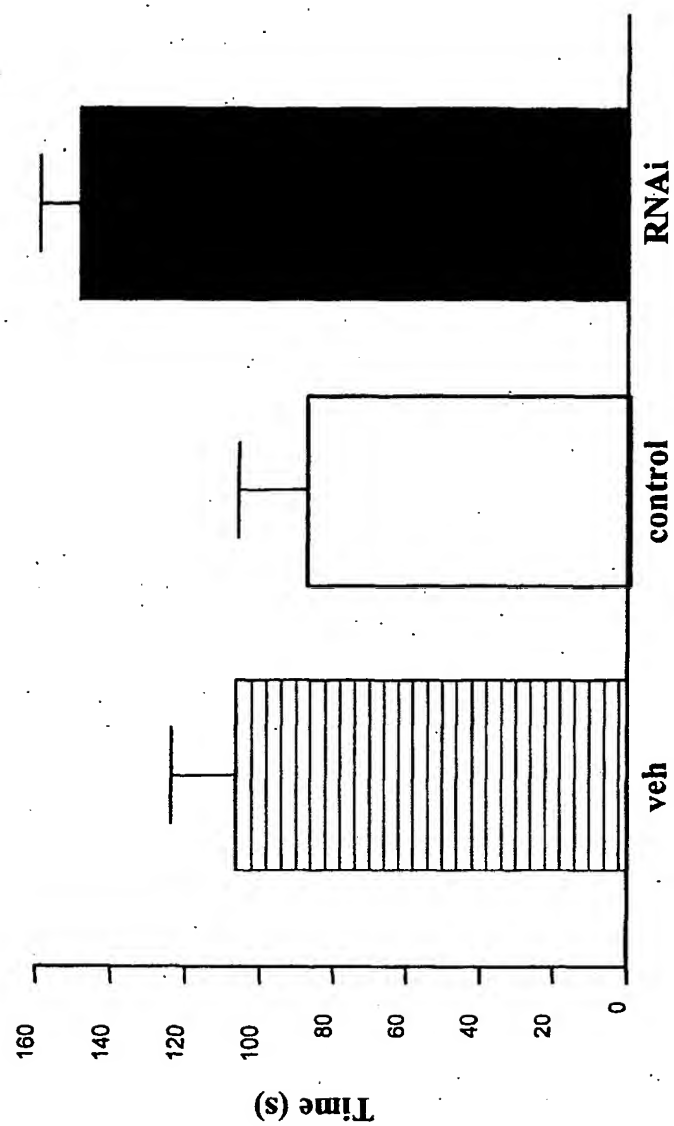


Figure 14

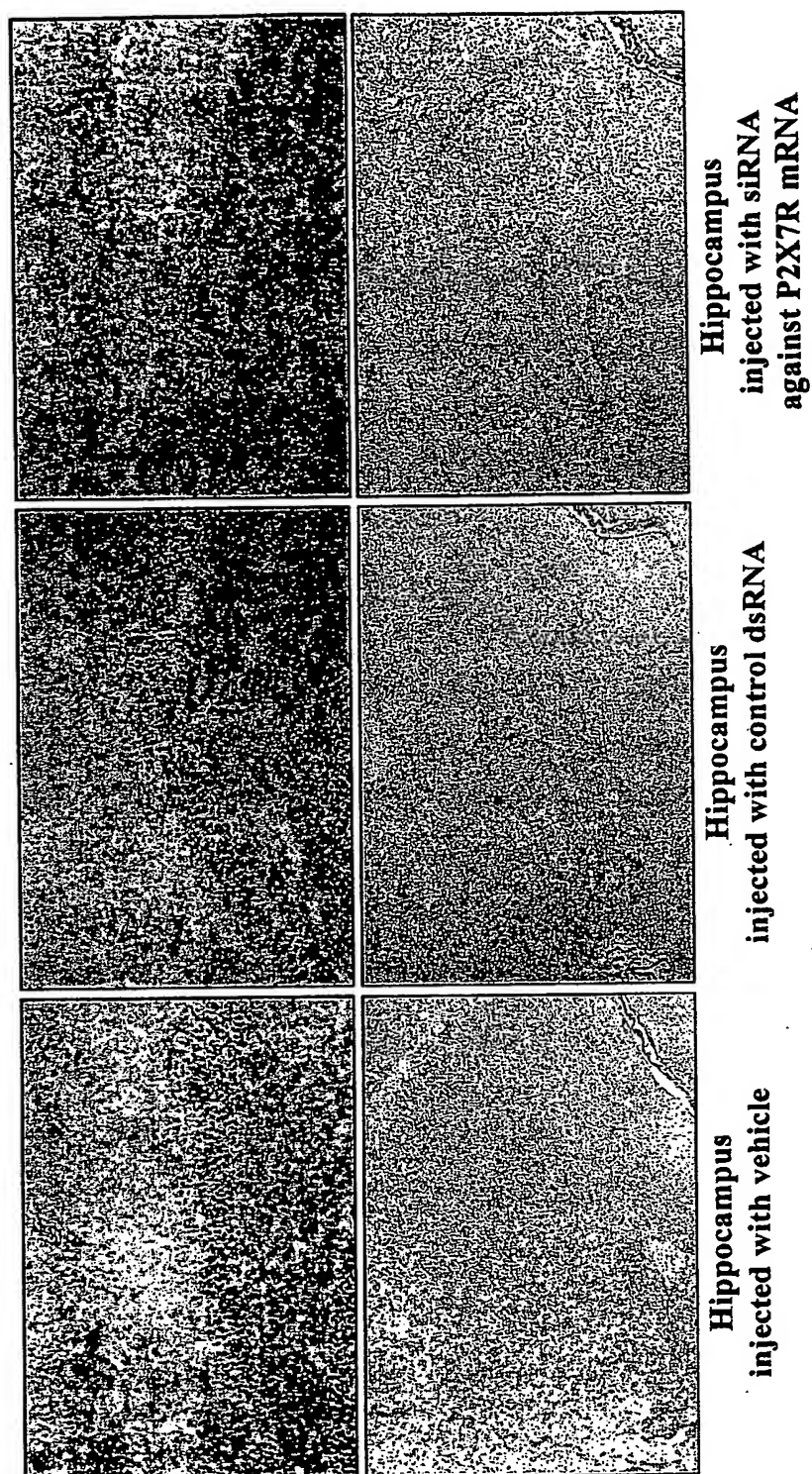


Figure 15

```

P2X7v01 MPACCCSDVFQYETNKVTRIQSMNYGTIKWFFHVIIIFSYYVCFALVSDKLYQRKEPVISS
P2X7v04 MPPVD-----AFPCLPFS---FALVSDKLYQRKEPVISS
P2X7v02 MPACCCSDVFQYETNKVTRIQSMNYGTIKWFFHVIIIFSYYVCFALVSDKLYQRKEPVISS
P2X7v03 MPACCCSDVFQYETNKVTRIQSMNYGTIKWFFHVIIIFSYYVCFALVSDKLYQRKEPVISS
      1.....10.....20.....30.....40.....50

P2X7v01 VHTKVKGIAEVKEEIVENGVKKL VHSVFDTADYTFPLQGN SFFVMTN FLKTEGQEQRLCP
P2X7v04 VHTKVKGIAEVKEEIVENGVKKL VHSVFDTADYTFPLQGN SFFVMTN FLKTEGQEQRLCP
P2X7v02 VHTKVKGIAEVKEEIVENGVKKL VHSVFDTADYTFPLQGN SFFVMTN FLKTEGQEQRLCP
P2X7v03 VHTKVKGIAEVKEEIVENGVKKL VHSVFDTADYTFPLQGN SFFVMTN FLKTEGQEQRLCP
      61.....70.....80.....90.....100.....110

```

Figure 16a

```

P2X7v01 EYPTRRTLCSDDRGCKKGWMDPQSKGIQTGRVCVVHEGNQKTCEVSAWCPIEAVEEAPRPA
P2X7v04 EYPTRRTLCSDDRGCKKGWMDPQSKGIQTGRVCVVHEGNQKTCEVSAWCPIEAVEEAPRPA
P2X7v02 EYPTRRTLCSDDRGCKKGWMDPQSKGLLS-----
P2X7v03 EYPTRRTLCSDDRGCKKGWMDPQSKGIQTGRVCVVHEGNQKTCEVSAWCPIEAVEEAPRPA
      121.....130.....140.....150.....160.....170

P2X7v01 LLNSAENFTVLIKNNIDFPGHNYTTRNILPGLNITCTFFHKTQNPQCPIFRLGDIFFRETGD
P2X7v04 LLNSAENFTVLIKNNIDFPGHNYTTRNILPGLNITCTFFHKTQNPQCPIFRLGDIFFRETGD
P2X7v02 -----
P2X7v03 LLNSAENFTVLIKNNIDFPGHNYTTRNILPGLNITCTFFHKTQNPQCPIFRLGDIFFRETGD
      181.....190.....200.....210.....220.....230

```

Figure 16b

```

P2X7v01 N FSDVAIQGGIMGIEIYWDCNLD RWFH HCHPKYSFRRLLDDKTTNVS LYPGYNFRYAKYYK
P2X7v04 N FSDVAIQGGIMGIEIYWDCNLD RWFH HCHPKYSFRRLLDDKTTNVS LYPGYNFRYAKYYK
P2X7v02 -----
P2X7v03 N FSDVAIQGGIMGIEIYWDCNLD RWFH HCHPKYSFRRLLDDKTTNVS LYPGYNFRYAKYYK
          241.....250.....260.....270.....280.....290
P2X7v01 E N NVEKRTL I K V F G I R F D I L V F G T G G K F D I I Q L V V Y I G S T L S Y F G L A A V F I D F L I D T Y S S
P2X7v04 E N NVEKRTL I K V F G I R F D I L V F G T G G K F D I I Q L V V Y I G S T L S Y F G L A A V F I D F L I D T Y S S
P2X7v02 -----
P2X7v03 E N NVEKRTL I K V F G I R F D I L V F G T G G K F D I I Q L V V Y I G S T L S Y F G L V R D S L F H A L G K W F G
          301.....310.....320.....330.....340.....350

```

Figure 16c

| | | | |
|---------|-------|--|--|
| P2X7v01 | NCCRS | HIYPWCKCCQPCVVNEYYRKKCESIVEPKPTLKYVSFVDESHIRMVNQQLLGRS | |
| P2X7v04 | NCCRS | HIYPWCKCCQPCVVNEYYRKKCESIVEPKPTLKYVSFVDESHIRMVNQQLLGRS | |
| P2X7v02 | | ----- | |
| P2X7v03 | EGSD | ----- | |
| | | 361.....370.....380.....390.....400.....410 | |
| P2X7v01 | LQDV | KGQEVPRPAMDFTDLSRLPLALHDTPPIPGQPEEIQLLRKEATPRSRDSPVWCQCG | |
| P2X7v04 | LQDV | KGQEVPRPAMDFTDLSRLPLALHDTPPIPGQPEEIQLLRKEATPRSRDSPVWCQCG | |
| P2X7v02 | | ----- | |
| P2X7v03 | | ----- | |
| | | 421.....430.....440.....450.....460.....470 | |

Figure 16d

| | | |
|---------|--|--|
| P2X7v01 | SCLPSQLPESHRCLEELCCRKKPGACITTSELFRLVLSRHVLQFLLLYQEPLALDVDS | |
| P2X7v04 | SCLPSQLPESHRCLEELCCRKKPGACITTSELFRLVLSRHVLQFLLLYQEPLALDVDS | |
| P2X7v02 | ----- | |
| P2X7v03 | ----- | |
| | 481.....490.....500.....510.....520.....530 | |
| P2X7v01 | TNSRLRHCA YRCYATWRFSGQDMADFAILPSCCRWRIRKEFPKSEGQYSGFKSPY | |
| P2X7v04 | TNSRLRHCA YRCYATWRFSGQDMADFAILPSCCRWRIRKEFPKSEGQYSGFKSPY | |
| P2X7v02 | ----- | |
| P2X7v03 | ----- | |
| | 541.....550.....560.....570.....580.....590 | |

Figure 16e

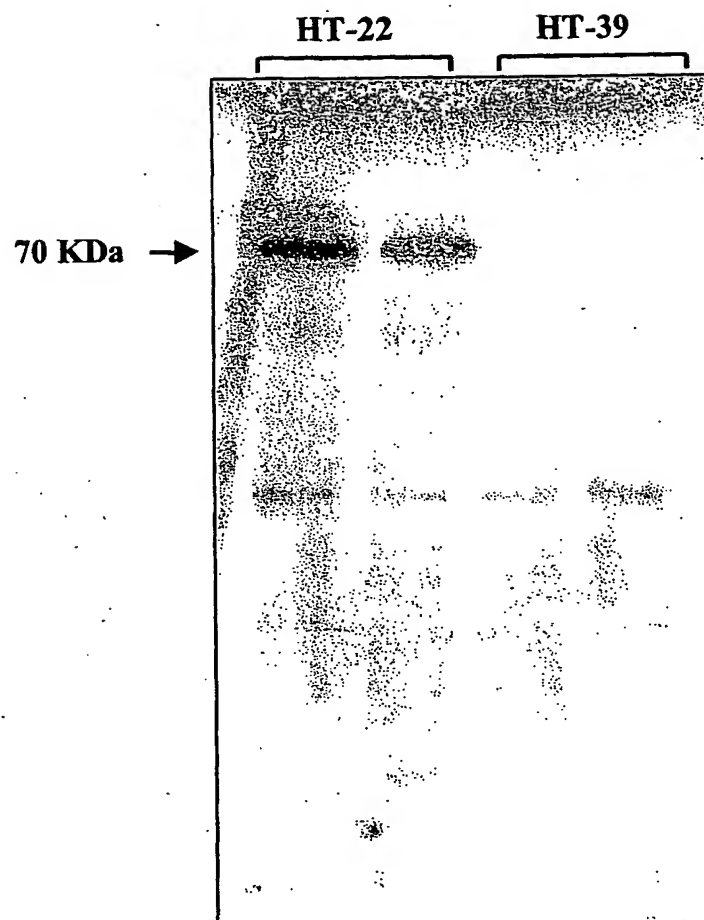


Figure 17

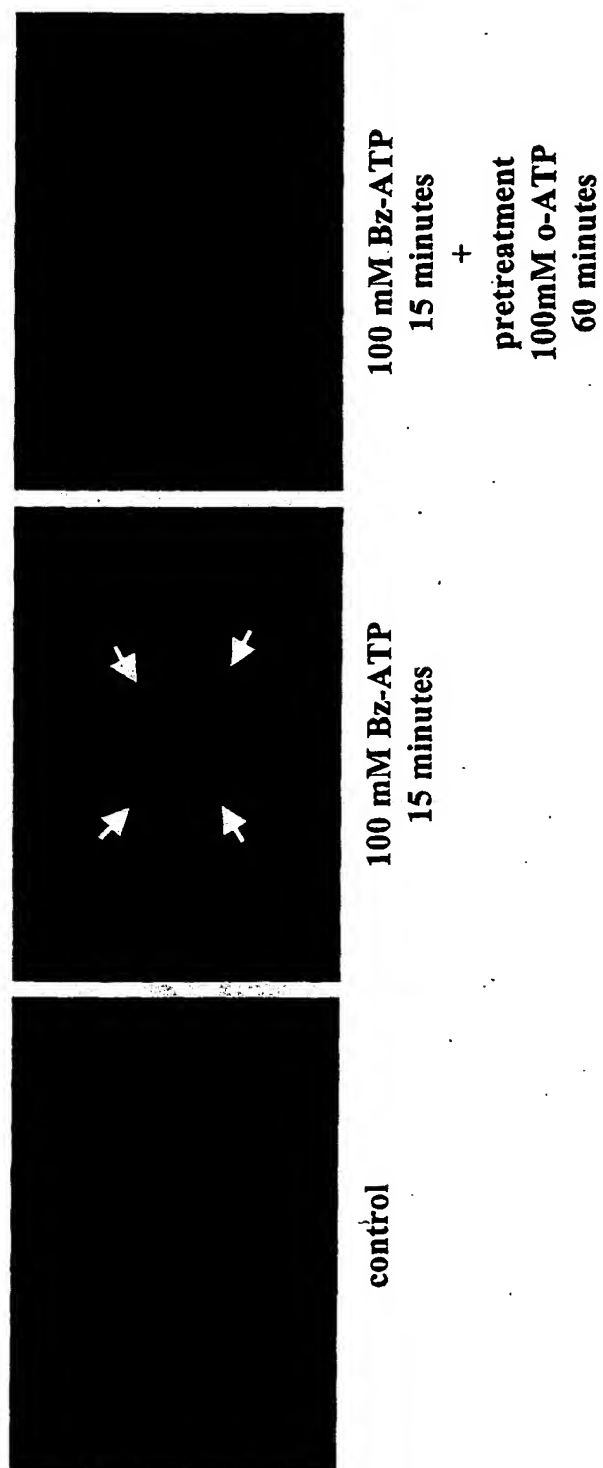


Figure 18

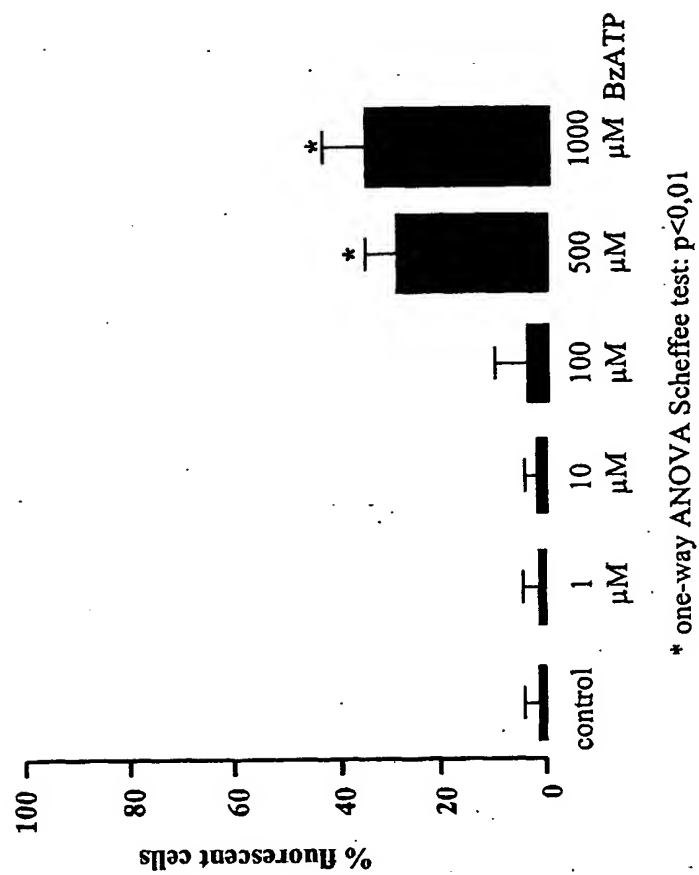


Figure 19a

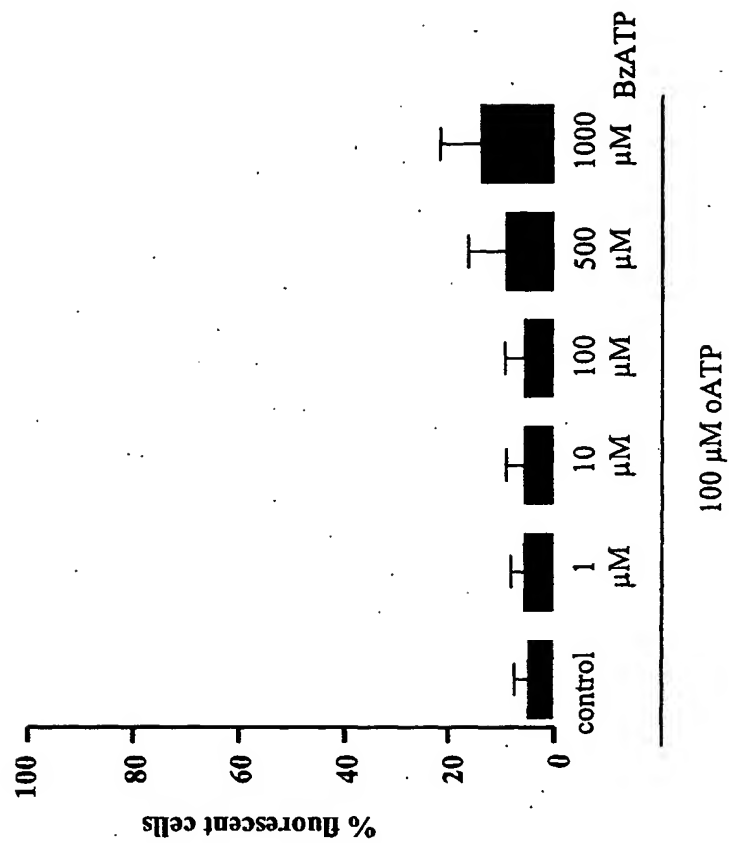


Figure 19b

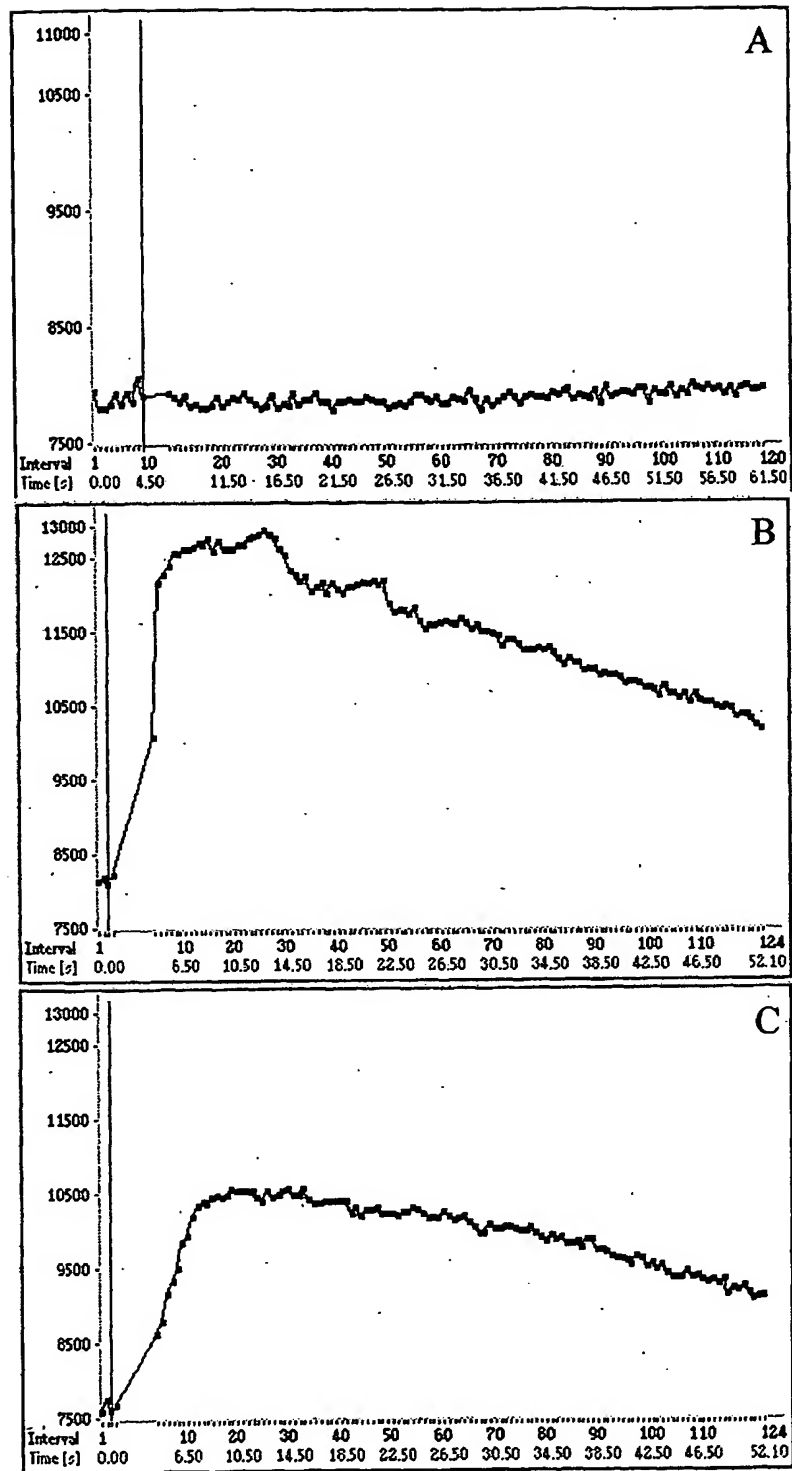


Figure 19c

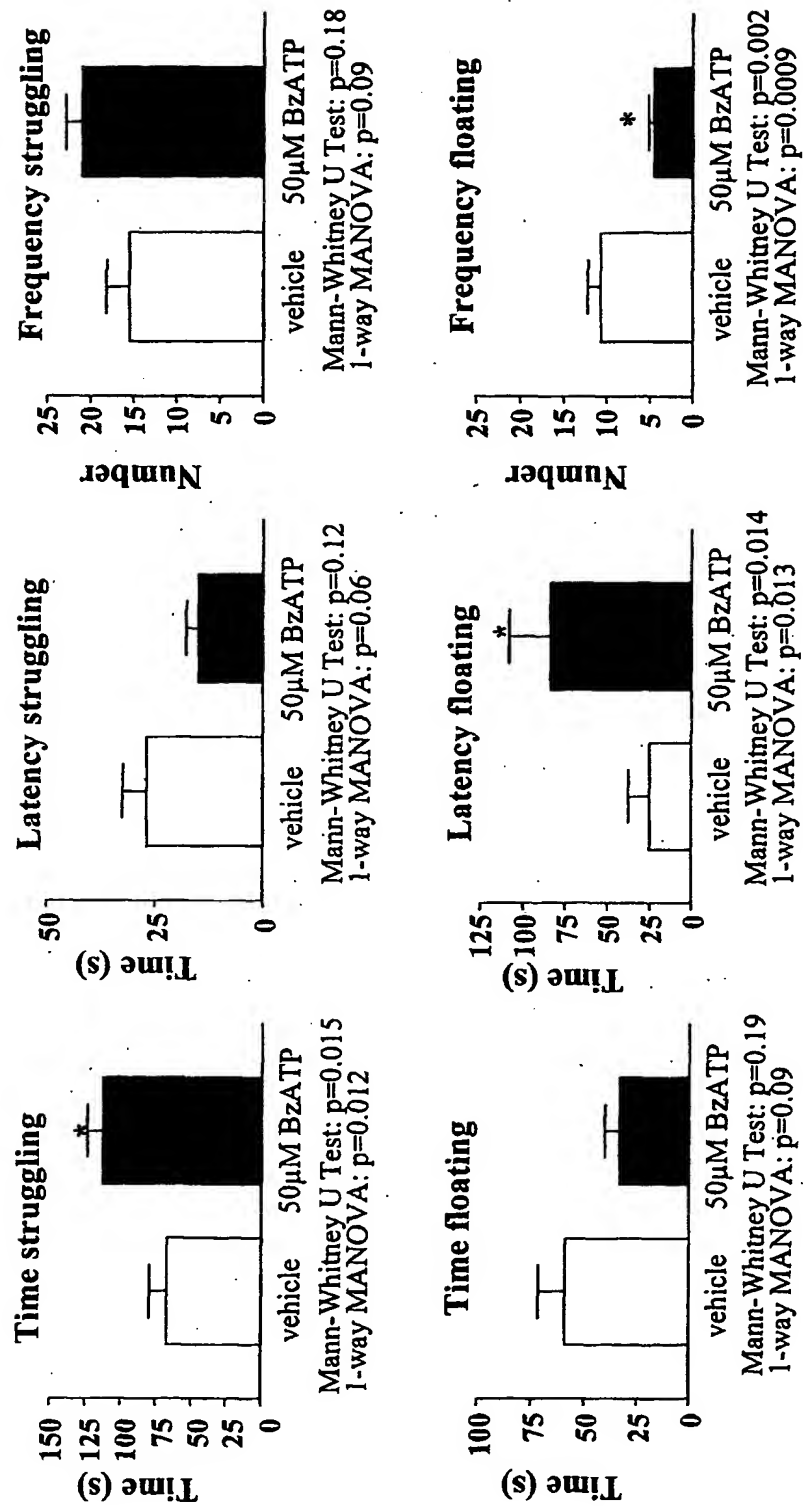


Figure 20

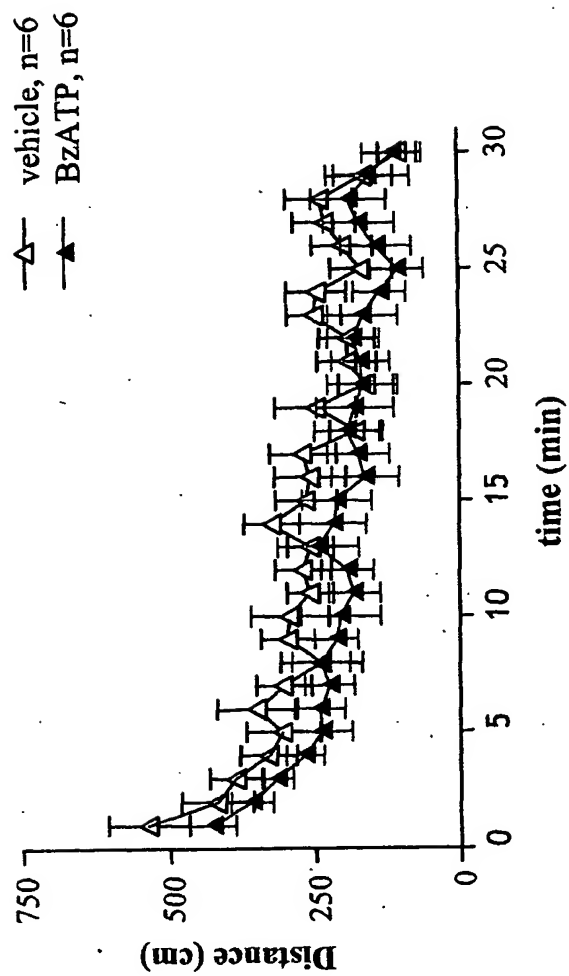


Figure 21

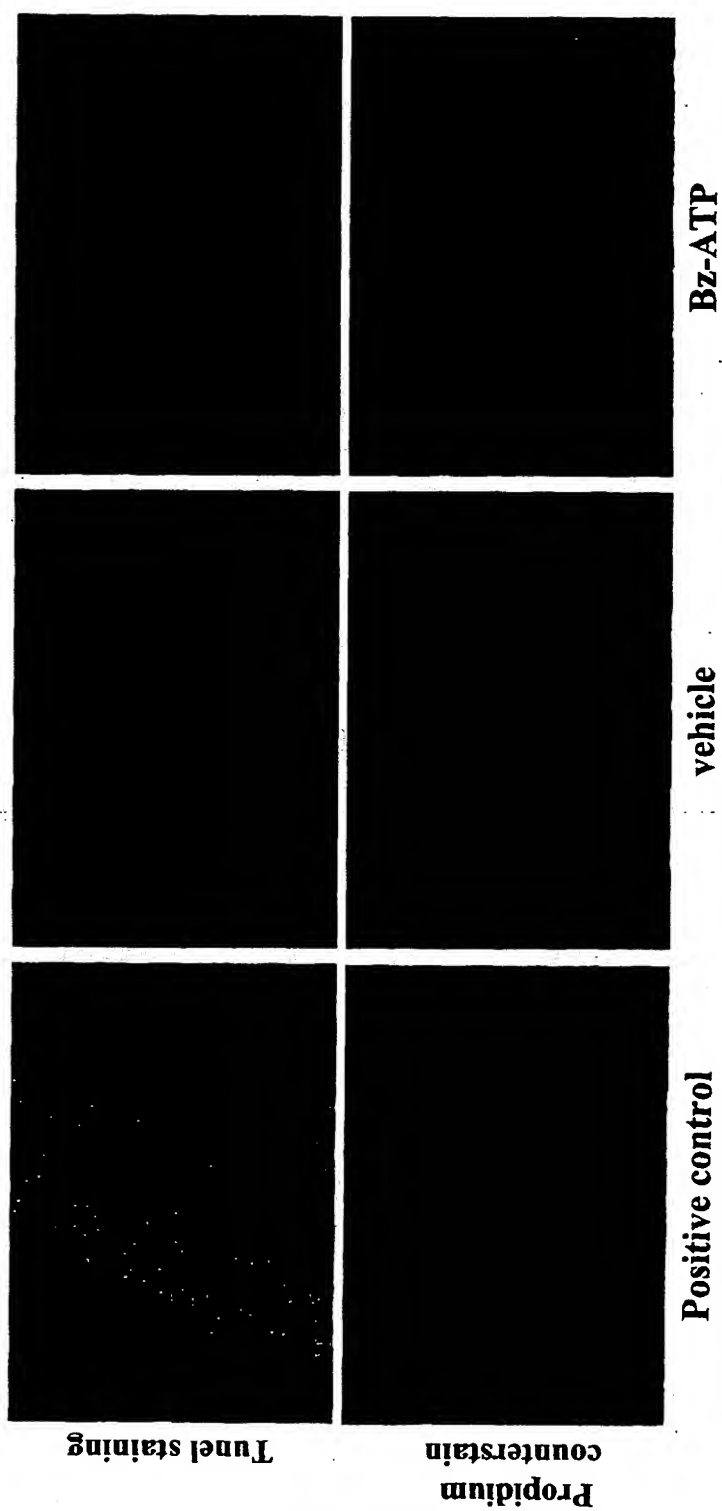


Figure 22

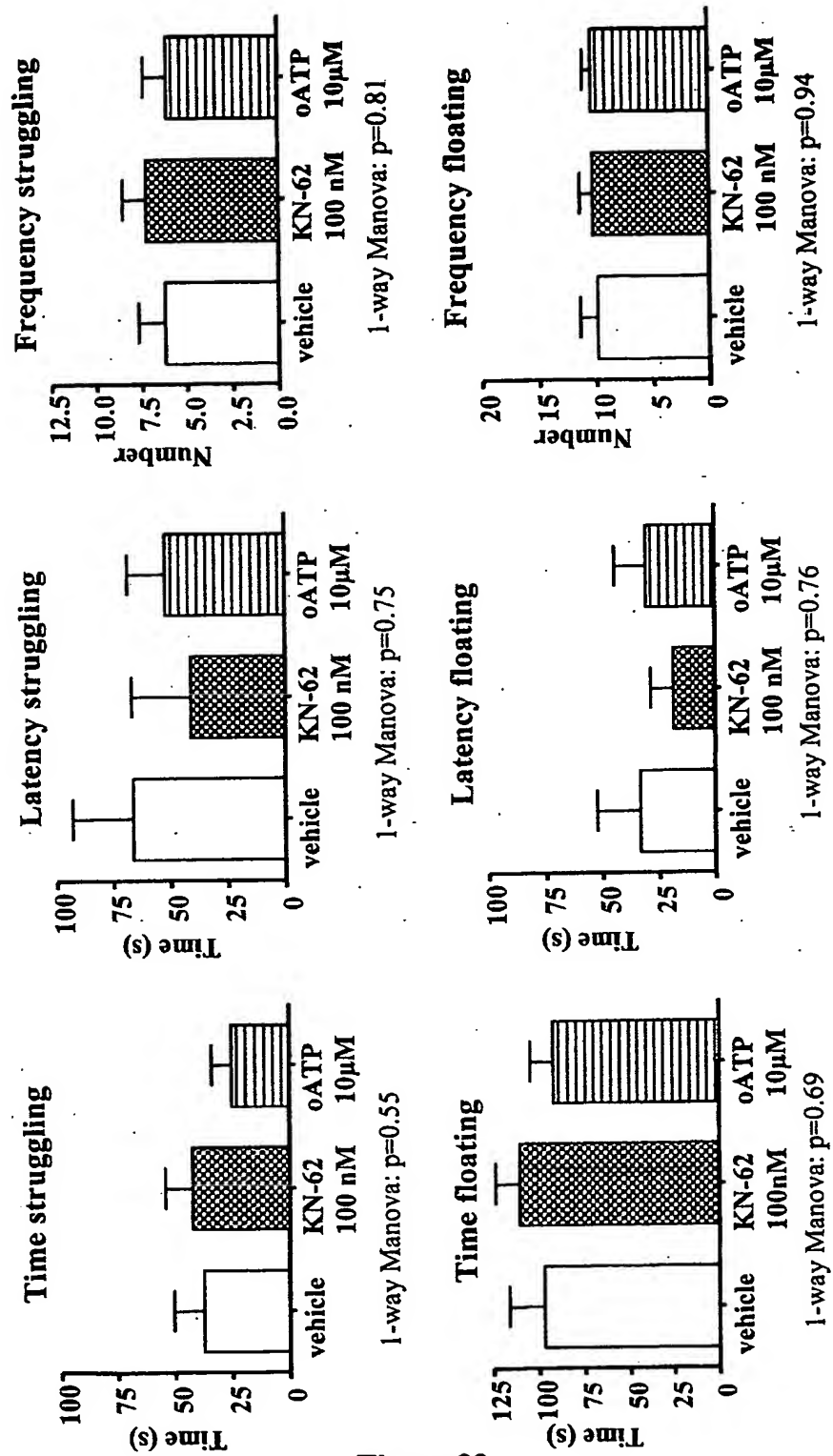


Figure 23

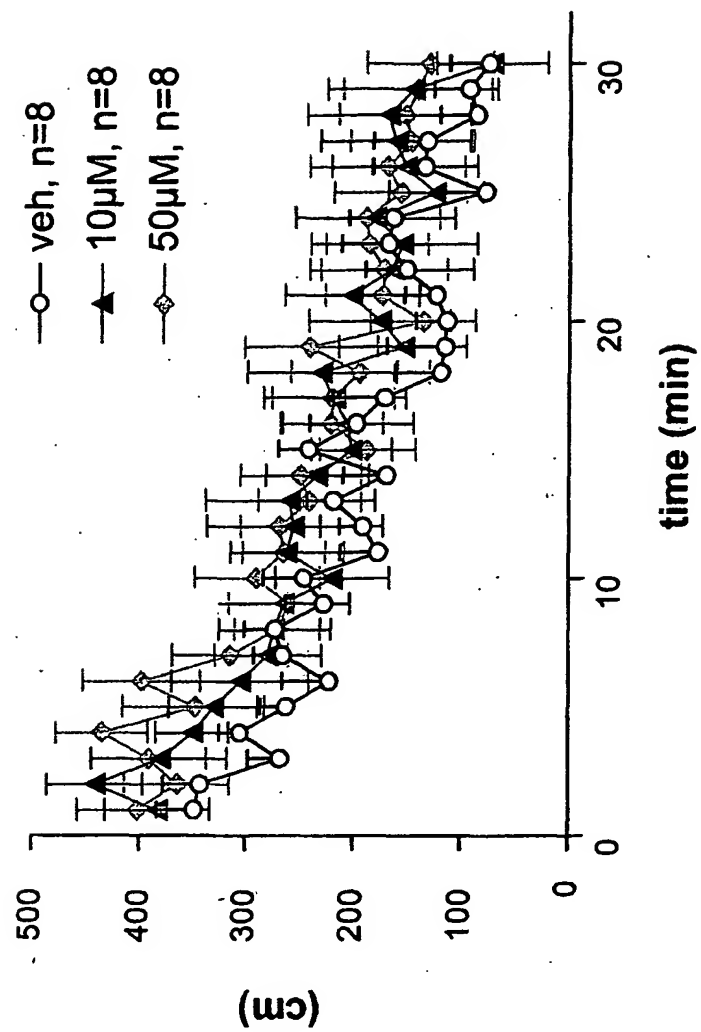
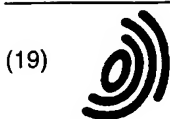


Figure 24



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European Patent Office
Office européen des brevets



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(74) Representative: **VOSSIUS & PARTNER
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(54) **Means and methods for diagnosing and treating affective disorders**

(57) The present invention relates to nucleic acid molecules, preferably genomic sequences, encoding an ATP-gated ion channel P2X7R which contain a mutation in the 5'UTR or 3'UTR regions, a mutation in exon 3, 5, 6, 8 or 13 or in introns 1, 3, 4, 5, 6, 7, 9, 11 or 12 or a deletion in exon 13, which allow to diagnose affective disorders. The invention further relates to polypeptides encoded by said nucleic acid molecules vectors and host cells comprising said nucleic acid molecules as well as to methods for producing polypeptides encoded by said nucleic acid molecules. The present invention also provides antibodies specifically directed to polypeptides encoded by said nucleic acid molecules and aptamers specifically binding said nucleic acid molecules.

Additionally, primers for selectively amplifying said nucleic acid molecules are provided in the present invention as well as kits, compositions, particularly pharmaceutical and diagnostic compositions comprising said nucleic acid molecules, vectors, polypeptides, aptamers, antibodies and/or primers. Moreover, the

present invention relates to methods for diagnosing affective disorders associated with a non-functional P2X7R protein, an altered ATP-gating of the P2X7R protein, an over- or underexpression of the P2X7R protein or associated with the presence of any one of the aforementioned nucleic acid molecules or polypeptides encoded thereby. Additionally, the present invention relates to uses and methods for treating affective disorders employing a functional or non-functional ATP-gated ion-channel P2X7R.

The present invention also relates to uses of modulators of P2X7R activity for treating affective diseases.

Furthermore, the present invention also relates to methods for identifying and characterizing compounds which are capable of specifically interacting with or altering the characteristics of the polypeptides of the present invention as well as to methods for the production of pharmaceutical compositions.

EP 1 469 072 A3



European Patent
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PARTIAL EUROPEAN SEARCH REPORT

Application Number

which under Rule 45 of the European Patent Convention shall be considered, for the purposes of subsequent proceedings, as the European search report

EP 04 00 9160

| DOCUMENTS CONSIDERED TO BE RELEVANT | | | |
|--|--|----------------------------------|---|
| Category | Citation of document with indication, where appropriate, of relevant passages | Relevant to claim | CLASSIFICATION OF THE APPLICATION (Int.Cl.7) |
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| | | | C07K C12Q A61K G01N |
| INCOMPLETE SEARCH <p>The Search Division considers that the present application, or one or more of its claims, does/do not comply with the EPC to such an extent that a meaningful search into the state of the art cannot be carried out, or can only be carried out partially, for these claims.</p> <p>Claims searched completely :</p> <p>Claims searched incompletely :</p> <p>Claims not searched :</p> <p>Reason for the limitation of the search:</p> <p>see sheet C</p> | | | |
| Place of search | | Date of completion of the search | Examiner |
| The Hague | | 28 September 2004 | Van der Schaal, C |
| CATEGORY OF CITED DOCUMENTS <p>X : particularly relevant if taken alone Y : particularly relevant if combined with another document of the same category A : technological background O : non-written disclosure P : intermediate document</p> <p>T : theory or principle underlying the invention E : earlier patent document, but published on, or after the filing date D : document cited in the application L : document cited for other reasons & : member of the same patent family, corresponding document</p> | | | |

EPO FORM 1503 03 02 (P4-C07)



European Patent
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INCOMPLETE SEARCH
SHEET C

Application Number
EP 04 00 9160

Although claims 30 34 42-45 are (partially) directed to a method of treatment of the human/animal body (Article 52(4) EPC), the search has been carried out and based on the alleged effects of the compound/composition.

PARTIAL EUROPEAN SEARCH REPORT

Application Number
EP 04 00 9160

| DOCUMENTS CONSIDERED TO BE RELEVANT | | | CLASSIFICATION OF THE APPLICATION (Int.Cl.7) |
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| | | | |



European Patent
Office

Application Number
EP 04 00 9160

CLAIMS INCURRING FEES

The present European patent application comprised at the time of filing more than ten claims.

☐ Only part of the claims have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims and for those claims for which claims fees have been paid, namely claim(s):

☐ No claims fees have been paid within the prescribed time limit. The present European search report has been drawn up for the first ten claims.

LACK OF UNITY OF INVENTION

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

see sheet 8

☐ All further search fees have been paid within the fixed time limit. The present European search report has been drawn up for all claims.

☐ As all searchable claims could be searched without effort justifying an additional fee, the Search Division did not invite payment of any additional fee.

☒ Only part of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the inventions in respect of which search fees have been paid, namely claims:

28-41 47-53 completely 1-12 17-20, 42-45 partially

☐ None of the further search fees have been paid within the fixed time limit. The present European search report has been drawn up for those parts of the European patent application which relate to the invention first mentioned in the claims, namely claims:



European Patent
Office

LACK OF UNITY OF INVENTION
SHEET B

Application Number
EP 04 00 9160

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

Invention 1: Claims 1-12 17-19 partially

nucleic acid molecule comprising a genomic nucleotide sequence according to SEQ ID NO 1 with substitution of nucleotide 362, or fragments containing the substitution, nucleotides hybridizing with the mutated sequence.

Inventions 2-6 :Claims 1-12 17-19 partially

nucleic acid molecule comprising a genomic nucleotide sequence according to SEQ ID NO 1 with substitution of nucleotide 532, 1100, 1122, 1171, 1702 respectively, fragments containing the substitutions and nucleotides hybridizing with the mutated sequences.

Inventions 7-13: claims 1-19 partially

polypeptides according to SEQ 3 or 4 with substitution of amino acid residue 117,150, 186, 191, 270, 568 or 578 respectively, nucleotides or fragments thereof encoding the mutated polypeptide(fragments), nucleotides hybridizing with the mutated nucleotide sequence and antibodies against the mutated polypeptide sequence

Inventions 14 and 15: claims 1-12 17-19 partially

nucleic acid molecule comprising a genomic nucleotide sequence according to SEQ ID NO 1 with substitution of nucleotide 32548 or 37633 respectively, fragments containing the substitutions and nucleotides hybridizing with the mutated sequences.

Invention 16: claims 1-19 partially

polypeptides according to SEQ 3 or 4 with a deletion of amino acids 488-494, nucleotides or fragments thereof encoding the mutated polypeptide(fragments), nucleotides hybridizing with the mutated nucleotide sequence and antibodies against the mutated polypeptide sequence.

Inventions 17-39: claims 1-12 17-19 respectively



European Patent
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LACK OF UNITY OF INVENTION
SHEET B

Application Number

EP 04 00 9160

The Search Division considers that the present European patent application does not comply with the requirements of unity of invention and relates to several inventions or groups of inventions, namely:

nucleic acid molecule comprising a genomic nucleotide sequence according to SEQ ID NO 1 with substitution of nucleotides mentioned in claim 1(e) and 1(f) respectively, fragments containing the substitutions and nucleotides hybridizing with the mutated sequences.

Invention 40. claims 21-27, 46 54-56 completely 20 42-45 partially

Use of P2X7R or its encoding nucleotides or variants thereof in diagnosis of affective disorder

Invention 41: claims 28-41 47-53 completely, claims 20 42-45 partially

Use of modulators of P2X7R activity as pharmaceutical against affective disorders

**ANNEX TO THE EUROPEAN SEARCH REPORT
ON EUROPEAN PATENT APPLICATION NO.**

EP 04 00 9160

This annex lists the patent family members relating to the patent documents cited in the above-mentioned European search report. The members are as contained in the European Patent Office EDP file on
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28-09-2004

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For more details about this annex : see Official Journal of the European Patent Office, No. 12/82

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